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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:53:49 ; Search time 228 Seconds
(without alignments)
5462.084 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 553

Sequence: 1 MVQRLLWSRLRRKRAQLL.....AIYFATQVVFQKSLAKYSA 553

Scoring table:

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 3

Total number of hits satisfying chosen parameters: 3387848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastp -SUFFIX=oligo -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR_SCORE=quality -THR_MIN=3 -ALIGN=45 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09593793@cgn.1.133 @runat_13022003_161425_21810 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6 -Fgapext=7
-YGAPOP=60 -YGAPEXT=60 -DBLOP=6 -DELEXT=7

Database :

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23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	553	100.0	1662	24	ABN81324	Human mast cell re
2	553	100.0	2582	24	ABK92217	Prostate cancer-as
3	553	100.0	3320	24	AAS14962	DNA encoding human
4	553	100.0	3410	19	AAV61201	Full length cDNA s
5	553	100.0	3410	19	AAV58586	Prostate tumour sp
6	553	100.0	3410	21	AAC79473	cDNA sequence of h
7	553	100.0	3410	21	AAO63349	Human immunogenic
8	553	100.0	3410	22	AAS63557	Human prostate cDN
9	553	100.0	3410	22	AAS10108	Human prostate tum
10	553	100.0	3410	22	AAH93465	Human prostate-spe
11	553	100.0	3410	22	AAH84779	Human prostate-spe
12	553	100.0	3410	22	AAH02530	Prostate tumour an
13	553	100.0	3410	24	ABL94929	Human L1-12 cDNA s
14	553	100.0	3410	24	ABL29017	Human breast tumou
15	501	90.6	2133	24	ABA91283	Thioredoxin-ubiqui
16	320	57.9	1593	24	ABA91284	Thioredoxin-ubiqui
17	320	57.9	4034	22	AAS64040	Human prostate cDNA
18	320	57.9	4034	22	AAH93868	P53S3 cDNA splice
19	320	57.9	4034	24	ABL95411	Human P53S3 splice
20	263	47.6	1203	22	AAS64153	Human /M. tubercul
21	263	47.6	1203	22	AAH93917	Ral2-P501S-E2 cons
22	263	47.6	1203	24	ABL95524	Ral2-P501S-E2 cons
23	263	47.6	3878	22	AAD05230	Human secreted pro
24	263	47.6	4894	22	AAS64038	Human prostate cDNA
25	263	47.6	4894	22	AAH93866	P53S3 cDNA splice
26	263	47.6	4894	24	ABL95409	Human P53S3 splice
27	263	47.6	6976	22	AAS64041	Human prostate cDNA
28	263	47.6	6976	22	AAH93869	P53S3 cDNA splice
29	263	47.6	6976	24	ABL95412	Human P53S3 splice
30	255	46.1	2133	21	AAC64928	Human prostate-rel
31	255	46.1	2133	22	AAH07155	Prostate gene PS10
32	255	46.1	2152	20	AAV71181	Consensus sequence
33	252	45.6	2124	21	AAC64927	Human prostate-rel
34	252	45.6	2124	20	AAH07601	Prostate gene PS10
35	252	45.6	2143	20	AAV71180	Clone 1711345IH, t
36	235	42.5	2904	22	AAS64039	Human prostate cDNA
37	235	42.5	2904	22	AAH93867	P53S3 cDNA splice
38	235	42.5	2904	24	ABL95410	Human P53S3 splice
39	209	37.8	2462	21	AAZ45677	cDNA sequence of a
40	187	33.8	3663	24	ABN81320	Human mast cell re
41	122	22.1	789	19	AAV61144	3' cDNA sequence o
42	122	22.1	789	19	AAV58487	3' fragment of pro
43	122	22.1	789	21	AAO6250	Human immunogenic
44	122	22.1	789	22	AAS63458	Human prostate cDN
45	122	22.1	789	22	AAS10009	Human prostate tum
46	122	22.1	789	22	AAH93366	Human prostate-spe
47	122	22.1	789	22	AAH84680	Human prostate-spe
48	122	22.1	789	22	AAH02431	Prostate tumour an
49	122	22.1	789	24	ABL94830	Human L1-12 3' cDN
50	85	15.4	258	20	AAV71166	PS108 gene-specifi
51	85	15.4	258	21	AAC63191	Human prostate-rel
52	85	15.4	258	22	AAH07587	Prostate gene PS10
53	82	14.8	247	20	AAV71169	PS108 gene-specifi
54	82	14.8	247	21	AAC63194	Human prostate-rel
55	82	14.8	247	22	AAH07590	Prostate gene PS10
56	76	13.7	742	21	AAZ45675	cDNA sequence of a
57	71	12.8	217	20	AAV71167	PS108 gene-specifi
58	71	12.8	217	21	AAC63192	Human prostate-rel
59	71	12.8	217	22	AAH07588	Prostate gene PS10
60	71	12.8	255	20	AAV71168	PS108 gene-specifi
61	71	12.8	255	21	AAC63193	Human prostate-rel
62	71	12.8	255	22	AAH07589	Prostate gene PS10
63	35	6.3	432	22	AAD05262	Human secreted pro
64	34	6.1	231	20	AAV71170	PS108 gene-specifi
65	34	6.1	231	21	AAC63195	Human prostate-rel
66	34	6.1	231	22	AAH07591	Prostate gene PS10
67	34	6.1	510	21	AAZ45681	cDNA sequence of a

68 32 5..8 828 24 ABK93112 Human prostate spe
69 26 4.7 271 24 ABK93110 Human prostate spe
70 24 4.3 612 24 ABK93111 Human prostate spe
71 20 3.6 60 22 AAS64154 Human prostate cDN
72 20 3.6 60 22 AAS64154 Human prostate cDN
73 20 3.6 60 22 AAS64154 Human prostate cDN
74 18 3.3 435 20 ABL95525 Human P501S epitop
75 12 2.2 57 22 ABL95525 Human secreted pro
76 12 2.2 57 22 ABL95525 Human prostate cDN
77 12 2.2 57 22 ABL95525 CD4 lepitopes of P5
78 10 1.8 30 22 ABL95525 Human P501S CD4 ep
79 10 1.8 30 22 ABL95525 Human prostate cDN
80 10 1.8 30 22 ABL95525 P501S epitope enco
81 10 1.8 30 22 ABL95526 Human P501S epitop
82 10 1.8 40 24 ABA91300 Prostate antigen P
83 10 1.8 75 24 ABA91299 Thiorodoxin-ubiqui
84 10 1.8 75 24 ABA91301 Prostate antigen P
85 10 1.8 208 22 ABL20168 Human breast cance
86 10 1.8 308 22 ABL20168 Human breast cance
87 10 1.8 1808 21 AAZ29231 Human cell signall
88 10 1.8 2352 23 ABV22257 Human prostate exp
89 9 1.6 27 22 AAS64156 Human prostate cDN
90 9 1.6 27 22 ABL95527 P501S epitope enco
91 9 1.6 27 22 ABL95527 Human P501S epitop
92 9 1.6 27 24 AAS14966 Human PROST 03 PCR
93 9 1.6 33 22 AAS63908 Human prostate cDN
94 9 1.6 33 22 AAS63908 Human prostate-spe
95 9 1.6 33 22 ABL95529 Human prostate-spe
96 9 1.6 33 22 ABL95529 Human PCR primer A
97 9 1.6 40 22 ABL95529 Human prostate cDN
98 9 1.6 40 22 ABL95529 Human prostate-spe
99 9 1.6 40 24 ABL95523 Human coding sequ
100 9 1.6 54 24 ABA91298 Thiorodoxin-ubiqui

ALIGNMENTS

RESULT 1
ABN81324
ID ABN81324 standard; cDNA; 1662 BP.
XX AC ABN81324;
XX 30-AUG-2002 (first entry)
XX Human mast cell related splice variant gene MC14 SEQ ID NO 12.
XX DE Human mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
XX KW vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
XX KW gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 1..1662
XX FT /*tag= a
XX FT /product= "MC14 alternatively spliced variant"
XX PN WO200246389-A2.
XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US46180.
XX PR 08-DEC-2000; 2000US-251835P.
XX PR 14-MAR-2001; 2001US-275479P.
XX PR 28-MAR-2001; 2001US-279115P.
XX PR 02-APR-2001; 2001US-280143P.
XX PA (UNIO) UCB SA.
XX PA Nocka K, Pirozzi G, Einstein R;
XX PI
XX

DR WPI; 2002-508560/54.
XX P-PSDB; ABB77575.
XX Novel isolated nucleic acids that are differentially expressed in mast
PT cells in patients with allergic hypersensitivity, encoding proteins
PT associated with mast cell regranulation and allergic hypersensitivity
PT
XX Claim 1; Page 115-117; 119pp; English.
XX The invention relates to isolated nucleic acid (ABN81319-ABN81324),
CC corresponding to genes differentially expressed in mast cells following
CC activation or in patients with allergic hypersensitivity disease, (I)
CC that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of
CC (II) if at least 6 amino acids. (II) is useful for identifying binding
CC partners. (I) or (II) is useful for diagnosing or treating a disease
CC state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,
CC urticaria or atopic dermatitis or mastocytosis) in a subject which
CC involves determining the level of expression of (I) or (II). A computer
CC system, comprising a database containing information identifying the
CC expression level in a tissue or at least one mast cell of (I), is useful
CC for presenting information to identify the relative expression level of
CC (I). (II) is used as a marker to detect, diagnose or identify an allergic
CC response in a patient. The protein can also serve as a target that
CC modulate gene expression or activity and as an antigen to raise
CC polyclonal or monoclonal antibodies. (II) is useful for identifying
CC agents that modulate expression of the protein or agents, such as
CC agonists or antagonists. The agonists or antagonists are useful for
CC modulating biological activity and function of (II) and thus are useful
CC for alleviating disease conditions such as allergic hypersensitivity,
CC seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
XX Sequence 1662 BP; 229 A; 551 C; 511 G; 371 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-593-793A-113 (1-553) x ABN81324 (1-1662)
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DB 1 ATGGTCCAGAGGCTGTGGTGAGCCGCTGTGGCGACCCGGAACCCAGCTCTGCTG 60
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrYrValPro 40
DB 61 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCAGGCATCACATATGTCG 120
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 121 CCTTGTCTGCTGGAGTGGGGGTAGAGAGAGTTCATGACCATGTGTCTGGGCATTTGGT 180
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 181 CCAGTGTCTGGGCTGTGCTGTCTGCGCTCTAGGCTCAGCCAGTACCCAGCTGGCTGGA 240
QY 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 241 CGTATATGGCGCGCGCGCTTCATCTGGGCACCTGCTCTGGGCATCTCTGTGAGCCTC 300
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 301 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTCTCTGGCCGATCCAGGCCCTG 360
QY 121 GluLeuAlaLeuIleLeuGlyValGlyValGlyLeuAspPheCysGlyGlnValCysPhe 140
DB 361 GAGTGGGCACTGCTCATCTGCGCTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 420
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

Db 421 ACTCCACTGGAGCCCTGCTCTGACCTCTTCCGGGACCGGACCACTGTGCCAGGCC 480
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 481 TACTCTGTCTATGCTTCATGATCATGCTTGGGGGCTGCTGGGTACCTCTGCTGCTGCC 540
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 541 ATTGACTGGACACAGTGCCTGGCCCCCTACCTGGGACCCAGGAGAGTGCCTCTTT 600
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 601 GGCCTGCTCACCTCATCTCTCTCACTGCTAGCAGCCACACTGCTGCTGGCTGAGGAG 660
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 661 GCAGCCTGGGCCCCACCGGACGAGAGGCTCTCGGCCCCCTCTCTGCTGGCCCCAC 720
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 721 TGTGTTCATGCGGGCCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTTCCCGGCTG 780
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 781 CACCAGCTGTGCTGCGCATGCGCCGACCCCTGCGCGGCTCTCTGCTGCTGAGCTGTC 840
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 841 AGCTGATGGCACTCATGACCTTCACGCTGTTTACACGGATTCGTGGCGAGGGGCTG 900
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 901 TACCAGGGGCTGCCAGAGCTGAGCGGACCGGAGCCCGGAGACACTATGATGAGGC 960
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 961 GTTCGATGGCAGCCTGGGGCTGTCTCTGAGTGGCCATCTCCCTGCTTCTCTCTG 1020
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1021 GTCATGGACCGGCTGGTGAGGATTCGGCACTCGAGCACTATTTGGCCAGTGTGCA 1080
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1081 GCTTTCCTGTGCTGCCGTGCCACATGCTCTGCCAGAGTGTGCCGTGGTGACAGCT 1140
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1141 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1200
Qy 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1201 TCCCTCTACCCCGGAGAGAGAGTGTCTCTGCCCAATACCGAGGGGACACTGGAGGT 1260
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1261 GCTACAGTGAGCAGCCTGTATGACCACTTCTCTGCCAGGCCCTTAGCCTGGAGCTCCC 1320
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1321 TTCCCTTAATGGACAGTGGGTCTGGAGCAGTGGCTCTCCACCTCCACCCCGGCTC 1380
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1381 TCGGGGGCTCTGCTCTGATGCTCTCGGTACGTGTGGTGGTGGGTGAGCCACCGAGGCC 1440
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1441 AGGGTGGTTCGGGGCGGGGATGTCCTGGACCTTCGGCATCCTGGATGCTTCCTG 1500
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520

Db 1501 CTGTCCAGGTGGCCCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1560
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Db 1561 ACTGCTATATGGTGTCTCCGAGCCCTGGGTCTGGTTCGCCATTACTTTGCTACACAG 1620
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1621 GTAGTATTGTGACAGAGCGACTTGGCCAAATACTCAGCG 1659
RESULT 2
ABK92217
ID ABK92217 standard; DNA; 2582 BP.
XX AC ABK92217;
XX DT 15-AUG-2002 (first entry)
XX DE Prostate cancer-associated DNA sequence #103.
XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
XX KW gene therapy; gene; ds.
XX OS Mammalia.
XX PN WO200230268-A2.
XX PD 18-APR-2002.
XX PF 12-OCT-2001; 2001WO-US32045.
XX PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX P-PSDB; ABG61900.
DR WPI; 2002-471335/50.
XX PT Detecting a prostate cancer-associated transcript in a cell in a
XX PT patient, useful for diagnosing prostate cancer (PC) or screening
XX PT modulators of PC, by determining if prostate cancer-associated genes
XX PT are expressed in a prostate tissue
PS Claim 22; Page 386; 436pp; English.
XX CC The present invention relates to methods of detecting a prostate
XX CC cancer-associated transcript in a cell from a patient. The method
XX CC comprises contacting a biological sample from the patient with
XX CC prostate cancer-associated polynucleotides (designated PC genes) that
XX CC selectively hybridise to a sequence that is at least 80% identical
XX CC to them. The prostate cancer-associated polynucleotide sequences
XX CC are differentially expressed in prostate tumour tissue or in
XX CC prostate cancer and are derived from the tissues of various
XX CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX CC The methods of the invention are useful for diagnosing and treating
XX CC prostate cancer in mammals. The prostate cancer-associated genes are
XX CC useful for diagnosing or treating prostate cancer, as well as for
XX CC identifying modulators of prostate cancer or agents that inhibit
XX CC prostate cancer. The nucleic acid sequences are particularly useful
XX CC in gene therapy, as a vaccine or in antisense applications.
XX CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
XX CC sequences.

XX SQ Sequence 2582 BP; 407 A; 822 C; 785 G; 566 T; 2 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2582
 Score: 533.00 Matches: 533
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-593-793a-113 (1-553) x ABK92217 (1-2582)

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 DB 370 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATCACTATGTGCGG 429
 QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
 DB 430 CCTCTGCTGCTGAAGTGGGGGTAGAGGAGAGTTTATGACCATGTGTGGGCATTGGT 489
 QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
 DB 490 CCAGTGTGGGCCCTGTCTGTCCCGCTCCTAGGCTCAGCCAGTCAACCACTGGCGTGA 549
 QY 81 ArgTyrgLysArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
 DB 550 CGTATGGCGCGCGCGCGCTTTCATCTGGGCACTGCTTGGGCATCTCTGTGAGCCTC 609
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 QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
 DB 670 GAGCTGGCACTGCTCATCTGGGCGTGGGCTGCTGTGACTTCTGTGCCAGGTGCTTTC 729
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 DB 730 ACTCCACTGGAGCGCTGCTCTGTGACCTTCTCCGGGACCGGACCACTGTGCCAGGCC 789
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 DB 790 TACTCTGTATGCCCTTCATGATCATCTTTGGGGGCTGGCTGGGCTTACCTTCTGCTGCC 849
 QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrrLeuGlyThrGlnGluCysLeuPhe 200
 DB 850 ATTGACTGGGACACCACTGCTTCTTCCAGCTGCGTGGGCGCCCTACCTGGGCGCCCTTT 909
 QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
 DB 910 GGCGCTGCTCACCTCATCTTCTTCCAGCTGCGTGGGCGCCCTGCTTCCCGCGCTG 969
 QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
 DB 970 GCAGCGCTGGGCGCCACCGAGCGCAGAGGCTGTGGCGCCCTTCTGTGCGCCCGCCAC 1029
 QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
 DB 1030 TGCTGTCCATGGCGGCGCGCTTGGCTTTCGGAACCTTGGGCGCCCTGCTTCCCGCGCTG 1089
 QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
 DB 1090 CACACAGCTGTGTGCGCGCATGCCCGCACCTGCGCGCGCTTCTTCTGGCTGAGCTGTGC 1149
 QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrrThrAspPheValGlyGlyLeu 300
 DB 1150 AGCTGGATGGCACTATGACCTTTCACGCTGTTTTACACGATTTCTGGCGGAGGGGCTG 1209

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrrAspGluGly 320
 DB 1210 TACCAGGGCGTCCAGAGCTGAGCCGCGCACCGAGCCGCGGAGACATATGATGAAGGC 1269
 QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
 DB 1270 GTTCGGATGGCAGCCTGGGCTGTTCCTGCAAGTGGCCATCTCCCTGGTCTCTCTG 1329
 QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrrLeuAlaSerValAla 360
 DB 1330 GTCATGACCGGCTGTGTGAGGATTCGGCAGCTCAGCAGTCTATTTGGCCAGTGTGGCA 1389
 QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
 DB 1390 GCTTTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCGGTGACAGCT 1449
 QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrrThrLeuAla 400
 DB 1450 TCAGCCGCGCTCACCGGGTTCACCTTCTCAGCCCTCAGATCCTGCCCTACACACTGGCC 1509
 QY 401 SerLeuTyrrHisArgGluLysGlnValPheLeuProLysTyrrArgGlyAspThrGlyGly 420
 DB 1510 TCCTCTACACCGGAGAGAGAGGTGTTCTGCCCCAATACCGAGGGGACACTGGAGGT 1569
 QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
 DB 1570 GCTAGCAGTGAGACAGCCTGATGACCACTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1629
 QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
 DB 1630 TTTCCCTAAATGGACACGTGGTGTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTC 1689
 QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGluProThrGluAla 480
 DB 1690 TGGCGGCGCTCTGCCCTGATGCTCTCCGTACGTGGTGGTGGTGGCCACCGAGGCC 1749
 QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
 DB 1750 AGGGTGTTCGGGCGGGGCACTGCTGCCAGCTGCCATCCTGGATAGTGCCTTCTCTG 1809
 QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
 DB 1810 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTC 1869
 QY 521 ThrAlaTyrrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrrPheAlaThrGln 540
 DB 1870 ACTGCCATATGTGTCTGCCGAGCCCTGGGTCTGTGCTGCCATTTACTTTGCTACACAG 1929
 QY 541 ValValPheAspLysSerAspLeuAlaLysTyrrSerAla 553
 DB 1930 GTAGTATTTGACAAGAGCAGCTTGGCCAAATACTACGCG 1968

RESULT 3
 AAS14962
 ID AAS14962 standard; cDNA; 3320 BP.
 XX
 AC AAS14962;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE DNA encoding human PROST 03.
 KW Human; PROST 03; metastasis; prostate cancer; tumour; immune response;
 KW cytostatic; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 282..1943
 FT /tag= a
 FT /product= "PROST 03"
 XX
 PN W0200181577-A2.

XX 01-NOV-2001.
XX PD
XX PF
XX 26-APR-2001; 2001WO-US13323.
XX PR
XX 27-APR-2000; 2000US-200065P.
XX PR
XX 20-APR-2001; 2001US-0200065.
XX (SCHD) SCHERING AG.
XX PA
XX Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Steinbrecher R;
PI Van Heut PT, Wu J;
XX WPI; 2002-041404/05.
DR P-PSDB; AAU10324.
XX
PT Novel PROST 03 polypeptides and polynucleotides useful in research,
PT diagnosis and therapeutic applications, particularly for use in cancer
PT therapeutics -
XX
PS Claim 6; Fig 1; 77pp; English.
XX
CC The invention relates to an isolated PROST 03 polypeptide (I) and to
CC the polynucleotide (II) encoding PROST 03. Fragments of (I) were used
CC to generate antibodies (III) to PROST 03. (III) is useful for selectively
CC destroying a cell expressing (I), and for treating a disease-state
CC associated with expression of PROST 03 in a human patient. (III) is
CC useful for diagnosing metastasis associated with (I), in a subject.
CC (I) is also useful for diagnosing and treating diseases of cell
CC proliferation such as prostate cancers. (I) is also useful for generating
CC antibodies to PROST 03. (III) is useful in detecting the levels of PROST
CC 03 polypeptides in cells and tissues, and in targeting drugs to primary
CC and metastatic tumours. (I) is also useful for stimulating immune
CC response to PROST 03 containing cells. (II) is useful in diagnostic
CC assays for detecting the levels of polynucleotides encoding PROST 03 in
CC cells and tissues. (II) is useful as DNA probes, as targets for antisense
CC and ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents
CC the coding sequence of human PROST 03.
XX

SQ Sequence 3320 BP; 585 A; 1013 C; 944 G; 778 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 3320
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x AA514962 (1-3320)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db ATGGTCCAGAGGCTGGGTGAGCGCCCTGCTGCGGACCCGAAAGCCAGCTCTTGCTG 341
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGACAGGCATCACCTATGTGCG 401
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db CCTCTGCTGCTGAAGTGGGGTAGAGGAGAGTTTCATGACCATGGCTGGGCATTTGGT 461
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db CCAGTGTGGGGCTGTGCTGTCTCCCGCTCTAGGCTCAGCCAGTACCTGGCGTGA 521
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db CGCTATGGCCGCCGCCGCCCTTTCATCTGGGCACTGTCTTGGGCATCCTGCTGAGCCTC 581

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db TTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCGATCCAGGCCCTG 641
QY 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db GAGCTGGCACTGCTCATCTGGCGCTGGGCTGCTGGAGTTCTGTGGCAGAGTGTCTTC 701
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db ACTCCACTGGAGGCGCTGCTCTACCTCTTCCGGGACCCGGACCACTGTCCGAGGCC 761
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db TACTCTGTATGCTTCATGATCAGTCTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 821
QY 181 IleAspTrpAspTrpSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db ATTGACTGGGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db GGCTGTGCTACCTCATCTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db GCAGCGCTGGGCGCCACCGAGCCAGAGAGGCTGTGGCGCCCTCTCTGTGCGCCAC 1001
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db TGCTGTCCATGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1061
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaLeuLeuCys 280
Db CACCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCGTGGCGAGGGCTG 1181
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCGAGGCGCCGAGACACTATGATGAAG 1241
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db GTTCGGATGGCGAGCCTGGGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db GTCATGGACCGGCTGGTGCAGCGATTCCGCACCTCGAGCAGTCTATTGGCCAGTGTG 1361
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db GCTTTCCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1421
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db TCAGCGCGCTCACCGGCTTACCTTCTCAGCCCTGCGAGATCCTGCTGCTGCTGCTGCT 1481
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db TCCCTCTACCAACCGGAGAGAGGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db GCTAGCAGTGGAGCAGCCTGATGACCACTTCTTCCCGAGGCGCTTAAGCCTGGAGCTCC 1601
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
Db TTCCCTAATGACAGCTGGGTGCTGGAGGAGTGGCTGCTCCCACTTCCACCTCCAGGCTC 1661
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480

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1662 TCGGGGCGCTCTCCCTGTGTGTCCTCCGTACGTGTGTGGTGGGTGAGCCACCGAGGCC 1721
481 AtgValValproGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
1722 AGGGTGGTTCGGGGCGGGGCGGACATCTCCGTGGACCTCGCCATCTGGATAGTGGCTTCCCTG 1781
501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
1782 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTCCAGTCCAGCCAGTCTGTC 1841
521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
1842 ACTGCCTATATGTGTCTGCGCAGGCGCTGGGTCTGGTGGCCATTTACTTTGCTACACAG 1901
541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
1902 GTAGTATTTGACAAGAGGACATTGGCCAAATCTCAGCG 1940

RESULT 4
ID AAV61201 standard; cDNA; 3410 BP.
XX
AC AAV61201;
XX
DT 06-JAN-1999 (first entry)
XX
DE Full length cDNA sequence of prostate tumour clone L1-12.
XX
KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN W09837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03492.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
XR WPI; 1998-609886/51.
DR P-PSDB; AAW71869.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 79-80; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-593-793a-113 (1-553) x AAV61201 (1-3410)
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1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
284 ATGGTCCACGAGGCTGTGGGTGAGCCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGGCTG 343
21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
344 GTCAACCTGCTAACCCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCCG 403
41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
404 CCTCTGCTCTGGAAGTGGGGGTAGAGAGAAAGTTTCATGACCATGGTGTGGGCATTTGGT 463
61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
464 CCAGTGTGGGCTGTGTGTGTCGCGCTCCTAGGCTCAGCCAGTACCACCTGGCGTGA 523
81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
524 CGCTATGGCGCGCGCGGCTTTCATCTGGGCACTGCTCCTTGGGCATCTCTGTGAGCCCTC 583
101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
584 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCAGGCCCTCG 643
121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
644 GAGTGGCACTGCTCATCTGGCGTGGGCTGCTGGACTCTGTGGCCAGGTGCTCTTC 703
141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
704 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGAGCCACCTGTGCCAGGCC 763
161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
764 TACTCTGTCTATGCCCTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 823
181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
824 ATTGACTGGGACACCAGTGCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 883
201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
884 GGCTGTCTCACCTCATCTTCTACCTGCTAGCAGCCACACTGTGTGGTGGCTGAGGAG 943
221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
944 GCAGGCTGGGCCCCCACCAGGACGAGGAGGCTGTCGGCCCCCTCTCTGTGCCGCCAC 1003
241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyValAlaLeuLeuProArgLeu 260
1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACCTGGCGGCCCTGCTTCCCCGGCTG 1063
261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
1064 CACCACTGTGTGGCGCATGCGCGCACCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1123
281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
1124 AGCTGGATGGCACTCATGACCTTTCACGCTGTTTACACGGATTTCTGGGCGAGGGGCTG 1183
301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
1184 TACCAGGGGCTGCCAGAGCTAGCGGGGACCGAGGCCCGGAGACACTATATGATGAGGC 1243
321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
1244 GTTCGGATGGCAGCGCTGGGCTGTTCCTGTCAGTGGCCATCTCCCTGCTCTCTCTG 1303
341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
1304 GTCATGGACCGGCTGTGCAGCGATTTCGCACTCGCAGCACTCTATTTGGCCAGTGGCA 1363
```

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGCTGGCTGCCAGTCCCTGTCCACAGTGTGGCTGGTACAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGTTCCACTTCTCAGCCCTGCAGATCCTGCCCTACACATGGCC 1483
Qy 401 SerLeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACACCGGAGAGAGAGTGTCTCTGCCCAATACCGAGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGGAGCAGCCTGATGACACAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTTAATGACAGCTGGGTGCTGGAGGAGTGGCTCTCCACCTCCACCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCTGTGATGTCTCCGTAGCTGTGTGGTGGTGGAGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCCGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCTGTTTATGGGCTCCATTTGTCCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTTCTGTCCGCGAGGCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGGACTTGGCCAAATACTCAGCG 1942
RESULT 5
AAV58586
ID AAV58586 standard; cDNA; 3410 BP.
XX
AC AAV58586;
XX
DT 08-DEC-1998 (first entry)
XX
DE Prostate tumour specific gene clone L1-12.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 284..1945
FT /*tag= a
XX
XX WO9837418-A2.
PN
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03690.
XX
PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-0806596.
PR 01-AUG-1997; 97US-0904809.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dallon DC, Xu J;
PI
XX

DR WPI; 1998-480805/41.
DR P-PSDB; AAW69385.
XX
PT Novel human prostate specific tumour protein and fragments - useful
for detecting and treating prostate cancers
XX
PS Claim 1; Page 84-85; 141pp; English.
XX
CC This sequence represents a human prostate tumour specific gene, and can
be used in the method of the invention. The method is for detecting
prostate cancer comprises contacting a biological sample with an agent
able to bind an immunogenic portion of a prostate protein (such as
encoded by this sequence). An antibody which binds to an immunogenic
portion of the prostate protein, and the method can be used to detect,
monitor progression of, or treat prostate cancers. The antibody may
also be conjugated to a therapeutic agent for use in therapy of prostate
cancers.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-09-593-793A-113 (1-553) x AAV58586 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCGCTGGGTGAGCGCTGCTGGCGACCGAAGCCAGCTTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCACCTGCTTAACCTTTGGCTGGAGGTGTGTTGGCGCGAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTCTGGGCATTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGCGCTGGTGTGTCCTCCGCTCTAGCTCAGCCAGTACCATGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCCCTTTCATCTGGGCACTGTCTTGGGCATCTCTGTAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGTGTCGCCGATCCCGAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCAGTGTCTCATCTGGCGTGGGCTGTGGACTTCTGTGGCAGAGTGTGCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGGGAGACCGGACCATGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTCGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCGCCCTACCTACCTGGGACCCAGGAGGAGTGTCTCTTT 883
Qy 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCCCTCATCTTCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGCGCTGGCGCCACCAGGAGCAGAGAGCGCTGTGGCGCCCTCTCTGTGTGGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGGGCGCGCTGGCTTTCGGAACCTGGGGCGCCCTGCTTCCCGGGCTG 1063
QY 261 HIsGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGTCGGGATGCGCGACCCCTGCGCGGCTCTTCTGGCTGAGCTGTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyLeu 300
|||||
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTCTTACACGATTTCTGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCGAGGGCCGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGGATGGCAGCGCTGGGGCTGTCTCTGACGTGCGCATCTCCCTGTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCTGGACCGCTGGTGCAGCGATTCGGCACTCCGACGAGTCTATTGGCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCTTCTCCCTGTGGCTGCGCGTCCCATGCTGCTCCACAGTGTGGCGTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCCCTCACCGGTTCACCTTCTCAGCCCTGCGAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1484 TCCTCTACCAACCGGAGAGCAGGTGTTCTGTCGCAATACCGAGGGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1544 GTAGCAGTGAGGACAGCTGATGACCACTTCTCTGCCAGGCGCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
|||||
Db 1604 TTCCCTAATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCCCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
Db 1664 TCGGGGCTCTGCTGCTGATGCTCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGGTTCCGGCGGGGCACTGCTGCTGGACCTCGCCATCTCTGGATGCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCCAAGTGGCCCAATCCCTGTTTATGGGCTCATTTGCTCCAGCTCAGCGAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCTATATGCTGTGCGCCAGCGCTGGGTCTGGTCCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1904 GTAGATTTTACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 6
AAC79473
ID AAC79473 standard; cDNA: 3410 BP.
XX

AC AAC79473;
XX 07-FEB-2001 (first entry)
XX
XX cDNA sequence of human breast tumour clone P501S.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy;
KW breast cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
XX WO200061756-A2.
PN
PD 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US09688.
XX
PR 09-APR-1999; 99US-0288950.
PR 02-JUL-1999; 99US-0346327.
XX
PA (CORI-) CORIXA CORP.
PI Reed SG, Xu J, Dillon DC;
XX
DR WPI; 2000-638568/61.
DR P-PSDB; AAB28527.
PT A novel isolated polypeptide comprising an immunogenic portion of a
PT breast cancer protein useful in the detection and treatment of breast
XX cancer -
PS Claim 26; Page 91-92; 95pp; English.
XX
CC The present sequence was isolated from a breast tumour cDNA library. It
CC is provided in a specification relating to compounds for immunotherapy
CC and diagnosis of breast cancer. Breast tumour antigens and the
CC polynucleotides that encode them may be used in the production of a
CC pharmaceutical composition to be used in the treatment of breast cancer.
CC Proliferated T cells and incubated antigen presenting cells are also
CC required. The polypeptides and polynucleotides may also be used to
CC produce a vaccine.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-593-793a-113 (1-553) x AAC79473 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCGCCTGCTGCGCACCGGAAAGCCAGCTCTGTCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 CTCACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGATTCATGACCATGGTGTGGCATTTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTCTGGGCTGTGTGTCTGCTCCGCTCTAGGCTCAGCCAGTGCACCTGGGTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGCGCGCGCGCCCTTCATCTGCGGACATGTCCTTGGGCATCTCTGTGAGCCTC 583

XX Sequence 3410 BP: 667 A; 1015 C; 945 G; 782 T; 1 other;

Alignment Scores:

Pred. No.: 0 Length: 3410
 Score: 553.00 Matches: 553
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-593-793a-113 (1-553) x AAA06349 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
 DB 284 ATGGTCCAGAGCGTGGGTGAGCGCGCTGCTGCGGCACCGAAGCCAGCTTGTGCTG 343
 QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
 DB 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCGG 403
 QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
 DB 404 CTTCTGCTGCTGAAAGTGGGGTAGAGGAGATTTCATGACCATGCTGGGCGATTGCT 463
 QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
 DB 464 CCAGTGTGCGGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
 QY 81 ArgTyrGlyArgArgProPheLeuLeuLeuSerLeuGlyIleLeuLeuSerLeu 100
 DB 524 CCCTATGGCGCGCGCGCGCTTCACTGGGCACTGTCTGGGCACTGCTGGGCACTGCT 583
 QY 101 PheLeuLeuProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
 DB 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTG 643
 QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
 DB 644 GAGCTGGCACTGCTCATCTGGCGCTGGGGCTGCTGGCACTTCTTGGCGAGGTGCTTC 703
 QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
 DB 704 ACTCACCAGGAGCGCTGCTCTGACCTCTTCGGGACCCGAGCAGCTGCTGCCAGGCG 763
 QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
 DB 764 TACTCTGTCTATGCTTCATGATCAAGTCTTGGGGGCTGCTGGGCTGCTGCTGCTGCC 823
 QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
 DB 824 ATTGACTGGGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 883
 QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
 DB 884 GAGCTGCTACCCCTATCTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
 QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
 DB 944 GCAGCGCTGGGCGCCACCGAGCCAGCAGAGGGCTGTGGGCGCCCTCTCTTGTGGCC 1003
 QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
 DB 1004 TGCTGTCCATGCGGCGCGCTTGGCTTCCGGAACCTGGGCGCGCTGCTTCCCGGCTG 1063
 QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgPheValAlaGluLeuCys 280
 DB 1064 CACCAGCTGTGCTGCGCATGCGCGCACCCCTGCGCGCGCTCTTCTGCTGCTGCTGCT 1123
 QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
 DB 1124 ACCTGGATGGCACTCATGACCTTCACGCTGTGTTTACAGGATTTCTGCTGGCGAGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
 DB 1184 TACCAGGGCGTCCAGAGCTGAGCGGGCACCGAGCGGCGGAGACACTATGATGAAGC 1243
 QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
 DB 1244 GTTCGATGGGAGCGCTGGGCTGTTCCTGAGTGGCGCATCTCCCTGGTCTTCTCTCTG 1303
 QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
 DB 1304 GTCATGGACCGCTGGTGCAGCGATTGCGCACTCGAGCAGTCTATTTGGCCAGTGGCA 1363
 QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
 DB 1364 GCTTTCCCTGTGGCTGCCGTTCCACATGCCTGTCCACAGTGTGGCGGTGACAGCT 1423
 QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
 DB 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACATGGC 1483
 QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
 DB 1484 TCCTCTACCAACCGGAGAGCAGGTTCCTGCCCAATACCGAGGGACACTGGAGT 1543
 QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
 DB 1544 GCTAGCAGTAGGACAGCGCTGATGACCACTTCTCTGCCAGGCCCTAAGCCTGGAGTCC 1603
 QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
 DB 1604 TTCCCTAATGAGACAGTGGGTGCTGGAGCAGTGGGCTGCTCCACCTCCACCCGCGCTC 1663
 QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
 DB 1664 TCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1723
 QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
 DB 1724 AGGTGGTTCGCGGCGGGGCACTGCTGCTGAGACCTCGCCATCCTGGATAGTGCCTCTG 1783
 QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
 DB 1784 CTGTCCCAAGTGGCGCCCACTCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCAGTCTG 1843
 QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
 DB 1844 ACTGCTATATGCTGCTGCCAGCGCTGGTCTGGTGGCCATTTACTTTGCTACACAG 1903
 QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
 DB 1904 GTAGTATTGTACAAGAGGCACTTGGCCAAATACTCAGCG 1942

RESULT 8

AAS63557

ID AAS63557 standard; cDNA; 3410 BP.

XX AAS63557;

XX 29-JAN-2002 (first entry)

XX Human prostate cDNA sequence #109.

XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

XX WO2001/73032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US09919.

XX 27-MAR-2000; 2000US-0536857.

PR

PR	09-MAY-2000; 2000US-0568100.
PR	12-MAY-2000; 2000US-0570737.
PR	13-JUN-2000; 2000US-0593793.
PR	27-JUN-2000; 2000US-0605783.
PR	10-AUG-2000; 2000US-0636215.
PR	29-AUG-2000; 2000US-0651236.
PR	06-SEP-2000; 2000US-0657279.
PR	02-OCT-2000; 2000US-0679426.
PR	10-OCT-2000; 2000US-0685166.
XX	(CORI-) CORIXA CORP.
PA	
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX	
DR	WPI: 2001-639232/73.
DR	P-PSDB; AAU69763.
XX	
PT	New human prostate-specific polypeptides and polynucleotides useful for
PT	the diagnosis and treatment of cancer, especially prostate cancer -
XX	
PS	Claim 1; Page 267-268; 579pp; English.
XX	
CC	The invention relates to isolated prostate-specific
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC	antibodies raised against the polypeptides (or antigenic epitopes
CC	derived from them) and antigen-presenting cells expressing the
CC	polypeptides. The antibodies are useful for detecting the presence of
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC	the antigen-presenting cells are useful for stimulating and/or expanding
CC	T cells specific for a tumour protein, and for inhibiting the development
CC	of cancer especially prostate cancer. Compositions comprising the
CC	polynucleotide and/or polypeptide are useful for stimulating an immune
CC	response, and for treating cancer. The oligonucleotide is useful for
CC	detecting cancer. The present sequence is a prostate specific
CC	polynucleotide of the invention.
XX	
SQ	Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:	
Pred. No.:	0 Length: 3410
Score:	553.00 Matches: 553
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	22 Gaps: 0
US-09-593-793A-113 (1-553) x AAS63557 (1-3410)	
Qy	1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db	284 ATGGTCAGAGCGTGTGGTGAGCCGCCCTGCTGCACCGCACCAGGAAGCCAGCTCTTCGCTG 343
Qy	21 ValAsnLeuLeuThrPhcglyLeuGluValCysLeuAlaLaAglyIleThrTyrrValPro 40
Db	344 GTCAACTGCTAAACCTTTGGCTGGAGGTGTGTTTGGCCGAGCATCACCTATGTCGCG 403
Qy	41 ProLeuLeuLeuGluValglyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db	404 CCTCTGCTGTGGAAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTCTGGCATTTGGT 463
Qy	61 ProValIleuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db	464 CCAGTGCTGGCCCTGTGCTGTGTCCCGCTCCCTAGGCTCAGCCAATGACCATGGCGTGA 523
Qy	81 ArgTyrrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db	524 CGTATGCGCCGCGCGGCCCTTCATCTGTGGCACTGTCTCTTGGGCATCTCTGCTGAGGCTC 593
Qy	101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db	584 TTTCATCATCCAAAGGCCGCGCTGCTAGCAGGGCTGTGTCCCGGATCCCAGGCCCTG 643

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QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGGTCCGGCGGGGCATCTGCTGGACCTCGCCATCTCGATAGTGCTTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCATCTCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCCTATATGGTGTCTGCCGAGCGCTGGGTCTGGTCTGCCATTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 1942

RESULT 9
AAS10108
ID AAS10108 standard; cDNA; 3410 BP.
XX
AC AAS10108;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human prostate tumour cDNA L1-12.
XX
KW Human; prostate tumour protein; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN US6262245-B1.
XX
PD 17-JUL-2001.
XX
PF 25-FEB-1998; 98US-0030607.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC;
XX
DR WPI; 2001-440862/47.
DR P-PSDB; AAU04961.
XX
PT Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient
XX
PS Claim 3; Column 118-121; 105pp; English.
XX
CC The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS10108 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCCAGAGGCTGTGGGTAGCCGCCCTGTCTGGCGCACCGGAAAGCCAGCTCTTGGCTG 343
```

```
... QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGAGGCATCACTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGAGAGTTTACCATGGTGTGTGGCATGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrPheGly 80
DB 464 CCAGTCTGGGCCCTGTGTCTGTCCCGCTCTAGGCTCAGCCAGTCACTGAGCCAGTGG 523
QY 81 ArgTyrGlyArgArgProPheIleTyrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGCCCTTTCATCTGGGCACCTGTCTTGGGCATCTCTGTGTAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCATCATCCCAAGGCGCGCTGGCTAGCAGGCTGTCTGTGCCCGGATCCAGGCCCTTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGTCTGACTTCTGTGCCAGGTGTCTCTTC 703
QY 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGGCCCTGTCTGTGACCTTTCGGGAGCCCGGAGCCACTGTCTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGTGTCTTGGGCTTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCTGCTGGCCCTCTCTGAGGACCCAGGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCTGCTCACCCCTCATCTTCTCACCTGCTAGCAGCCACACTGCTGGTGGGTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCGCTGGGCCCCACCGAGCGAGCAGAGAGGCTGTGGCCCTCTTGTGTGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTGTCCATGCCGGCGCGCTGGCTTTCCGGAACCTGGCGCCCTGTCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCAGCTGTGTGCGCATGCCCGCACCTTGGCGGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
DB 1124 AGCTGGATGGCATCTCATACCTTCACGCTGTTTACCGGATTTCTGTGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGGCTGCCAGAGCTGAGCGGGCAGCGAGCCCGGAGACACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGCAGCGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGGCTGTGTGAGCGATTCGGCACTTCGAGCAGTCTATTGTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGCTGCCACATGCTCTGCCAGTGTGCCGCTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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Db 1424 TCAGCGCCCTCACCGGGTTCACTTCTCAGCCCTCAGATCCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACACACGGGAGAGCAGGTGTTCTTCCGCCAAATACAGAGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGACACAGCCTGATGACCACTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACACGTGGGTGCTGAGGACGTGGCTCTGCCACCTCCACCCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCCCTGATGCTCCGTACGTGGTGGTGAGGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTTTCCGGCGGGGACATCTGCCCTGGACCTGCCCATCTGGATAGTGCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTCCCGAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGGACAAGCGGACTTGGCCAAATACTACAGC 1942
RESULT 10
AAH93465
ID AAH93465 standard; cDNA; 3410 BP.
XX AAH93465;
AC
XX
DT 04-OCT-2001 (first entry)
DE Human prostate-specific full length cDNA sequence L1-12.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI: 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 265-266; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode

CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-593-793a-113 (1-553) x AAH93465 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGGTGAGCCGCTGCTGGCGCAGCGAAGCCAGCTCTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTCATGACCATGTGCTGGCGATTG 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTGTGTCCTGCTAGGCTCAGCCAGTGACCATGTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGCGCGCGCGCCCTTCATCTGGGCATGTCTTGGGCATCTGCTGAGCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAAGGCCCTG 643
Qy 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGGCGTGGGCTGCTGGACATTCTGTGGCAGAGTGTCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGACCATGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 764 TACTGTGTATATGCTTTCATGATCAGTCTTGGGGCTGCTGGGTACTCTCTGCTGCC 823
Qy 181 IleAspTTPAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGACACAGTGGCCCTTACCTTGGGACCCAGGAGAGTGCCTCTTT 883
Qy 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GSCCTGCTCACCTTCATCTTCTCACCTGGGTAGCAGCCACACTGCTGCTGGTGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003

```
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGTGTTCATGCGCGCGCGCTGGCTTTCGGAACCTGGCGCGCTGCTTCCCGCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCAGCTGTGTGCGCGATGCCCGCACCTCGCGCGCTCTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCAGCGTGTTCACCGATTTCTGGCGGAGGGCGTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
DB 1184 TACCAGGCGCTGCCAGAGCTGAGCGCGGCACCGAGCGCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGACCGCGCTGTGTCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCTGTGCTGCCGTGCCATGCTGCTCCACAGTGTGCCGTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrClyPheThrPheSerAlaLeuGlnIleLeuProThrThrLeuAla 400
DB 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCGCTGCAGATCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCCTCTACACCGGAGAGAGAGGTGTTCTCGCCCAATACGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGACAGCTGATGACAGCTTCTGCCAGGCGCTAAGCGTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
DB 1604 TTTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCGCTCTCCACCTCCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGGGGGCTCTGCTGTGATGCTCTCCGTACGTGTGGTGGTGAGGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGTTCGGCGCGGGGCATCTGCCCTGGACCTCGCCATCTGGATAGTGCCTCCG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCATCTCCCTGTATTATGGCTCCATTTGTCAGCTCAGCCAGCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCTATATGTTGTCGCCGAGCGCTGGGTCTGGTCCCATTTACTTCTGCATACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 11
AAH84779
ID AAH84779 standard; cDNA; 3410 BP.
XX
AC AAH84779;
XX
DT 25-SEP-2001 (first entry)
XX
```

Human prostate-specific cDNA sequence L1-12/P501S.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
chromosome 22q11.2; prostate-specific protein; chromosome 1;
prostate specific antigen; PSA; ss.

Homo sapiens.

WO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;

WPI; 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a
prostate-specific protein, useful in the diagnosis and therapy of
prostate cancer -

Claim 5; Page 164-165; 325pp; English.

The present invention describes an isolated polypeptide (P1) comprising
at least an immunogenic portion of a prostate-specific protein, or its
variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
(N1) have cytostatic activity and can be used in vaccine production.
The polypeptides, nucleic acids and antibodies from the present
invention are useful in the diagnosis and therapy of prostate cancer.
Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
region. Prostate specific antigen (PSA) P501S was located on
chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
polynucleotide and polypeptide sequences used in the exemplification
of the present invention.

Sequence 3410 BP: 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:

Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-593-793A-113 (1-553) x AAH84779 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

DB 284 ATGGTCCAGAGGCTGTGGGTGAGCGCGCTGCTGCGCACCGGAAAGCCAGCTCTGTGCTG 343

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrThrValPro 40

DB 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGGCATCATGTGTCGCG 403

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

DB 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAAGATTCTATGACCATGGTGTCTGGCATTTGT 463

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisThrArgGly 80

DB 464 CCAGTGTGGGCTGTGCTGTCTGCCGCTCTAGGCTCAGCCAGTCACCCACTGGCGTGA 523

QY 81 ArgTyrGlyArgArgProPheIleThrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

Db	524	CGTATGGCGCGCGCGCCCTTCATCTCGGGGACATGTCTCTGGGGCATCCTCGCTGAGCCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGCCCCGATCCCGAGGCCCTG	643
Qy	121	GlulLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCGGCGCTGGGGCTGCTGGACTTCTGTGTGGCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGluAla	160
Db	704	ACTCCACTGGAGGCCCTGCTCTGACCTCTCCGGGACCCGGACCACTGTGCGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGCTATGCGCTTCATGATCAGTCTTGGGGCTGCTGGGTACTCTCGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTGCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT	883
Qy	201	GlyLeuLeuThrIleuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGCTCACCTCATCTCTCACTTCGCTAGCAGCACACACTGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCAGGACGACGAAAGGGCTGTGGGCCCTCTCTGTGCGCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATCGCGGCGCGCTGGCTTTCCGGAACTGGGCGCCCTCTCTTCCC CGGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCACTGTGTGCGCGATGCGCGCACCCCTGCGCGCGCTCTTCTGGGTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGTGTGTTTTACCGGATTTCTGTGGCGGAGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly	320
Db	1184	TACCAGGGCTGCCCCAGACTGAGCGGGCACCGGAGCCCGGAGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTTCGATGGGACCGCTGGGGCTGTCTCTGCACTGCGCATCTCCCTGGTCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCAATGGACCGCTGTGTGAGCGATTCGGCACTCAGCAGACTATTTGGCCAGGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValIleThrAla	380
Db	1364	GCCTTCCCTGTGGCTGCCGTCACATGCCTGTCCCACAGTGTGGCGCTGGTGCACGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGACTCTGCCCTACACACTGGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACACCGGGAAGCAGGTGTCTCTGCCCCAATACCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGAAGACACCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTTAATGGACACTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTC	1663

Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGCCCTCTCCCTGTATCTCCGTACGTGTGGTGGAGCCACCGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGGTGGTTCCGGCGCGGGGCATCTGCCTGGACCTCGGCATCCYGGATAGTGCCTTCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTGCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTTCACAGCTCAGCAGCTGTGC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCCTATATGGTGTCGCCCGAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTTCACAAAGCGCATTGGCCAAATACTCCAGCG	1942

RESULT 12

AAH02530	AAH02530 standard; cDNA; 3410 BP.
AAH02530;	
14-JUN-2001	(first entry)
Prostate tumour antigen determined full length cDNA sequence for L1-12	
Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine; ss.	
Homo sapiens.	
WO200125272-A2.	
12-APR-2001.	
04-OCT-2000; 2000WO-US27464.	
04-OCT-1999; 99US-0157455.	
(CORI-) CORIXA CORP.	
Xu J, Skeiky YAW, Reed SG, Cheever MA;	
WPI; 2001-245062/25.	
P-PSDB; AAB74800.	
Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer	

Claim 4; Page 155-156; 276pp; English.

The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74921 and AAB74830 are sequences used in the exemplification of the present invention.

XX	Sequence	3410 BP	667 A	1014 C	945 G	783 T	1 other
SQ							

Alignment Scores:

Pred. No.:	0	Length:	3410
Score:	533.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0
US-09-593-793A-113 (1-553) x AAH02530 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
Db	284	ATSGTCCAGAGGCTGTGGGTGAGCGCCCTGCTGCGCACCGGAAAGCCAGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro	40
Db	344	GTC AACCTGTAACTTTGGCTTGGAGGTGTGTGTTGGCGCAGGAGCATCACCTATGTGCGG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCCTGCTGCTGGAGTGGGGGTAGAGGAGAAGTTCAATGACCATGGTGCTGGGCAATGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTGTGGGCCTGTCTGTGTGCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGTATATGGCGCGCGCGCCCTTCATCTGGGACATGTCTCTTGGGCAATCCTGTGAGCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGGCCGCGTGGCTAGCAGAGGCTGTGTGCCCCGAGTCCCAGGCCCCCTG	643
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyValLeuValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCTGGGCGTGGGCGTCTGGACTTCTGTGGCCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCCCTGTCTCTGACCTCTCTCCGGGACCCGGACCACTGTCTGCCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTCTATGCTTTCATGATCACTCTTGGGGCTGCTTGGGCTACTCTCTGCTGCCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTAGTCCCTTGGCCCCCTACCTTGGGCACTCCAGAGGAGTGTCTCTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCCTGCTCACCCCTCATCTTCTCTCACTGCTAGCAGCACACACTGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCGAGCGACAGAGAAGGCTGTGCGGCCCTCTCTTGTGCGCCCA	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCCGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTCTGCTTCCCGGGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCACTGTGCTGCCGATGCCGCCGCCACCTTGCGCCCGGCTCTTCTGTGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGATTTCTGCTGGCGAGGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAAGGGGCTGCCAGACTAGCCGGGACCCGAGCGCCGAGACACTATGATGAAGGC	1243

[illegible]

PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.

XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2002-255649/30.

XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -

XX Claim 1; SEQ ID NO 110; 87pp; English.

XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.

XX SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:

Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-593-793A-113 (1-553) x ABL94929 (1-3410)

Qy 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

Db 284 ATGGTCCAGAGCGTGTGGGTGAGCCCTGCTGCGGACCCGGAAGCCAGCTCTTGCTG 343

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCCG 403

Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAGTGGGGTAGAGGAAGTTCATGACCATGCTGGCGCATTTGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTCTGCTCCCGCTCTAGCTAGCTAGCCAGTCACCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCCGCCCTTCTATCTGGGCATGCTCTGGGCATCCTGTGTAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGCCCGGATCCAGAGCCCTTG 543
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCAGCTGCTCATCTGGGCGTGGGGCTGCTGGAGCTTCTGTGGCCAGGTGTCTC 703
Qy 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTCTATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 883
Qy 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCTCATCTCTCCTCCTGCTAGCAGCCACACTGCTGCTGCTGCTGCTGCTG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGGCTGCTGCTTCCGGAACCTGGGCGCTGCTTCCCGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCGTGGCGGAGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCAGGCGCCGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGTCAGTGGCCATCTCCTGCTGCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGTGTGCGAGCGATTCGGCACTCAGCAGAGTCTATTTGGCCAGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGGTCCACATGCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCAGGGTTCACCTTCTCAGCCCTGCGAGATCCTGCTGCTGCTGCTGCTG 1483

QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACACCGGAGAGAGGTGTTCTCCCAAAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGGACAGCCTGATGACACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCTGCTCCACACTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGGGGGCGCTCTCCCTGTATGTCTCCGTACGTGTGTGTGGTGGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTGTTCCGGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCCTTCCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGTGCTGCCGAGGCGCTGGGTCTGGTCCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGACGCGACTTGGCCAAATACTACGCG 1942

RESULT 14

ABK29017
ID ABK29017 standard; cDNA; 3410 BP.
XX AC ABK29017;
XX DT 23-APR-2002 (first entry)
XX DE Human breast tumour polypeptide full length cDNA clone #3.
XX KW Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic; immunostimulant.
XX OS Homo sapiens.
XX PN W0200198339-A2.
XX PD 27-DEC-2001.
XX PF 12-JUN-2001; 2001WO-US19032.
XX PR 22-JUN-2000; 2000US-0602877.
XX PR 12-OCT-2000; 2000US-0687507.
XX PR 06-FEB-2001; 2001US-0778381.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX WPI; 2002-147792/19.
XX DR Polynucleotides encoding breast tumour polypeptides, useful for treating breast cancer or stimulating an immune response -
XX PT
XX PS Claim 1; Page 143-144; 150pp; English.
XX CC The invention relates to polynucleotides encoding breast tumour polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a

CC cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences ABK28920-ABK29025 represent cDNA clones encoding human breast tumour polypeptides of the CC invention.

XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABK29017 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGTGCGGCACCGGAAACCCAGCTCTTGGCTG 343
... QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGAGGCATCATGTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGAAAGTTTACCATCATGTTGTGGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTCTGGGCTGTGTCTGTCCGCGCTCTAGGCTCAGCCAGTGCACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTTCATCTGGGCATCTCTTGGGCATCTCTGTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGCGCGGCTGGCTAGCAGGGCTCTGTGCGCGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGCTTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGTGACCTTTCGCGGACCCGAGCACCCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCATCTTGGGGGTGCTTGGGCTACCTCTGCGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGATGGGACACCACTGCTGCTGGGCGGCTACCTGTGGCACCAGGAGGAGTGCCTTCT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCCTCATCTTCTCACCTGCTAGCAGCCACACTGTGTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCGGCCACCGAGCGAGAGGGGCTGTGCGGCCCTCTCTGTGTGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTGTCTCCCGGCTG 1063


```
Oy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTGCGCATGCCCGCACCCCTGCGCGGCTCTTCGTGCTGAGCTGTGC 1123
Oy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGCGGCGAGGGGTG 1183
Oy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGGCGCACCGAGGCGGAGACACTATGATGAAGGC 1243
Oy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGCAGCTGGGGCTGTCTCGAGTCGCGCATCTCCCTGCTCTCTCTCTG 1303
Oy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCAATGGACCGGCTGGTGCAGCGATTCGCGCACTCGAGCAGTCTATTGGCCAGTGTGCA 1363
Oy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGGTGCACATGCCGTGCCACAGTGTGGCGGTGGTGCACACT 1423
Oy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCCTCACCGGTTACCTTCTCAGCGCTGCAGATCTCCCTACACACTGGCC 1483
Oy 401 SerLeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCCCGGGAAGCAGGTGTCTCTGCCAATACCGAGGGGACACTGGAGGT 1543
Oy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGGAGCAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
Oy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACACCTGGGTGCTGGAGGCAGTGGCTTCCCACTCCACCCCGCGCTC 1663
Oy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TGCGGGGCTTGGCTGTGATGCTTCCGTACGTGTGGTGGGTGAGCCACCCAGGCC 1723
Oy 481 ArgValValProGlyArgGlyCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCGCGGCGGGGCGCATCTGCCTGGACCTCGCCATCTCGGATAGTTCCTG 1783
Oy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCCAAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCAGCTCAGCCAGTCTGTC 1843
Oy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCATATGGTGTCTGCGCGCAGGCGCTGGGTCTGTCGCCATTTACTTTGCTACACAG 1903
Oy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAGAGCGACTTGGCCAAATACTACGCG 1942

RESULT 15
ID ABA91283
XX ABA91283 standard; DNA; 2133 BP.
XX AC ABA91283;
XX DT 08-APR-2002 (first entry)
XX DE Thioredoxin-ubiquitin-P501S(aa55-553)His triple gene fusion.
XX KW Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
XX KW cancer; vaccine; therapy; human; gene; ds.
XX
```

```
OS Chimeric - Homo sapiens.
OS Chimeric - Escherichia coli.
XX
PN WO200200892-Al.
XX
PD 03-JAN-2002.
XX
PF 19-JUN-2001; 2001WO-EP06952.
XX
PR 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PI Cabezon Silva TEV, Delisse AEF;
XX
XX WPI; 2002-147888/19.
DR P-PSDB; AAM50661.
XX
XX Novel DNA sequence encoding triple fusion protein comprising ubiquitin
fused between thioredoxin and polypeptide of interest, useful for
producing recombinant polypeptide of interest suitable for medicinal
use
XX
XX Example 5; Fig 9a; 87pp; English.
XX
XX The present sequence is that of a triple gene fusion comprising,
from the 5' end, the trxA thioredoxin gene from Escherichia coli,
the human ubiquitin coding sequence, the prostate antigen P501S
(amino acids 55-553) coding sequence, and DNA encoding a histidine
tail. The triple fusion was constructed in plasmid pRIT5063,
which included the Saccharomyces cerevisiae CUP1 promoter and
yeast alpha prepro signal sequence. The triple fusion protein
(see AAM50661) was produced in E. coli G1724 transformants. This
is an example of the production of triple fusion proteins of the
invention comprising ubiquitin fused between thioredoxin and a
protein of interest, in this case P501S(aa55-553). A claimed method
of producing a recombinant protein of interest involves: culturing
a host cell (preferably E. coli) under conditions which allow
for co-expression of the triple fusion and a ubiquitin-specific
endoprotease (especially UBPI from Saccharomyces cerevisiae);
and recovering the recombinant protein directly from the bacterial
cells after it has been subjected to the action of the
ubiquitin-specific endoprotease in vivo. In the present case,
a p501-like protein of 509 amino acids is generated. The
recombinant protein can used as a vaccine for cancer therapy.
XX
SQ Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;

Alignment Scores:
Pred No.: 0 Length: 2133
Score: 501.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.60% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABA91283 (1-2133)
Oy 53 MetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGly 72
Db 604 ATGACCATGGTGTGGGCATTGGTCCAGTGTGGGCCCTGCTGTGTCCTCCGCTCCTAGGC 663
Oy 73 SerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeu 92
Db 664 TCAGCCAGTGACCACTGGCGTGGACGCTATGGCGCCGCCCTTCATCTCGGCACTG 723
Oy 93 SerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeu 112
Db 724 TCCCTGGGCATCCTGCTGAGCCTCTTCTCATCCAGGCGCGGCTGCTGCTAGCAGGGCTG 783
Oy 113 LeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeu 132
```

Db 784 CTGTGCCCCGGATCCACAGGCCCTGGAGCTGGCACTGCTCATCTGGGGCTGGGGCTGCTG 843
Qy 133 AspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArg 152
Db 844 GACTTCTGTGGCCAGGTGTCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGG 903
Qy 153 AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGly 172
Db 904 GACCCGGACCACTGTGCGCAGGCCCTACTCTGTCTATGCTTCTATGATCATGCTTGGGGC 963
Qy 173 CysLeuGlyTyrIleuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeu 192
Db 964 TGCTGGGCTACCTCTGCTGCCATGACTGGGACACAGTGCCTGGCCCTACCTG 1023
Qy 193 GlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAla 212
Db 1024 GGCACCCAGAGAGTGCCTCTTTGGCTGCTCACCTCATCTTCTCACCTGCGTAGCA 1083
Qy 213 AlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGlyLeu 232
Db 1084 GCCACACTGCTGCTGGCTGAGGAGGAGGCTGGGGCCCCACCGAGCCAGCAGAGGGCTG 1143
Qy 233 SerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsn 252
Db 1144 TCGGGCCCCCTCTGTGCGGCCCACTGCTGTCTCCATGCGGGGCCGCTTGGCTTTCCGGAAC 1203
Qy 253 LeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArg 272
Db 1204 CTGGGGCCCTCTTCCCGGCTGACACAGCTGTGCTGCCGATGCCCGCACCTGCGC 1263
Qy 273 ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyr 292
Db 1264 CGGCTCTTCTGCTGCTGAGCTGTCAGCTGTCATGGCCTCATGACCTTACCGCTGTTTAC 1323
Qy 293 ThrAspPheValGlyGluClyLeuTyrGlnGlyValProArgAlaGluProGlyThrGlu 312
Db 1324 ACGGATTTCTGGGGAGGGGCTGTACACAGGCGGTGCCAGAGCTGAGCGGGCACCGAG 1383
Qy 313 AlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCys 332
Db 1384 GCCCGAGACACTATGATGAAGCGGTTCGGATGGCAGGCTGGGGCTGTCTCTGCACTGC 1443
Qy 333 AlaIleSerLeuValIlePheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArg 352
Db 1444 GCATCTCTCCCTGCTTCTCTCTGCTGATGGACCGGCTGGTCAGCGATTCCGCACCTCGA 1503
Qy 353 AlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 1504 GCAGTCTATTTGGCCAGTGTGGCAGCTTTCCTGTGGCTGCCGGTGCACATGCTGTGCC 1563
Qy 373 HisSerValAlaValIleThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeu 392
Db 1564 CACAGTGTGGCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTTCACTTCTCAGCCCTG 1623
Qy 393 GlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuPro 412
Db 1624 CAGATCTGCCCTACACACTGGCCCTCCCTCTACCACCGGGAGAGCAGGTGTCTCTGCC 1683
Qy 413 LysTyrArgGlyAspThrClyAlaSerSerGluAspSerLeuMetThrSerPheLeu 432
Db 1684 AAATACCGAGGGGACACTGGAGGTGCTAGCAGTAGGAGAGCCTGATGACCACTTCTCTG 1743
Qy 433 ProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGly 452
Db 1744 CCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACAGTGGGTGCTGGAGGAGTGGC 1803
Qy 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472
Db 1804 CTGCTCCCACTCCACCGCGCTCTGCGGGGCTCTGCTGTGTGTCTCTCTGCTGTGTGTG 1863
Qy 473 ValValGlyGluProThrClnAlaArgValValProGlyArgGlyIleCysLeuAspLeu 492
Db 1864 GTGGTGGGTGTAGCCACCGAGGCCAGGGTGGTTCGGGGCCGGGGCATCTGCTGTGACCTC 1923

Qy 493 AlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySer 512
Db 1924 GCATCTCTGGATAGTGCCTTCTCTGCTGCCAGTGGCCCCATCCCTGTTTATGGGCTCC 1983
Qy 513 IleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeu 532
Db 1984 ATTGTCCAGCTCAGCAGTCTGTCTACTGTCTATATGTTGCTCTGCCGAGCCCTGGGCTCG 2043
Qy 533 ValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSer 552
Db 2044 GTCGCATTTACTTTGCTACAGGTAGTATTGTGACAGCGACTTGGCCAAATACTCA 2103
Qy 553 Ala 553
Db 2104 GCG 2106
RESULT 16
ID ABA91284
XX ABA91284 standard; DNA; 1593 BP.
AC ABA91284;
XX 08-APR-2002 (first entry)
DT 08-APR-2002 (first entry)
DE Thioredoxin-ubiquitin-P501S(aal-320)His triple gene fusion.
KW Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
KW cancer; vaccine; therapy; human; gene; ds.
XX Chimeric - Homo sapiens.
OS Chimeric - Escherichia coli.
FH Key Location/Qualifiers
FT CDS 1..1593
FT /tag= a
FT /trans_except= (pos:607..609,aa:Xaa)
FT /note= "Xaa not given in amino acid sequence of
Figure 12b (AAM50662), which has a Val
residue at amino acid position 208 not
not encoded by the present sequence"
XX WO200200892-A1.
PN 03-JAN-2002.
PD 19-JUN-2001; 2001WO-EP06952.
XX 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
PA Cabezón Silva TEV, Delisse AEF;
PI WPI; 2002-147888/19.
XX P-PSDB; AAM50662.
DR Novel DNA sequence encoding triple fusion protein comprising ubiquitin
PT fused between thioredoxin and polypeptide of interest, useful for
PT producing recombinant polypeptide of interest suitable for medicinal
PT use
XX Example 8; Fig 12b; 87pp; English.
PS The present sequence is that of a triple gene fusion comprising,
CC from the 5' end, the trxA thioredoxin gene from Escherichia coli,
CC the human ubiquitin coding sequence, the prostate antigen P501S
CC (amino acids 1-320) coding sequence, and DNA encoding a histidine
CC tail. The triple fusion was constructed in plasmid pRIT15115,
CC under the control of the lambda pL promoter. Triple fusion
CC protein (see AAM50662) was produced in E. coli G1724 transformants.
CC This is an example of the production of triple fusion proteins of

CC the invention comprising ubiquitin fused between thioredoxin and a
CC protein of interest, in this case p501S(aal-320). A claimed method
CC of producing a recombinant protein of interest involves: culturing
CC a host cell (preferably *E. coli*) under conditions which allow
CC for co-expression of the triple fusion and a ubiquitin-specific
CC endoprotease (especially UBP1 from *Saccharomyces cerevisiae*);
CC and recovering the recombinant protein directly from the bacterial
CC cells after it has been subjected to the action of the
CC ubiquitin-specific endoprotease in vivo. In the present case,
CC expression was controlled by addition of tryptophan. The
CC recombinant protein can be used as a vaccine for cancer therapy.

XX Sequence 1593 BP; 308 A; 472 C; 461 G; 352 T; 0 other;

Alignment Scores:

Pred. No.: 3 93e-288 Length: 1593
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABA91284 (1-1593)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 604 ATGGTCCAGAGGCTGTGGGTGAGCGCGCTGCTGGCGCACCGAAGCCAGCTCTGTG 563
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyLeuThrTyrValPro 40
DB 664 GTCAACCTGCTAACCTTTGGCGTGGAGGTGCTTTGGCGCGAGGCATCACCTATGTGCG 723
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyLeGly 60
DB 724 CCTCTGCTGCTGGAGTGGGGTAGAGGAGAGTTCATGACCATGGCTGGCGCATTTGGT 783
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 784 CCAGTGTGGGCTGTGCTGTCTCCGCTCTCTAGGCTAGCCAGTACCAGCTGGCGTGA 843
QY 81 ArgTyrGlyArgArgArgProPheLeuTrpAlaLeuSerLeuGlyLeuLeuSerLeu 100
DB 844 CGCTATGGCGCGCGCGCGCTTCTCTGTGGCACCTGCTTGGGCATCCTGTGAGCCTC 903
QY 101 PheLeuLeuProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 904 TTTCATCCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCCAGGCCCTG 963
QY 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 964 GAGCTGGCACCTGCTATCTCTGGCGTGGGGCTGCTGGACTCTGTGGCAGGTGTGCTTC 1023
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 1024 ACTCCACTGGAGCGCTGCTCTCTACCTCTTCCGGGACCGCACCTGTGCGCAGGCC 1083
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 1084 TACTGTGTATGCTTCATGATCATGCTTGGGGCTGCCTGGGTACCTCCCTGCTGCC 1143
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
DB 1144 ATTGACTGGACACAGTGCCTTGGCCCCCTTACCTTGGGCACCGAGAGGTGCTCTTT 1203
QY 201 GlyLeuLeuThrLeuLeuPheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 1204 GGCCTGCTCACCTCATCTTCTACCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 1263
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 1264 GCAGGCTGGGCCCCACCGAGCAGAGAGGGCTGTGCGGCCCTCTCTGTGCGCCCCAC 1323
QY 241 CysCysProCysArgAlaAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260

DB 1324 TGCTGTCCATGCGGCGCGCTTGGCTTCCGGAACCTGGCGCCCTGCTTCCCGGCTG 1383
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
DB 1384 CACCAGCTGTGCTGCCGATGCCGCCGCCCTGCCCGGCTCTTGGCTGAGCTGTGC 1443
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
DB 1444 ACCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCTGGCGCAGGGCTG 1503
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
DB 1504 TACCAGGGCGTCCCGAGAGCTGAGCGCGGCGCACCGGAGCCGAGACACTATGATGAAGC 1563
RESULT 17
AAS64040
ID AAS64040 standard; cDNA; 4034 BP.
XX
AC AAS64040;
XX
XX 29-JAN-2002 (first entry)
XX
DE Human prosate cDNA P553S splice variant #3.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US099919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick JS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 483-484; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.

SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

Alignment Scores:
Pred. No.: 9.75e-288 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS64040 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 281 ATGGTCAGAGGCTGTGGTGTAGCGCGCTGCTGCGGCACCGAAGCCAGCTTGTGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
DB 341 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGACGACATCACTATGTGCCG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGlyPheMetThrMetValLeuGlyIleGly 60
DB 401 CCTCTGCTGTGAGTGGGGGTAGAGGAGAGTTATGACCATGTGTGCTGGGCATTGGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 461 CCAGTGTGGCCCTGGTGTGTCGCCGCTCTAGGCTCAGCCAGTGCACCTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 521 CGTATATGGCCGCGCGCGCTTCATCTGGGCACCTGTCTGGGCATCTCTGTGAGCCCT 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 581 TTTCTCATCCAGAGCGCGCTGCTAGCAGGCTGCTGTGCCCGATCCAGCCGCCCTG 640
QY 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 641 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGCTGTGACTTCTGTGGCCAGGTGTGCTTC 700
QY 141 ThrProLeuAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 701 ACTCCACTGGAGCGCTGCTCTGACCTCTCCGGACCGGACCACTGTCCGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 761 TACTCTGTCTATGCTTCATGATCAGTCTTGGGGCTGCTGTGGCTACCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
DB 821 ATTGACTGGGACACCACTGCTGCTGGCCCTTACCTGGCCACCCAGGAGGAGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 881 GGCTGCTCACCTCATCTTCCTCACCTGCTAGCAGCCACACTGTGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGGCCCTCTCTGTGTGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1001 TGCTGTCCATGCGCGGCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1061 CACACAGCTGTGTGCCGATATGCCCGCACCTCTGCCGCGCTCTTCGTGGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
DB 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCTGTGGCGAGGCGTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320

DB 1181 TACCAGGGCTGCCAGAGCTGAGCCGGCAGCGGACCGGACACTATGATGAGGT 1240

RESULT 18

AAH93868

ID AAH93868 standard; cDNA; 4034 BP.

XX AC AAH93868;

XX DT 04-OCT-2001 (first entry)

XX P553S cDNA splice variant P553S-10.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

KW cytostatic; gene therapy; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200151633-A2.

XX 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US01574.

XX PR 14-JAN-2000; 2000US-0483672.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Fanger GR, Day CH, Retter MW, Stoik JA, Skeiky YAW;

PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for

PT diagnosing, monitoring and treating prostate cancer in a patient and

PT for use in vaccines -

XX Claim 1; Page 460-461; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

Alignment Scores:

Pred. No.: 9.75e-288 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAH93868 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

DB 281 ATGGTCAGAGGCTGTGGTGTAGCGCGCTGCTGCGGCACCGAAGCCAGCTTGTGCTG 340

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40

Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCAGCATCACCTATGTGGCG 400
Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyLeGly 60
Db 401 CCTCTGCTGCTGAAGTGGGGGTAGAGAGAGTTCTATGACCATGGTCTGGGCATTGGT 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGGCTGGGCTGTCTGTGCTCCCGCTCTAGCTCAGCCAGTGACCACTGGCGTGA 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCTCTGGGCACTGTCTTGGGCATCTGTGAGCCCTC 580
Qy 101 PheLeuIleProAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTCTCATCCCAAGGCGCGGTGGCTAGCAGGGCTGTGTGCGCGGATCCCAAGGCCCTG 640
Qy 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGTGACTTCTGTGGCAGGTGTGCTTC 700
Qy 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGACCACTGTGCGCAGGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuProAla 180
Db 761 TACTCTGTCTATGCCCTCATGATAGTCTTGGGGGCTGCTGGGCTACTCTGCTGCTGCC 820
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 821 ATTGACTGGACACAGTGCCTGCGCCCTACCTGGGCGCCACCCAGGAGGTGCTCTTT 880
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCTGTCTACCTCATCTTCTCACCTGCGGTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCGCCACCGACGACGAGAGGCTGTGCGCCCTCTCTGTGCGCCAC 1000
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATCGCGGCGCGCTTGCTTCCGGAACCTGGGCGCCCTCTCCCGGCTG 1060
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTGCGCGCATGCCCGCACCTGCGCGGCTCTTCTGCTGGCTGAGCTGTGC 1120
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 ACCTGGATGGCACTCATGACCTTACCGTGTGTTACAGGATTTGCTGGGCGAGGGGCTG 1180
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGCGGTGCCAGAGTGGCGGCGCACCGGAGCCCGGAGACACATGATGAGGT 1240

RESULT 19
ABL95411
ID ABL95411 standard; cDNA; 4034 BP.
XX
AC ABL95411;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P53S splice variant SEQ ID NO 704.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX

US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 98US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
PS Claim 1; SEQ ID NO 704; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
Alignment Scores:
Pred. No.: 9,75e-288 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABL95411 (1-4034)		DT	29-JAN-2002 (first entry)
QY	1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	XX	Human /M. tuberculosis fusion protein RAL2-P50IS-E2 cDNA.
Db	281 ATGGTCACAGGCTGGGGTGGAGCGCCCTGCTGGGCACCGAGAGCCAGCTCTTGCTG 340	XX	Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
QY	21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40	OS	Chimeric - Homo sapiens.
Db	341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGACAGCATCACCTATGTGCGG 400	XX	Chimeric - Microbacterium tuberculosis.
QY	41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60	XX	WO200173032-A2.
Db	401 CCTCTGCTGCTGAAGTGGGGTAGAGGAGAGTTTCATGACCATGGTGTGGGCATTGGT 460	PD	04-OCT-2001.
QY	61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80	XX	27-MAR-2001; 2001WO-US09919.
Db	461 CCAGTCTGGGCTGTGCTGTGCGCTCCCTAGGCTCAGCCAGTACACCATGGCGTGA 520	PR	27-MAR-2000; 2000US-0536857.
QY	81 ArgTrpGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuSerLeu 100	PR	09-MAY-2000; 2000US-0568100.
Db	521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCCTGCTGAGCCCTC 580	PR	12-MAY-2000; 2000US-0570737.
QY	101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120	PR	13-JUN-2000; 2000US-0593793.
Db	581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCTG 640	PR	27-JUN-2000; 2000US-0605783.
QY	121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140	PR	10-AUG-2000; 2000US-0636215.
Db	641 GAGTGGCACTGCTCATCTCGGGGTGGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 700	PR	29-AUG-2000; 2000US-0651236.
QY	141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160	PR	06-SEP-2000; 2000US-0657279.
Db	701 ACTCCACTGGAGCCCTGCTCTGACCTCTTCCGGGACCCGACCATGTGCCAGGCC 760	PR	02-OCT-2000; 2000US-0679426.
QY	161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180	PR	10-OCT-2000; 2000US-0685166.
Db	761 TACTCTGTATGCCTTCATGATCATGCTTGGGGGTGCTGGGTACCTCTGCTGCTGCC 820	XX	(CORI-) CORIXA CORP.
QY	181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200	XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
Db	821 ATTGACTGGGACACCATGCTGCTGGCCCTTACCTGGGCACCCAGAGGAGTCCCTTT 880	PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
QY	201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220	PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
Db	881 GGCTGCTCACCTCATCTTCCTACCTGCTGAGCAGCCACACTGCTGTGCTGAGGAG 940	XX	WPI; 2001-639232/73.
QY	221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240	DR	P-PSDB; AAU69907.
Db	941 GCAGCGCTGGGCCCCACCGAGCCAGAGAGGCTGTGCGCCCTCTCTTGTGCGCCAC 1000	XX	New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer - Example 17; Page 542-543; 579pp; English.
QY	241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyValAlaLeuProArgLeu 260	CC	The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
Db	1001 TGCTGTCCATGCGGGCGCGCTGGCTTTCGGAACCTTGGCGCGCTCTCCCGGGCTG 1060	XX	Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
QY	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	Alignment Scores:	
Db	1061 CACCACTGTGCTGGCGATGCCCGCACCTTACCTGGCGGCTCTTGTGGCTGAGTGTGC 1120	Pred. NO.:	3.85e-235 Length: 1203
QY	281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGlyLeu 300	Score:	263.00 Matches: 263
Db	1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTCTGTGGCGAGGGCTG 1180	Percent Similarity:	100.00% Conservative: 0
QY	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTrpAspGluGly 320	Best Local Similarity:	100.00% Mismatches: 0
Db	1181 TACCAGGGCGTCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTATGATGAAGGT 1240	Query Match:	47.56% Indels: 0
RESULT 20		DB:	22 Gaps: 0
ID	AA564153	US-09-593-793A-113 (1-553) x AA564153 (1-1203)	
XX	AA564153 standard; cDNA: 1203 BP.	QY	36 IleThrTyrValProProLeuLeuLeuGluValGlyValGluGlyPheMetThrMet 55
AC	AA564153;	Db	412 ATCACCTATGTGCCGCCCTCTGCTGTGGAAGTGGGGTAGAGGAAGTTCATGACCATG 471
XX		QY	56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
XX		Db	472 GTGCTGGCATTTGGTCCAGTGTGGGGCTGGTGTGTGTCGCCGCTCTAGGCTCAGCCAGT 531

Db 892 GAGGAGTGGCTCTTTGGCTGTGCTACCCCTCATCTTCTCACCTGCGTAGCAGCCACATG 951
Qy 216 LeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGGAGGAGCGCTGGGGCCACCGAGCCAGAGGGCTGTGGGCCCGC 1011
Qy 236 SerLeuSerProHisCysCysProCysArgAlaAlaGluAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCTTGTGCGCCACATGCTGTCCATCGCGGGCCGCTTGGCTTCCGGAACCTGGCGGC 1071
Qy 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGGCTGCACAGCTGTGCTGCGCATGCCCGCACCTGGCGCGCTCTTC 1131
Qy 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCAGCTCATGACCTTCACGCTGTTTACACGGATTTC 1191
Qy 296 ValGlyGlu 298
Db 1192 GTGGCGAG 1200

RESULT 22

ABL95524

ID ABL95524 standard; cDNA; 1203 BP.

XX ABL95524;

AC ABL95524;

XX 19-JUL-2002 (first entry)

DE Ra12-P501S-E2 construct cDNA sequence SEQ ID NO 851.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;

KW gene therapy; gene; ss.

XX Chimeric - Mycobacterium tuberculosis.

OS Chimeric - Homo sapiens.

XX US2002022248-A1.

PN 21-FEB-2002.

XX 12-JAN-2001; 2001US-0759143.

XX 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

PR 09-FEB-1998; 98US-0020956.

PR 25-FEB-1998; 98US-0030607.

PR 14-JUL-1998; 98US-0115453.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 99US-0232149.

PR 09-APR-1999; 99US-0288946.

PR 13-JUL-1999; 99US-0352616.

PR 12-NOV-1999; 99US-0439313.

PR 18-NOV-1999; 99US-0443686.

PR 14-JAN-2000; 2000US-0483672.

PR 27-MAR-2000; 2000US-0536857.

PR 09-MAY-2000; 2000US-0568100.

PR 12-MAY-2000; 2000US-0570737.

PR 13-JUN-2000; 2000US-0593793.

PR 27-JUN-2000; 2000US-0605783.

PR 10-AUG-2000; 2000US-0636215.

PR 29-AUG-2000; 2000US-0651236.

PR 06-SEP-2000; 2000US-0657279.

PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.

XX (XUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISK/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX Example 17; SEQ ID NO 851; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 3,85e-235 Length: 1203
Score: 283.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 24 Gaps: 0
US-09-593-793A-113 (1-553) x ABL95524 (1-1203)
Qy 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGluLysPheMetThrMet 55
Db 412 ATCACCTATGTCCGCTCTGCTGTGGAAGTGGGGTAGAGAGAAGTTCATGACCATG 471
Qy 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCATTGGTCCAGTGTGGGCTGTGTGTCTCCCTCCTAGGCTCAGCCAGT 531
Qy 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCGTGGAGCTATGGCGCGCGCGCTTCATCTGGGCACTGTCTTGGGC 591
Qy 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCTGCTGAGCCTCTTCTTCATCCAGGCGCGGTGGCTAGCAGGCTGTGTGCCG 651
Qy 116 AspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCGCTGAGCTGCGCTGCTATGCTGGGCTGGGCTGTGACTTCTGT 711
Qy 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GGCCAGGTGTGTTCACTCCACTGGAGGCGCTGCTCTGACCTCTCCGGGACCGGAC 771
Qy 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGCGCAGGCTTACTCTCTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 831
Qy 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACCTCTCTGCTGCCATTGACTGGGACACAGTGGCGCTGGCGCTTACCTGGGCACTCCAG 891


```
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
    |||||
Db 892 GAGGAGTGCTCTTGGCCGTCTACCCCTCATCTCTCTACCTGGTAGCAGCCACACTG 951

QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
    |||||
Db 952 CTGGTGGCTGAGAGGACGCTGGGCCCCACCGAGCAGCAGAGGGCTGTGCGGCCCC 1011

QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
    |||||
Db 1012 TCCCTGTGCCCACTGCTGTCCATGCCGGGCCCTTGGCTTCCTCGGAACCTGGGCGCC 1071

QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
    |||||
Db 1072 CTGCTTCCCGCTGCACACAGCTGTGCTGCCGATGCCCGCACCTGCGCGGCTCTTC 1131

QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTrpThrAspPhe 295
    |||||
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTC 1191

QY 296 ValGlyGlu 298
    |||||
Db 1192 GTGGGCGAG 1200

RESULT 23
AAD05230
ID AAD05230 standard; cDNA; 3878 BP.
XX
AC AAD05230;
XX
DT 18-JUL-2001 (first entry)
DE Human secreted protein-encoding gene 11 cDNA clone HWBARI4, SEQ ID NO:21.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnery; binding partner identification;
KW gene therapy; ss.
XX
OS Homo sapiens.
FX
FH Key Location/Qualifiers
CDS 152..1267
    /*tag= a
    /product= "Human secreted protein"
    /transl_except= (pos:209..211, aa:xaa)
    /note= "Xaa corresponds to any of the naturally occurring
    L-amino acids"
    sig_peptide 152..295
    /*tag= b
    mat_peptide 296..1264
    /*tag= c
    /product= "Mature human secreted protein"
XX
WO200134629-A1.
PN
XX
PD 17-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US30654.
XX
PR 12-NOV-1999; 99US-0164835.
PR 27-JUL-2000; 2000US-0221142.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;
```

XX

DR WPI; 2001-308779/32.

P-PSDB; AAE01362.

XX

New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or preservative -

XX

PS Claim 1; Page 388-389; 490pp; English.

XX

AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode. AAE01415-AAE01433 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA).

CC The present sequence represents a human secreted protein-encoding cDNA of the invention.

XX

SQ Sequence 3878 BP; 709 A; 1164 C; 1044 G; 951 T; 10 other;

Alignment Scores:

Pred No.:	1,21e-234	Length:	3878
Score:	263.00	Matches:	263
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
DB:	22	Gaps:	0

US-09-593-793A-113 (1-553) x AAD05230 (1-3878)

QY

58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77

Db

245 GGCATTGGTCCAGTCTGGGCTGTGTGTCTCCCGCTCTAGCTAGCCAGTGACCAC 304

QY

78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97

Db

305 TGGCGWGGACGCTATGGCCGCCGCCCTTCATCTCTGGGCACCTCTCTGGGCATCCTG 364

QY

98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117

Db

365 CTGAGCCCTCTTTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 424

QY

118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137

Db

425 AGGCCCCGTGGAGCTGGCACTCTCATCTCTGGCGCTGGGGCTGCTGGACTTCTGTGGCCAG 484

QY

138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157

Db

485 GTGTGCTTCACTCCACTGGAGGCCCTGTCTCTACCTCTTCCCGGACCCCGACCATGTG 544

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
OS Homo sapiens.
XX US2002022248-A1.
PN 21-FEB-2002.
XX 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 09-SEP-2000; 2000US-0651236.
PR 26-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX Claim 1; SEQ ID NO 702; 87pp; English.
PS
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
SQ Alignment Scores:

Pred. No.: 1.52e-234 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 24 Gaps: 0
US-09-593-793a-113 (1-553) x ABL95409 (1-4894)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1311 GGCATTGGTCCAGTGTGGCCCTGTGTGTCGCCGCTCCTAGGCTCAGCCAGTACCAC 1370
QY 78 TrpA:qGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1371 TGGCGTGGACGCTATGGCCGCCGCCCTTCATCTGGGCACTGTCTTGGGCATCTCG 1430
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProaspPro 117
Db 1431 CTGAGCCTCTTTCTCATCCAAAGGCCGGCTGGCTAGCAGGGCTGTCTGTCCCGGATCCC 1490
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1491 AGGCCCTGGAGCTGGCACTGCTCATCTGGCGGGGCTGCTGCACTTCTGTGCCAG 1550
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProaspHisCys 157
Db 1551 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGACCTTCTCCGGGACCCGACCACTGT 1610
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1611 CGCCAGGCTACTGTCTATGCCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTC 1670
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
Db 1671 CTGCTGCCATTGACTGGGACACCACTGCCCTGCCCTGCTGCTGGCACCAGGAGGAG 1730
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1731 TGCTCTTTGGCTGCTCACCTCATCTTCTCCTCACCTGCTAGCAGCACCACTGTCTGTG 1790
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1791 GGTAGGAGGAGCGCTGGGCCACCCAGCAGCAGCAGAGGGCTGTCGGCCCTCTCTTG 1850
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1851 TCGCCCCACTGCTGTCCATGGCGGGCCGCTTGGCTTTCCGGAACTGGGCCCTCTT 1910
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1911 CCCCAGCTGCACCACTGTGTGTCGCCGATGCCGCCACCTGCGCGGCTCTTCTGTGGCT 1970
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGC 2030
QY 298 GluGlyLeuTyrGlnClyValProArgAlaGluProGlyThrGluAlaArgHisTyr 317
Db 2031 GAGGGGCTGTACCAGGGCTGCCAGAGCTAGCGGGGACCGAGGGCCCGGAGACACTAT 2090
QY 318 AspGluGly 320
Db 2091 GATGAAGGT 2099
RESULT 27
AAS64041
ID AAS64041 standard; cDNA: 6976 BP.
XX
AC AAS64041;
XX
DT 29-JAN-2002 (first entry)
XX

DE Human prostate cDNA P553s splice variant #4.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
FA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR P-PSDB; AAU69873.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 484-486; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Alignment Scores:
Pred. No.: 2.15e-234 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS64041 (1-6976)

Qy 58 GlylleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGGCTGGGGCTGGTCTGTCTCCCGCTCTAGGCTCAGCCAGTGACCAC 1261
Qy 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCGTGGACCGCTATGGCCCGCCGGCCCTTCATCTGGGCACTGTCTTGGGCATCCTG 1321
Qy 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
XX

Db 1322 CTGAGCCTCTTTCTCATCCCAAGGCGCGGTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 1381
Qy 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
XX
Db 1382 AGGCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1441
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
XX
Db 1442 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCGGACCACCTGT 1501
Qy 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
XX
Db 1502 CGCCAGGCTACTGCTGTATGCTTTCATGATCATGCTTGGGGCTGCTGGGTACCTC 1561
Qy 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
XX
Db 1562 CTGCTGCCATTTGACTGGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
Qy 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
XX
Db 1622 TGCCTCTTTGGCCTGCTCACCTCATCTTCTCACCTGCTGCTGCTGCTGCTGCTGCTG 1681
Qy 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
XX
Db 1682 GCTGAGGAGGAGCGCTGGGCCCCACGAGCAGCAGAGGCTGTGGGCCCTCCTTG 1741
Qy 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
XX
Db 1742 TCGCCCTCTTGGCCTGCTCACCTCATCTTCTCACCTGCTGCTGCTGCTGCTGCTGCTG 1801
Qy 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
XX
Db 1802 CCCCGGCTGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1861
Qy 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrLeuPheThrAspPheValGly 297
XX
Db 1862 GAGCTGTGACGCTGGATGGCACTCATGACCTTACGCTGTTTACACGGAATTCGTGGGC 1921
Qy 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyr 317
XX
Db 1922 GAGGGGCTGTACCAAGGGCGTGGCCAGAGCTGAGCGGGGACCGGAGGAGGAGACACTAT 1981
Qy 318 AspGluGly 320
XX
Db 1982 GATCAAGGT 1990
RESULT 28
AAH93869
ID AAH93869 standard; cDNA; 6976 BP.
XX
AC AAH93869;
XX
DT 04-OCT-2001 (first entry)
XX
DE P553s cDNA splice variant P553S-6.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;

PI Wang A, Meagher MJ;

DR WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -

XX Claim 1; Page 461-463; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Alignment Scores:

Pred. No.: 2,15e-234 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAH93869 (1-6976)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1202 GGCATTGGTCCAGTGTGGCGCTGCTGTGTCGCCGCTCCTAGGCTAGCCAGTACCCAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1262 TGGCGTGGACGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCCTGGGCACTCTG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
DB 1322 CTGAGCCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGGCTGCTGTGCCCGGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
DB 1382 AGGCCCTTGGAGCTGGCACTGCTCATCTGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
DB 1442 GTGTGCTTCACTCCACTGAGGCGCTGCTCTGACCTTCTCGGGACCCCGGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
DB 1502 CGCCAGGGCTACTCTGTCTATGCCCTCATGATCATAGTCTTGGGGGCTGCTGGGTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
DB 1562 CTGCGCTGCCATTGATGGACACCACTGCCCTGGCCCCCTACCTGGGCACTCCAGGAGGAG 1621
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
DB 1622 TGCCCTTTTGGCGCTGCTCACCGCTCATCTCTCCTACCTGCTAGCAGCCACACTGCTGTG 1681
QY 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
DB 1682 GCTGAGGAGGAGCGCTGGGCCCCACCGAGCCAGCAGGAAGGCGTGTGCGGCCCTTCCTTG 1741

QY 238 SerProHisCysCysProCysArgAlaArgIleuAlaPheArgAsnLeuGlyAlaLeuLeu 257
DB 1742 TCGCCCCACTGCTGTCCATGCGGGCGCTGTGCTTTCCGGAACCTGGCGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAla 277
DB 1802 CCGCGGCTGCAACAGCTGTGCTGCGCATGCCCGCACCCCTGCGCGGCTCTTCTGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
DB 1862 GAGCTGTCCAGCTGGATGGCACTCATGACCTTCAGGCTGTTTACACGATTTCTGTGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
DB 1922 GAGGCGCTGTACCAAGGCGCTGCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTAT 1981
QY 318 AspGluGly 320
DB 1982 GATGAAGCT 1990
RESULT 29
ABL95412
ID ABL95412 standard; cDNA; 6976 BP.
XX
AC ABL95412;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P553S splice variant SEQ ID NO 1705.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
XX
XX Claim 1: SEQ ID NO 705; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
SQ
Alignment Scores:
Pred. NO.: 2,15e-234 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 24 Gaps: 0
US-09-593-793a-113 (1-553) x ABL95412 (1-6976)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGTGGCTGGCTGTGTCTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCTGGACGCTATGGCGCGCGCGCTTCATCTGGGCACCTCTCTGGGCATCTG 1321
QY 98 LeuSerLeuPheLeuIleProAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1322 CTGAGCCTCTTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTGGAGCTGGCACTGCTCATCTGGCGTGGGGCTGTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCACTCCACTGGAGCCCTGCTCTGACCTCTTCCGGACCCGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCGCTACTGTCTATGCTTATGATCATGCTCTGGGGGCTGGCTGGGCTACCTC 1561
QY 178 LeuProAlaIleAspTTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
Db 1562 CTGCTGCGCATGTAGTGAGACACAGTGCCTGGCCCTACCTGGGACCCAGAGGAG 1621
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1622 TGCCTCTTTGGCGTCTCACCTCATCTTCTCCTACCTGGCTAGCAGCCACACTGCTGGTG 1681
QY 218 AlaGluGluAlaLeuLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1682 GCTGAGGAGGCGGCTGGGGCCCAACCGAGGAGGAGGCTGTGGGCCCTCTCTTGTG 1741

QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1742 TCGCCCACTGCTGCTCCATGCGGGCCGCTGGCTTCCGAACTGGGGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1802 CCCCGGCTGCACAGCTGTGCTGCGCATGCCCGCACCCCTGCGCGGCTCTTCTGGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGACGCTGGATGGCACTCATGACCTTCAGCTGTTTACACGATTTTCGTGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGCTGTACAGGGGCTGCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTAT 1981
QY 318 AspGluGly 320
Db 1982 GATGAAGGT 1990
RESULT 30
AAC64928
ID AAC64928 standard; DNA; 2133 BP.
XX
XX AAC64928;
AC
XX
DT 07-FEB-2001 (first entry)
XX
XX Human prostate-related PS108 partial coding sequence SEQ ID NO: 16.
DE
XX
XX Human; prostate cancer; PS108; antibody; tumour; metastasis; ds.
KW
XX
XX Homo sapiens.
OS
XX
XX US6130043-A.
PN
XX
PD 10-OCT-2000.
XX
XX
PF 01-MAY-1998; 98US-0071710.
XX
XX
PR 02-MAY-1997; 97US-0850713.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
PI Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
PI Kratochvil JD, Russell JC, Hodges SC;
XX
XX WPI; 2000-655655/63.
DR
XX
PT Methods for detecting target prostate-specific polynucleotides or
PT diseases of the prostate (e.g. prostate cancer), comprising detecting
PT the presence of any of PS108 nucleic acid sequences in a test sample -
XX
XX
PS Claim 1; Column 77-80; 55pp; English.
XX
XX The present invention is related to a number of partial coding and
CC protein sequences for the human prostate tissue protein PS108. These
CC sequences can be used in the diagnosis and prognosis of prostate
CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.
XX
XX Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 1,92e-227 Length: 2133
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 21 Gaps: 0

```
US-09-593-793a-113 (1-553) x AAC64928 (1-2133)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGGTGCCAGAGCTGAGCCGGGACCGAGCGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCCGATGGCAGCCCTGGGCTGTTCTCCAGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGTGTCAGCGGATTCGGCACTCGAGCAGTCTATTTTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGGCCGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCTCCCTTACCACCGGAGAGCAGAGTGTCTCTGCCCAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGTAGCAGTGAGACAGCTGTATGACCACTTCTCTCCAGGCCCTAAGCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTCCCTTAATGGACACCTGGGTGTGGAGCAGTGGCTGCTCCACCTCCACCC 481
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 482 GGCTCTGTGGGGGCTCTGCTCCCTGTATGTCTCCGTACGTGTGGTGGGTGAGGCCACC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGGTGTTCGGGGCGGGGCATCTGCTCGGACCTCGCCATCTCGATAGTGCC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCTCTGTCTCCAGGTGGCCCATCTCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCCTATATGTTGTCTCCGAGGCCCTGGGTCTGTGGTCCCATTTACTTTGCT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTGTGACAAAGACGACTTGGCCAAATACTCAGCG 766
RESULT 31
ID AAS07155
XX AAS07155 standard; cDNA; 2133 BP.
AC AAS07155;
XX
DT 23-OCT-2001 (first entry)
XX
DE Prostate gene PS108-specific cDNA (EST) consensus sequence.
XX
KW Prostate; PS108; immunogen; drug screening; image localisation;
KW diagnostic; therapeutic; prostate tissue disease; cancer; metastasis;
KW expressed sequence tag; EST; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 1..799
```

/*tag= a
/product= "Prostate-specific protein PS108"

US6252047-B1.
26-JUN-2001.
15-MAR-2000; 2000US-0525397.
01-MAY-1998; 98US-0071710.
02-MAY-1997; 97US-0850713.
(ABBO) ABBOTT LAB.
Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
Russell JC, Stroupe SD, Yu H;
WPI; 2001-424488/45.
P-PSDB; AAU04205.
Novel PS108 polypeptide useful in assays for detecting antibodies to
prostate tissue, and as immunogens to produce PS108 antibodies -
Example 1; Fig 1; 55pp; English.
The sequence represents the prostate gene PS108-specific expressed
sequence tag (EST) consensus sequence. The sequence was produced from
overlapping PS108 ESTs sequences to produce a full length consensus
sequence. This sequence was then used to produce PS108 polypeptides which
are useful in assays for detecting antibodies to prostate tissue, and as
immunogens to produce antibodies. The polypeptide is useful for screening
compounds which specifically bind to the polypeptide and for screening
for drugs, compounds, or any other agent which can be used to treat
diseases associated with PS108. The antibody is useful to detect, or for
image localisation of, PS108 antigen in a patient, for detecting or
diagnosing a disease or condition, as delivery agents for therapeutic
agents as well as for diagnostic tests and for screening for diseases or
conditions associated with PS108, especially cancer. The antibody is also
useful for generating chimeric antibodies for therapeutic use, for
inhibiting the biological activity of PS108, in therapy (for e.g. to
treat prostate tissue disease including prostate cancer and its
metastases), and to detect the presence of any polypeptide in a test
sample which shares one or more antigenic determinants with the PS108
polypeptide.
SQ Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;

Alignment Scores:
Pred. No.: 1.92e-227 Length: 2133
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAS07155 (1-2133)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGGTGCCAGAGCTGAGCCGGGACCGAGCGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCCGATGGCAGCCCTGGGCTGTTCTCCAGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGTGTCAGCGGATTCGGCACTCGAGCAGTCTATTTTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGGCCGTGGTG 241


```
QY 379 ThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||
Db 242 ACAGCTTCAGCGCCCTCACCGGGTTCACTTCTCAGCCCTCAGATCTGCCCTACACA 301
|||||
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||
Db 302 CTGGGCTCCCTCTACACCGGGAGAGACAGGTGTTCTGCCCAATACCGAGGGACACT 361
|||||
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
Db 362 GGAGGTGCTAGCAGTGAGACACCTTGATGACCAAGCTTCTGCCAGGCCCTAAGCCCTGGA 421
|||||
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyLysGlySerGlyLeuLeuProProPro 458
|||||
Db 422 GCTCCCTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCC 481
|||||
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
|||||
Db 482 GCGCTCTGGGGGCTCTGCCCTGTATGTCCTCGTACGTGTGGTGGGTGAGCCACCC 541
|||||
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||
Db 542 GAGGCCAGGGTGGTCCGGGCGGGGCACTGCTGGAGCTCGCCATCTGGATAGTGGC 601
|||||
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
Db 602 TTCCTGCTGCTCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAG 661
|||||
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
|||||
Db 662 TCTGTCACTGCTATATGTGTCTGCCGAGGCTGGGTGCTGGTCCCATTTACTTTGCT 721
|||||
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 722 ACACAGGTAGTATTGACAAGACGACTTGGCCAAATACTCAGCG 766
|||||
RESULT 32
AAV71181
ID AAV71181 standard; cDNA; 2152 BP.
XX
AC AAV71181;
XX
DT 12-FEB-1999 (first entry)
XX
DE Consensus sequence of the PS108 gene derived from overlapping clones.
XX
KW PS108 gene; prostate disease; benign prostatic hyperplasia; BPH;
KW prostatitis; prostatic intraepithelial neoplasia; PIN; cancer;
KW drug screening; gene therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..769
FT /*tag= a
XX
PN W098050567-AL.
XX
PD 12-NOV-1998.
XX
PF 01-MAY-1998; 98WO-US089930.
XX
PR 02-MAY-1997; 97US-0850713.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Billington-Medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 1999-034731/03.
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DR P-PSDB; AAW85068.
XX
PT New isolated prostate-specific polynucleotides - used to develop
PT products for the diagnosis and treatment of prostate diseases, e.g.
PT benign hyperplasia, prostatic or prostate cancer
XX
PS Claim 1; Fig 1A-E; 122pp; English.
XX
CC The present sequence represents the consensus sequence for a PS108
CC gene. The sequence is derived from overlapping clones AAV71166-79. The
CC clone sequences are PS108 gene-specific. They are used in the method
CC of the invention. The specification describes a method for detecting the
CC presence of a target PS108 polynucleotide in a test sample. The method
CC comprises contacting the test sample with at least 1 PS108-specific
CC polynucleotide or complement, and detecting the presence of the target
CC PS108 polynucleotide. The products can be used for detecting,
CC diagnosing, staging, monitoring, prognosticating, in vivo imaging,
CC preventing or treating, or determining predisposition to diseases or
CC conditions of the prostate such as benign prostatic hyperplasia (BPH),
CC prostatitis, prostatic intraepithelial neoplasia (PIN) and cancer. In
CC particular the products can be used in drug screening and gene therapy.
XX
SQ Sequence 2152 BP; 419 A; 622 C; 569 G; 542 T; 0 other;
Alignment Scores:
Pred. No.: 1.93e-227 Length: 2152
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 20 Gaps: 0
US-09-593-793a-113 (1-553) x AAV71181 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
|||||
Db 2 GGGCTGTACACGGGCTGCCAGAGCTGAGCGGCGGACCGAGCGCGGAGACACTATGAT 61
|||||
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheGlnCysAlaIleSerLeuValPhe 338
|||||
Db 62 GAAGGCGTTCGGATGGGACGCTGGGGCTGTCTTCGAGTGGCCATCTCCCTGCTCTTC 121
|||||
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
|||||
Db 122 TCTCTGGTTCATGACCGCGCTGTGTCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCACT 181
|||||
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
|||||
Db 182 GTGGCAGCTTTCCTGTGGCTGCCGTGCCACATGCTGCCACAGTGTGCCCGTGTG 241
|||||
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||
Db 242 ACAGCTTCAGCGCCCTCACCGGGTTCACTTCTCAGCCCTCAGATCTGCCCTACACA 301
|||||
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||
Db 302 CTGGGCTCCCTCTACACCGGGAGAGACAGGTGTTCTGCCCAATACCGAGGGACACT 361
|||||
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
Db 362 GGAGGTGCTAGCAGTGAGACACCTTGATGACCAAGCTTCTGGAGGAGTGGCTGCTCCACTCCACCC 481
|||||
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyLysGlySerGlyLeuLeuProProPro 458
|||||
Db 422 GCTCCCTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCC 481
|||||
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
|||||
Db 482 GCGCTCTGGGGGCTCTGCCCTGTATGTCCTCGTACGTGTGGTGGGTGAGCCACCC 541
|||||
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||
Db 542 GAGGCCAGGGTGGTCCGGGCGGGGCACTGCTGGAGCTCGCCATCTGGATAGTGGC 601
|||||
```

QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
Db 602 TTCTCTGCTGCCAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCTACGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
|||||
Db 662 TCCTGCTACTGCCCTATATGTTGCTGCGCAGGCTGGTCTGGTCTGCCCATTTACTTTGCT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 722 ACACAGGTAGTATTTGACAAAGCGACTTGGCCAAATACTACGCG 766
RESULT 33
AAC64927
ID AAC64927 standard; DNA; 2124 BP.
AC AAC64927;
XX
DT 07-FEB-2001 (first entry)
XX
XX Human prostate-related PS108 partial coding sequence SEQ ID NO: 15.
DE Human prostate cancer; PS108; antibody; tumour; metastasis; ds.
XX
KW Human; prostate cancer; PS108; antibody; tumour; metastasis; ds.
XX
OS Homo sapiens.
XX
XX US6130043-A.
XX
XX 10-OCT-2000.
PD
XX
XX 01-MAY-1998; 98US-0071710.
XX
XX 02-MAY-1997; 97US-0850713.
XX
XX (ABBO) ABBOTT LAB.
PA
PI Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
PI Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
PI Kratochvil JD, Russell JC, Hodges SC;
XX
XX WPI; 2000-655655/63.
DR
XX
XX Methods for detecting target prostate-specific polynucleotides or
PT diseases of the prostate (e.g. prostate cancer), comprising detecting
PT the presence of any of PS108 nucleic acid sequences in a test sample -
XX
XX Claim 1; Column 75-78; 55pp; English.
PS
CC The present invention is related to a number of partial coding and
CC protein sequences for the human prostate tissue protein PS108. These
CC sequences can be used in the diagnosis and prognosis of prostate
CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.
XX
SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:
Pred. No.: 1.19e-224 Length: 2124
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AAC64927 (1-2124)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
|||||
Db 3 CAGGGCGTCCCGACAGCTGAGCGCGGCACCGAGGCCGCGAGACACTATGATGAGCGCTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
|||||

Db 63 CGGATGGCAGCCCTGGGGCTGTTCCTCGAGTGGCCATCTCCCTGGTCTCTCTGGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
|||||
Db 123 ATGAGCCGGCTGGTGGCAGGATTTCGACACTCGAGCAGTCTATTGTGGCAGTGGGAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
|||||
Db 183 TTCCCTGTGGCTGCGGTGCCACATGCCCTGTCCACAGTGTGGCCGTGGTGACAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
|||||
Db 243 GCGGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCTCC 302
QY 402 LeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
|||||
Db 303 CTCTACACCGGAGAGCAGGTGTTCTCGCCCAAAATACCGAGGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
|||||
Db 363 AGCAGTGAGGACAGCCTGATGACACAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTC 422
QY 442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 461
|||||
Db 423 CCTAATGGACACGTGGGTGCTGGAGGCAGTGGCTGCTCCACCTCACCCGCGCTGTC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
|||||
Db 483 GGGGCTCTGCTGCTGATGTCTCCGTACGTGTGTGGTGGGTGAGCCACCGAGGCCAGG 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
|||||
Db 543 GTGTTCCGGCGCGGGGCATCTGCTGGACCTCGCCATCTCGCATAGTGGCTTCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
|||||
Db 603 TCCAGGTTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGCTACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
|||||
Db 663 GCGTATGTGTGTCGCCGAGCGCTGGGTCTGTGCGCCATTACTTTGCTACACAGGTA 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 723 GTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 758
RESULT 34
AAS07601
ID AAS07601 standard; cDNA; 2124 BP.
XX
AC AAS07601;
XX
DT 23-OCT-2001 (first entry)
XX
DE Prostate gene PS108-specific cDNA clone 17113461H.
XX
KW Prostate; PS108; immunogen; drug screening; image localisation;
KW diagnostic; therapeutic; prostate tissue disease; cancer; metastasis;
KW expressed sequence tag; EST; ss.
OS Homo sapiens.
XX
PN US6252047-B1.
XX
PD 26-JUN-2001.
XX
PF 15-MAR-2000; 2000US-0525397.
XX
PR 01-MAY-1998; 98US-0071710.
PR 02-MAY-1997; 97US-0850713.
XX
PA (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD, Yu H;
 XX WPI: 2001-424488/45.
 DR Novel PS108 polypeptide useful in assays for detecting antibodies to
 XX prostate tissue, and as immunogens to produce PS108 antibodies -
 PT Example 1; Fig 1; 55pp; English.
 PS The sequence represents the coding sequence of prostate gene PS108-
 XX specific expressed sequence tag (EST) cDNA clone 17113461H. The sequence
 CC was used along with other overlapping cDNA clones to produce a full
 CC length consensus sequence (see AAS07155). This sequence could then be
 CC used to produce PS108 polypeptides which are useful in assays for
 CC detecting antibodies to prostate tissue, and as immunogens to produce
 CC antibodies. The polypeptide is useful for screening compounds which
 CC specifically bind to the polypeptide and for screening for drugs,
 CC compounds, or any other agent which can be used to treat diseases
 CC associated with PS108. The antibody is useful to detect, or for image
 CC localisation of PS108 antigen in a patient, for detecting or diagnosing a
 CC disease or condition, as delivery agents for therapeutic agents as well
 CC as for diagnostic tests and for screening for diseases or conditions
 CC associated with PS108, especially cancer. The antibody is also useful for
 CC generating chimeric antibodies for therapeutic use, for inhibiting the
 CC biological activity of PS108, in therapy (for e.g. to treat prostate
 CC tissue disease including prostate cancer and its metastases), and to
 CC detect the presence of any polypeptide in a test sample which shares one
 CC or more antigenic determinants with the PS108 polypeptide.
 XX
 SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:
 Pred. No.: 1.19e-224 Length: 2124
 Score: 252.00 Matches: 252
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 45.57% Indels: 0
 DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS07601 (1-2124)

Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
 Db 3 CAGGCGTGCACAGCTGACCGGGACCGAGGCGGAGACACATATGATGAGGCGTT 62
 Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
 Db 63 CGGATGGCAGCCTGGGCGCTGCTCTGCAGTGCAGCCATCTCCCTGGTCTTCTCTGTC 122
 Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
 Db 123 ATGACCGGCTGGTGCACAGGATCGGCACACTCGACAGTCTATTGGCCAGTGGCAGCT 182
 Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
 Db 183 TTCCTGTGGCTGGCGTGCACATGCTGCTCCACAGTGGCGGCTGGTGCAGCTTCA 242
 Qy 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
 Db 243 GCCGCCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCC 302
 Qy 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
 Db 303 CTCATACACCGGGAGAGAGCTGTCTCTGCCCAATACCGAGGGGACACTGGAGGTGCT 362
 Qy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
 Db 363 AGCAGTGGAGACGCTGATACAGCTTCTGTCAGGCCCTAAGCCTGGAGCTCCCTTC 422
 Qy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuGlyCys 461

Db 423 CCTATGACACGCTGGGTGCTGGAGGCAGTGGCTGCCCTCCACCTCCACCGCGCTCTGC 482
 Qy 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
 Db 483 GGGGCGCTCTGGCTGTGATGTCTCCGTAGCTGTGGTGGTGGAGCCACCGAGGCCAGG 542
 Qy 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
 Db 543 GTGGTTCGGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTCTCTCTGCTG 602
 Qy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
 Db 603 TCCAGGTGGGCCCATCTGTTATGGCTCCCATTTGCCAGTCCAGCTCTGCTCACT 662
 Qy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
 Db 663 GCCATATATGGTGTGCGCCAGGCTGGGTCTGGTGGCCATTTACTTTTGTACACAGGTA 722
 Qy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
 Db 723 GTATTGACAGAGCGACTTGGCCAAATACTCAGCG 758
 RESULT 35
 AAV71180
 ID AAV71180 standard; cDNA; 2143 BP.
 XX AC AAV71180;
 AC AAV71180;
 DT 12-FEB-1999 (first entry)
 XX
 DE Clone 17113461H, the PS108 gene contig full length sequence.
 XX
 KW PS108 gene; prostate disease; benign prostatic hyperplasia; BPH;
 KW prostatitis; prostatic intraepithelial neoplasia; PIN; cancer;
 KW drug screening; gene therapy; ss.
 OS Homo sapiens.
 XX
 PN WO9805067-A1.
 PD 12-NOV-1998.
 XX
 PF 01-MAY-1998; 98WO-US08930.
 XX
 PR 02-MAY-1997; 97US-0850713.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI: 1999-034731/03.
 XX
 PT New isolated prostate-specific polynucleotides - used to develop
 PT products for the diagnosis and treatment of prostate diseases, e.g.
 PT benign hyperplasia, prostatic or prostate cancer
 XX
 PS Claim 1; Fig 1A-E; 122pp; English.
 XX
 CC The present sequence represents the full length contig of the PS108
 CC gene, as represented by clone 17113461H. This clone is the contig of
 CC overlapping clones AAV71166-79. The clone sequences are PS108
 CC gene-specific. They are used in the method of the invention. The
 CC specification describes a method for detecting the presence of a
 CC target PS108 polynucleotide in a test sample. The method comprises
 CC contacting the test sample with at least 1 PS108-specific polynucleotide
 CC or complement, and detecting the presence of the target PS108
 CC polynucleotide. The products can be used for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing or
 CC treating, or determining predisposition to diseases or conditions of
 CC the prostate such as benign prostatic hyperplasia (BPH), prostatitis,

CC prostatic intraepithelial neoplasia (PIN) and cancer. In particular the
CC products can be used in drug screening and gene therapy.

XX
SQ Sequence 2143 BP; 418 A; 621 C; 563 G; 541 T; 0 other;

Alignment Scores:
Pred. No.: 1.2e-224 Length: 2143
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 20 Gaps: 0

US-09-593-793A-113 (1-553) x AAV711180 (1-2143)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
DB 3 CAGGGCGTCCAGAGCTGAGCGCGGACCGAGGCCGAGACATATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
DB 63 CGGATGGGAGCGCTGGGCTGTCTCGAGTGGCGCATCTCCTCTCTCTCTCTCTCTCT 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
DB 123 ATGGACCGGCTGGTCAGCGATTTCGGCATCTCGAGCAGTCTATTGGCCAGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
DB 183 TTCCTGTGGCTGGCGGCGCCACATGCTCCAGTGTGGCGTGGCGTGGCGTGGCGTTC 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
DB 243 GCGCGCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCTGCCCTACACACTGGCCCTCC 302
QY 402 LeuTyrHisArgGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyAla 421
DB 303 CTCTACCAACCGGAGAGCAGGTGTCTGTCGCAATACCGAGGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
DB 363 AGCAGTGGACAGCTGATGACAGCTTCTGCCAGGCCCTTAAGCTGGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
DB 423 CCTAATGGACAGCTGGTGTCTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
DB 483 GGGGCTCTGCTGTGTCTCCGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 542
QY 482 ValValProGlyArgGlyTleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
DB 543 GTGGTTCGGGGCGGGGATCTGCTGGACCTTCGTCATCTGGATAGTGTCTCTGTGTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
DB 603 TCCAGAGTGGCCCATCTCTGTTATGGCTCCATTTGTCAGCTCAGCCAGCTGTCTACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
DB 663 GCGTATATGGTGTCTGCGCGAGCGCTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 723 GTATTGTGAAGAGCGACTTGGCCAAATACACAGCG 758

RESULT 36
AAS64039
ID AAS64039 standard; cDNA: 2904 BP.
XX
AC AAS64039;
XX

DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA P553S splice variant #2.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.
OS
PN WO200173032-A2.
XX
PD 04-OCT-2001.

XX
PF 27-MAR-2001; 2001WO-US09919.

XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.

PA (CORI-) CORIXA CORP.

XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fangder GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -

XX Claim 1; Page 482-483; 579pp; English.

CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.

XX SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:
Pred. No.: 1.12e-208 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS64039 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGGTTCGATGGGAGCGCTGGGGGTGTCTGTGAGTGGCCATCTCCTGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGTGTATGGACCGGCTGGTGGAGCATTCGGCACTTCGAGCAGTCTATTTGGCCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378

```
Db 930 GTGGCAGCTTCCCTGTGGCTCCGGTGCACATGCTCTCCACAGTGTGGCTGGTG 989
Qy 379 ThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCGCTCACCAGGTTCACTTCTCAGCCCTCAGATCGCCCTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACCACCGGAGAGCAGAGGTCTCTCCCAATACCGAGGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGGTGTAGCAGTACAGACACCTGTATGACACAGCTTCTGCCAGCGCCTAAGCCTGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 1170 GCTCCCTTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCTCTCCACCTCCACCC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTGGGGGCTCTGCTGCTGATGTCCTCGTACGTGTGTGGTGGTGGTGGTGGT 1289
Qy 479 GluAlaArgValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGTGTTCGGGGCGGGGCATCTGCTGGACCTGCCATCTCGTATAGTGCC 1349
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTGTGCTGCCAGGTGGCCCATCCCTGTTTATGAGCTCCATTTGTCAGCTCAGCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTGTCTGCCGAGGCCCTGGGCTCTGGTGGTGGTGGTGGT 1469

RESULT 37
AAH93867
ID AAH93867 standard; cDNA; 2904 BP.
AC AAH93867;
DT 04-OCT-2001 (first entry)
XX P553S cDNA splice variant p553S-12.
DE Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX Homo sapiens.
XX WO200151633-A2.
PN 19-JUL-2001.
XX 16-JAN-2001; 2001WO-US01574.
PF 14-JAN-2000; 2000US-0483672.
XX (CORI-) CORIXA CORP.
PA Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI; 2001-425873/45.
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
```

```
XX Claim 1; Page 459-460; 543pp; English.
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:
Pred. No.: 1,12e-208 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAH93867 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGGTTCGGATGGCAGCCTGGGGCTGTCTCTGCAGTGGCCATCTCCCTGCTCTTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTCCCTGTGGCTGGCTGCCATGCTCCATGCTCCACAGTGTGGCCGTGGTG 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCGCTCACCAGGTTCACTTCTCAGCCTCGACATCTCGCTTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACCACCGGAGAGCAGAGGTGTCTCTGCCCAATACCGAGGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGGTGTAGCAGTACAGACACCTGTATGACACAGCTTCTGCCAGCGCCTAAGCCTGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 1170 GCTCCCTTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCTCTCCACCTCCACCC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTGGGGGCTCTGCTGCTGATGTCCTCGTACGTGTGTGGTGGTGGTGGTGGTGGT 1289
Qy 479 GluAlaArgValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGTGTTCGGGGCGGGGCATCTGCTGGACCTGCCATCTCGTATAGTGCC 1349
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTGTGCTGCCAGGTGGCCCATCCCTGTTTATGAGCTCCATTTGTCAGCTCAGCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTGTCTGCCGAGGCCCTGGGCTCTGGTGGTGGTGGTGGTGGT 1469
```

QY 539 ThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1470 ACACAGGTAGTATTGACAGGCGGACTTGCCCAATACTACGCG 1514

RESULT 38

ABL95410
ID ABL95410 standard; cDNA; 2904 BP.
AC ABL95410;
XX

DT 19-JUL-2002 (first entry)
XX

DE Human P553S splice variant SEQ ID NO 703.
XX

KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
gene therapy; gene; ss.
XX

OS Homo sapiens.
XX

PN US2002022248-A1.
XX

PD 21-FEB-2002.
XX

PF 12-JAN-2001; 2001US-0759143.
XX

PR 25-FEB-1997; 97US-0806099.
PR

PR 01-AUG-1997; 97US-0904804.
PR

PR 09-FEB-1998; 98US-0020956.
PR

PR 23-FEB-1998; 98US-0030607.
PR

PR 14-JUL-1998; 98US-0115453.
PR

PR 23-SEP-1998; 98US-0159812.
PR

PR 15-JAN-1999; 99US-0232149.
PR

PR 09-APR-1999; 99US-0288946.
PR

PR 13-JUL-1999; 99US-0352616.
PR

PR 18-NOV-1999; 99US-0439313.
PR

PR 14-JAN-2000; 2000US-0483672.
PR

PR 27-MAR-2000; 2000US-0536857.
PR

PR 09-MAY-2000; 2000US-0568100.
PR

PR 12-MAY-2000; 2000US-0570737.
PR

PR 13-JUN-2000; 2000US-0593793.
PR

PR 27-JUN-2000; 2000US-0605783.
PR

PR 10-AUG-2000; 2000US-0636215.
PR

PR 29-AUG-2000; 2000US-0651236.
PR

PR 06-SEP-2000; 2000US-0657279.
PR

PR 02-OCT-2000; 2000US-0679426.
PR

PR 10-OCT-2000; 2000US-0685166.
XX

(XUJ/) XU J.
PA

(DILL/) DILLON D C.
PA

(MITC/) MITCHAM J L.
PA

(HARL/) HARLOCKER S L.
PA

(JIAN/) JIANG Y.
PA

(KALO/) KALOS M D.
PA

(FANG/) FANGER G R.
PA

(RETT/) RETTER M W.
PA

(STOL/) STOLK J A.
PA

(DAYC/) DAY C H.
PA

(VEDV/) VEDVICK T S.
PA

(CART/) CARTER D.
PA

(LISX/) LI S X.
PA

(WANG/) WANG A.
PA

(SKEI/) SKEIKY Y A W.
PA

(HEPL/) HEPLER W T.
PA

(HEND/) HENDERSON R A.
XX

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX

XX WPI; 2002-255649/30.
XX

PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX
PS Claim 1; SEQ ID NO 703; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:

Pred. No.: 1-12e-208 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABL95410 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
|||||

Db 810 GAGGGCGTTCCGATGGCAGCGCTGGGCTGTTCTCGAGTGGCCATCTCCCTGGTCTTC 869
|||||

QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
|||||

Db 870 TCTCTGGTCATGGACCGCTGGTGGCAGCATTCGGACATCGAGCAGTCTATTGGCCAGT 929
|||||

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
|||||

Db 930 GTGGCAGCTTTCCTGTGGCTGCCGTGCCACATGCTGTCACACAGTGTGGCCGTGGTG 989
|||||

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||

Db 990 ACAGCTTTCAGCGCCCTACCCTCCGCTTCTCAGCTTCTCAGCTTCTGCTGCTTACACA 1049
|||||

QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||

Db 1050 CTGGCCCTCCCTCTACACCGGAGAGCAGGTGTTCTCCCAAAATACCGAGGGGACACT 1109
|||||

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||

Db 1110 GGAGGTGCTAGCAGTGCAGCAGCAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGA 1169
|||||

QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
|||||

Db 1170 GCTCCCTTCCCTAAATGGACACGTTGGGTGCTGGAGGCGAGTGGCTGCTCCACCTCCACCC 1229
|||||

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
|||||

Db 1230 GCGCTCTGCGGGGCTCTGCTGCTGATGTTCTCCGTACGTGTTGGTGGGTGAGGCCACC 1289
|||||

QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||

Db 1290 GAGGCCAGGGTGGTTCGCGGGCGGGGCATCTGCTGGACCTGCCATCTCGGATAGTGGC 1349
|||||

QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||

Db 1350 TTCTCTGCTGCTCCAGGTGGCCCATCCCTGTTTATGGGTCCATTTGTCAGCTTCAGCCAG 1409
|||||

QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
|||||

Db 1410 TCTGTACCTGCTATATGTTGTTCTGCCGAGGCGCTGGGTGCTGCTGCTGCTTGTCTT 1469
|||||

QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||

Db 1470 ACACAGGTAGTATTTCACAGGAGCGGACTTGCGCCAAATACTACGCG 1514
|||||

RESULT 39
AAZ45677

```

ID AA245677 standard; cDNA; 2462 BP.
XX
AC AA245677;
XX
DT 06-APR-2000 (first entry)
XX
DE cDNA sequence of a novel prostate cancer-associated gene.
XX
KW prostate cancer-associated gene; Incyte clone 1864683; bone cancer;
KW cell proliferation; cancer; adrenal gland cancer; bladder cancer;
KW prostate cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 376..1071
FT FT /*tag= a
FT FT /product= "prostate cancer-associated protein"
FT sig_peptide 376..516
FT FT /*tag= b
XX
XX W09967384-A2.
XX
XX 29-DEC-1999.
XX
XX 15-JUN-1999; 99WO-US13524.
XX
XX 22-JUN-1998; 98US-0102615.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Walker MG, Volkmath W, Klingler TM, Sprinzak EA;
XX
XX WPI; 2000-126631/11.
XX
XX P-PSDB; AAY54369.
XX
XX Identifying biomolecules for the diagnosis and treatment of diseases
XX associated with cell-proliferation -
XX
XX Claim 8; Page 47-48; 52pp; English.
XX
XX The present sequence is derived from a prostate cancer-associated
XX gene, and is represented by Incyte clone number 1864683. The sequence
XX is used in the method of the invention. The specification
XX describes a method for identifying biomolecules for the diagnosis or
XX treatment of diseases associated with cell proliferation. The method
XX comprises examining polynucleotides, consisting of prostate cancer-
XX specific genes, and genes of unknown function, expressed in cDNA
XX libraries. The patterns of both gene sets are compared to identify
XX genes of unknown function with similar expression patterns to the
XX prostate cancer-specific genes. The biomolecules identified by the
XX method form pharmaceutical compositions useful for the diagnosis and
XX treatment of diseases associated with cell proliferation. Such diseases
XX include cancer of the adrenal gland, bladder and bone, but especially
XX prostate cancer. The method may also be applied using other disease-
XX specific genes. The prostate cancer-specific genes facilitate the
XX diagnosis and treatment of cell proliferation disorders.
XX
XX Sequence 2462 BP; 483 A; 726 C; 632 G; 621 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1.6e-184 Length: 2462
XX Score: 209.00 Matches: 209
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 37.79% Indels: 0
XX DB: 21 Gaps: 0
XX
XX US-09-593-793a-113 (1-553) x AA245677 (1-2462)
XX
XX 320 GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSer 339
XX Db 367 GCGGTTGCGATGGGCGAGCTGGGGCTGTCTCTGCAGTGGCCATCTCCCTGGTCTTCT 426

```

```

QY 340 LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal 359
XX |||||||
DB 427 CTGGTCATGGACCGCTGGTCAGCGATTGGCACTCAGCAGTCTATTGGCCAGTGTG 486
XX |||||||
QY 360 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThr 379
XX |||||||
DB 487 GCAGCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTGCCACAGTGTGCCGTGTGTGACA 546
XX |||||||
QY 380 AlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeu 399
XX |||||||
DB 547 GCTTCAGCCGCCCTCACCGGTTCTACCTTCTCAGCCCTGCAGATCCTCCCTACACACTG 606
XX |||||||
QY 400 AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly 419
XX |||||||
DB 607 GCCTCCCTCTACCACCGGGAGACGAGTGTCTCTGCCCAATACCGAGGGGACACTGGA 666
XX |||||||
QY 420 GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAla 439
XX |||||||
DB 667 GGTGCTAGCAGTAGGACAGCCTGATGACAGCTTCTCCCTGCCAGGCCCTTAAGCCTGGAGCT 726
XX |||||||
QY 440 PropheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAla 459
XX |||||||
DB 727 CCTTCCCTAATGGACACGTGGGTGCTGGAGGCAAGTGCCCTGCTCCACCTCCACCCCGC 786
XX |||||||
QY 460 LeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGlu 479
XX |||||||
DB 787 CTCTCGGGGGCTCTGCTCTGTGTGTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGG 846
XX |||||||
QY 480 AlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPhe 499
XX |||||||
DB 847 GCCAGGGTGGTTCGGGGCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTC 906
XX |||||||
QY 500 LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer 519
XX |||||||
DB 907 CTGCTGTCCAGTGGCCCATCCTCTGTATGGCTTATGGCTCCTATGTCCAGCTCAGCAGTCT 966
XX |||||||
QY 520 ValThrAlaTyrMetValSerAlaAla 528
DB 967 GTCACCTATATATGGTGTCTGCCGCA 993
XX |||||||
RESULT 40
ABN81320
ID ABN81320 standard; cDNA; 3663 BP.
XX
AC ABN81320;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human mast cell related gene MC14 SEQ ID NO 3.
XX
KW Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
KW vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT CDS 294..746
XX FT FT /*tag= a
XX FT FT /product= "MC14-1"
XX FT CDS 1238..2218
XX FT FT /*tag= a
XX FT FT /product= "MC14-2"
XX
XX W0200246389-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US46180.
XX
XX 08-DEC-2000; 2000US-251835P.
XX
XX 14-MAR-2001; 2001US-275479P.
XX

```

PR 28-MAR-2001; 2001US-279115P.
XX 02-APR-2001; 2001US-280143P.
PA (UNIO) UCB SA.
XX
PI Nocka K, Pirozzi G, Einstein R;
XX
DR WPI; 2002-508560/54.
XX P-PSDB; ABB77570, ABB77571.
XX
PT Novel isolated nucleic acids that are differentially expressed in mast
PT cells in patients with allergic hypersensitivity, encoding proteins
PT associated with mast cell regranulation and allergic hypersensitivity
PT
XX
PS Claim 1; Page 98-102; 119pp; English.
XX
CC The invention relates to isolated nucleic acid (ABN81319-ABN81324),
CC corresponding to genes differentially expressed in mast cells following
CC activation or in patients with allergic hypersensitivity disease, (I)
CC that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of
CC (II) if at least 6 amino acids. (II) is useful for identifying binding
CC partners. (I) or (II) is useful for diagnosing or treating a disease
CC state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,
CC urticaria or atopic dermatitis or mastocytosis) in a subject which
CC involves determining the level of expression of (I) or (II). A computer
CC system, comprising a database containing information identifying the
CC expression level in a tissue or at least one mast cell of (I), is useful
CC for presenting information to identify the relative expression level of
CC (I). (II) is used as a marker to detect, diagnose or identify an allergic
CC response in a patient. The protein can also serve as a target that
CC modulate gene expression or activity and as an antigen to raise
CC polyclonal or monoclonal antibodies. (II) is useful for identifying
CC agents that modulate expression of the protein or agents, such as
CC agonists or antagonists. The agonists or antagonists are useful for
CC modulating biological activity and function of (II) and thus are useful
CC for alleviating disease conditions such as allergic hypersensitivity,
CC seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
XX
SQ Sequence 3663 BP; 740 A; 1058 C; 985 G; 880 T; 0 other;

Alignment Scores:
Pred. No.: 7.44e-164 Length: 3663
Score: 187.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.82% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABN81320 (1-3663)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1331 GGCAATTTGGTCCAGTGTGGGCTGGTCTGTGTCCTCCGCTCCTAGGCTACGCCAGTACCAC 1390
QY 78 TrpArgGlyYargTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1391 TGGCGTGGACGTATGGCGCGCGCGCTTCATCTGGGCACTGTCCTTGGGCATCTCG 1450
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
DB 1451 CTGAGCCTCTTTCTCATCCAAAGGCGCGCTGCTAGCAGGCTGCTGTGCCCGGATCCC 1510
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
DB 1511 AGCCCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGCTGCTGGACTCTGTGGCCAG 1570
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
DB 1571 GTGTGCTTCACCTCCACTGGAGGCCCTGCTCTGACCTCTTCGGGAGCCCGGACCACTGT 1630
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177

DB 1631 CGCCAGGCGCTACTCTCTCTATGCTTATGCTTTCATGATCAGTCTTTGGGGGCTGCTGGGCTACCTC 1690
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
DB 1691 CTGCGCTGCCATTGACTGGGACACCACTGCTGGCCCTTACTGGCACCCAGAGGAG 1750
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
DB 1751 TGCCTCTTTTGGCTGCTCACCTCATCTTCTCCTGCTAGCAGCCACACACTGCTGGTG 1810
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
DB 1811 GCTGAGGAGGAGCGCTGGGCCCCACCGAGCCAGAGGGCTGTGCGCCCCCTCTCTTG 1870
QY 238 SerProHisCysCysProCys 244
DB 1871 TCGCCCCACTGCTGTCCATGC 1891
RESULT 41
ID AAV61144 standard; cDNA; 789 BP.
XX AAV61144;
AC AAV61144;
XX
DT 06-JAN-1999 (first entry)
XX
DE 3' cDNA sequence of prostate tumour clone LI-12.
XX
KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN W09837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03492.
XX
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI; 1998-609886/51.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 38-39; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subcloned cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:
Pred. No.: 6.07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 19 Gaps: 0

US-09-593-793A-113 (1-553) x AAV61144 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376

Db 12 GCACGTGGCAGCTTCCCTGTGGCTGGCGGTGCACATGCTGTCCACACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 72 GTGGTGACAGCTTCAGCCGCCCTCACCAGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCTCCCTCTACCAACCGGAGAGCAGGTCTTCTGCCCAATACCGAGG 191
QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGCTAGCAGTAGGACAGCCCTGATGACAGCTTCTGTGCCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuPro 456
Db 252 CCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCTGTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCGCGCTCTGGGGGCCCTGTGCTGTGATGTCTCCGTACGTGTGGTGGGTGAG 371
QY 477 ProThr 478
Db 372 CCCACC 377
RESULT 42
AAV58487
ID AAV58487 standard; cDNA; 789 BP.
XX
AC AAV58487;
XX
DT 08-DEC-1998 (first entry)
XX
DE 3' fragment of prostate tumour specific gene LI-12.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03690.
XX
PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-080596.
PR 01-AUG-1997; 97US-0904809.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
WPI; 1998-480805/41.
XX
PT Novel human prostate specific tumour protein and fragments - useful
PT for detecting and treating prostate cancers
XX
PS Claim 1; Page 39; 141pp; English.
XX
CC This sequence represents a human prostate tumour specific gene, and can
CC be used in the method of the invention. The method is for detecting
CC prostate cancer comprises contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as
CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may
CC also be conjugated to a therapeutic agent for use in therapy of prostate
XX cancers.

SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
Alignment Scores:
Pred. No.: 6.07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 19 Gaps: 0
US-09-593-793a-113 (1-553) x AAV58487 (1-789)
QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
Db 12 GCCAGTGTGGCAGCTTCCCTGTGGCTGGCGGTGCACATGCTGTCCACACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 72 GTGGTGACAGCTTCAGCCGCCCTCACCAGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCTCCCTCTACCAACCGGAGAGCAGGTCTTCTGCCCAATACCGAGG 191
QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGCTAGCAGTAGGACAGCCCTGATGACAGCTTCTGTGCCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuPro 456
Db 252 CCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCTGTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCGCGCTCTGGGGGCCCTGTGCTGTGATGTCTCCGTACGTGTGGTGGGTGAG 371
QY 477 ProThr 478
Db 372 CCCACC 377
RESULT 43
AAA06250
ID AAA06250 standard; cDNA; 789 BP.
XX
AC AAA06250;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:10.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX

DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein
XX
XX
PS Claim 1; Page 99; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
XX
Alignment Scores:
Pred. No.: 6,07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AA06250 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
DB 12 GCCAGTGGGAGCTTCCTCTGGCTGGCGGTGCCAGATGCTGTCCACAGTGTGGCC 71

QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
DB 72 GTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCACGCCCTGCAGATCCTGCC 131

QY 397 TyrThrLeuAlaSerLeuTyHisArgGluLysGlnValPheLeuProLysTyArgGly 416
DB 132 TACACACTGGCTTCCTCTACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191

QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
DB 192 GACACTGGAGGTGCTAGCAGTACGACAGCTGTGATGATGATGATGATGATGATGATG 251

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456
DB 252 CCTGGAGCTCCCTTCCTTAATGGACAGCTGGGTGTGGAGGAGTGGCTGTCCACCT 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
DB 312 CCACCGCGCTCTGGGGGCTCTGCCTGTGATGATGATGATGATGATGATGATGATGATG 371

QY 477 ProThr 478
DB 372 CCCACC 377

RESULT 44
ID AAS63458
XX AAS63458 standard; cDNA; 789 BP.
XX
AC AAS63458;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #10.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX

OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
XX
DR New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 232-233; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
XX
Alignment Scores:
Pred. No.: 6,07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS63458 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
DB 12 GCCAGTGGGAGCTTCCTCTGGCTGGCGGTGCCAGATGCTGTCCACAGTGTGGCC 71

QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
DB 72 GTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCACGCCCTGCAGATCCTGCC 131

QY 397 TyrThrLeuAlaSerLeuTyHisArgGluLysGlnValPheLeuProLysTyArgGly 416
DB 132 TACACACTGGCTTCCTCTACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191

QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
DB 192 GACACTGGAGGTGCTAGCAGTACGACAGCTGTGATGATGATGATGATGATGATGATG 251

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OY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
|||||
Db 252 CCTGGAGCTCCCTCCCTAATGCACACGCTGGGTGCTGGAGGAGTGGCTGCCACCT 311
|||||
OY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
|||||
Db 312 CCACCCGGCGCTCTGGGGGCGCTCTGCCTGTGATGTCCTCGGTACGTTGGTGGGTGAG 371
|||||
OY 477 ProThr 478
|||||
Db 372 CCCACC 377

RESULT 45
AAS10009
ID AAS10009 standard; cDNA; 789 bp.
AC AAS10009;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human prostate tumour cDNA L1-12 #1.
KW Human; prostate tumour protein; prostate cancer; ss.
XX
XX Homo sapiens.
OS
PN US6262245-B1.
XX
PD 17-JUL-2001.
XX
XX 25-FEB-1998; 98US-0030607.
XX
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC;
PI
XX WPI; 2001-440862/47.
DR
XX
XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient
XX
XX Example 1; Column 32-33; 105pp; English.
PS
XX
XX The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.
XX
SQ Sequence 789 bp; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:
Pred. No.: 6.07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAS10009 (1-789)

OY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
|||||
Db 12 GCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGTGCCACATGCCGTGCCACAGTGTGGCC 71
|||||
OY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
|||||
Db 72 GTGGTGACAGCTTACCGCGCGCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCC 131
|||||
```

```
OY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
|||||
Db 132 TACACACTGGCGCTCCCTCTACCCACGGGAGAGCAGGTGTTCTGCCCCAAATACCGAGGG 191
|||||
OY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
|||||
Db 192 GACACTGGAGGTGCTAGCAGTGAGGACAGCCCTGATGACAGCTTCTGCCAGGCCCTAAG 251
|||||
OY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
|||||
Db 252 CCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGCTGGAGGAGTGGCTGCCACCT 311
|||||
OY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
|||||
Db 312 CCACCCGGCGCTCTGGGGGCGCTCTGCCTGTGATGTCCTCGGTACGTTGGTGGGTGAG 371
|||||
OY 477 ProThr 478
|||||
Db 372 CCCACC 377
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Run on: February 19, 2003, 05:11:24 ; Search time 53 seconds

(without alignments)
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Title: US-09-593-793a-113

Perfect score: 553

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Word size: 3

Total number of hits satisfying chosen parameters: 706526

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Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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-NO_XLPY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAEXT=60 -FGAPOP=6 -FGAEXT=7
-YGAPOP=60 -YGAEXT=60 -DELOP=6 -DELEXT=7

Database :

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1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Score	Query Match Length	Description

1	553	100.0	Sequence 110, App
2	553	100.0	Sequence 110, App
3	553	100.0	Sequence 110, App
4	553	100.0	Sequence 110, App
5	553	100.0	Sequence 110, App
6	553	100.0	Sequence 110, App
7	553	100.0	Sequence 110, App
8	320	57.9	Sequence 702, App
9	263	47.6	Sequence 705, App
10	263	47.6	Sequence 705, App
11	255	46.1	Sequence 16, Appl
12	255	46.1	Sequence 16, Appl

13	252	45.6	2143	3	US-09-071-710-15	Sequence 15, Appl
14	235	45.6	2143	4	US-09-525-397-15	Sequence 15, Appl
15	235	45.6	2904	4	US-09-605-785-703	Sequence 703, App
16	122	22.1	789	4	US-09-020-956-10	Sequence 10, Appl
17	122	22.1	789	4	US-09-030-607-10	Sequence 10, Appl
18	122	22.1	789	4	US-09-605-785-10	Sequence 10, Appl
19	122	22.1	789	4	US-09-439-313-10	Sequence 10, Appl
20	122	22.1	789	4	US-09-352-616A-10	Sequence 10, Appl
21	122	22.1	789	4	US-09-232-149A-10	Sequence 10, Appl
22	85	15.4	258	3	US-09-071-710-1	Sequence 1, Appl
23	85	15.4	258	4	US-09-525-397-1	Sequence 1, Appl
24	82	14.8	247	3	US-09-071-710-4	Sequence 4, Appl
25	82	14.8	247	4	US-09-525-397-4	Sequence 4, Appl
26	71	12.8	217	3	US-09-071-710-2	Sequence 2, Appl
27	71	12.8	217	4	US-09-525-397-2	Sequence 2, Appl
28	71	12.8	255	3	US-09-071-710-3	Sequence 3, Appl
29	71	12.8	255	4	US-09-525-397-3	Sequence 3, Appl
30	34	6.1	231	3	US-09-071-710-5	Sequence 5, Appl
31	34	6.1	231	4	US-09-525-397-5	Sequence 5, Appl
32	9	1.6	33	4	US-09-605-785-888	Sequence 488, App
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37	9	1.6	903	4	US-08-944-604-15	Sequence 15, Appl
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41	8	1.4	357	2	US-08-673-190A-6	Sequence 6, Appl
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50	8	1.4	1214	4	US-09-605-785-225	Sequence 225, App
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53	8	1.4	1214	4	US-09-232-149A-225	Sequence 225, App
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55	8	1.4	1215	4	US-09-439-313-326	Sequence 326, App
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58	8	1.4	1248	4	US-09-020-956-171	Sequence 171, App
59	8	1.4	1248	4	US-09-030-607-171	Sequence 171, App
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64	8	1.4	1265	4	US-09-020-956-173	Sequence 173, App
65	8	1.4	1265	4	US-09-030-607-173	Sequence 173, App
66	8	1.4	1265	4	US-09-605-785-173	Sequence 173, App
67	8	1.4	1265	4	US-09-439-313-173	Sequence 173, App
68	8	1.4	1265	4	US-09-352-616A-173	Sequence 173, App
69	8	1.4	1265	4	US-09-232-149A-173	Sequence 173, App
70	8	1.4	1320	1	US-08-176-412-1	Sequence 1, Appl
71	8	1.4	1320	2	US-08-555-268A-1	Sequence 1, Appl
72	8	1.4	1320	2	US-08-495-695B-1	Sequence 1, Appl
73	8	1.4	1320	5	PCT-US94-14436-1	Sequence 1, Appl
74	8	1.4	1386	2	US-08-897-340-1	Sequence 1, Appl
75	8	1.4	1386	3	US-09-252-329-1	Sequence 1, Appl
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78	8	1.4	2737	4	US-09-484-970B-129	Sequence 29, Appl
79	8	1.4	4571	1	US-08-232-144-5	Sequence 5, Appl
80	8	1.4	7400	1	US-09-116-032-1	Sequence 1, Appl
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82	8	1.4	11531	1	US-08-442-806-1	Sequence 1, Appl
83	8	1.4	17415	3	US-08-486-343A-1	Sequence 1, Appl
84	8	1.4	17415	5	PCT-US95-07349-1	Sequence 1, Appl
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Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 36, Appl
Sequence 485, App
Sequence 485, App
Sequence 20, Appl
Sequence 20, Appl

100 7 1.3 46 1 US-08-794-153-20

ALIGNMENTS

RESULT 1

US-09-020-956-110

: Sequence 110, Application US/09020956

: Patent No 6261562

: GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun

: APPLICANT: Dilllin, Davin C.

: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO

: NUMBER OF SEQUENCES: 178

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: SEED AND BERRY LLP

: STREET: 6300 Columbia Center, 701 Fifth Avenue

: CITY: Seattle

: STATE: WA

: COUNTRY: USA

: ZIP: 98104

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patentin Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/020,956

: FILING DATE: 09-FEB-1998

: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:

: NAME: Maki, David J.

: REGISTRATION NUMBER: 31,392

: REFERENCE/DOCKET NUMBER: 210121.427C2

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (206) 622-4900

: TELEFAX: (206) 682-6031

: INFORMATION FOR SEQ ID NO: 110:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3410 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

: ORIGINAL SOURCE:

: ORGANISM: Homo sapiens

US-09-020-956-110

Alignment Scores:

Pred. No.: 0 Length: 3410

Score: 553.00 Matches: 553

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-020-956-110 (1-3410)

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284 ATGGTCCAGAGCTGTGGGTGAGCGCCCTGCTGCGGCACCGGAAAGCCAGCTCTTGCTG 343

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGGATCATCACTATGTGCGG 403

Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

404 CCTCTGCTGCTGCAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGCTGTGGCATTTGCT 463

Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

464 CCAAGTCTGGGCTGCTGTCTCCGCTCCTAGAGTCCAGCCAGTGCACCATGGGCTGGA 523

Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

524 CGCTATGGCCGCCCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTCTGCTGACCTC 583

Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120

584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCGATCCAGGCCCTG 643

Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140

644 GAGCTGGCACTGCTCATCTCGGGCGTGGGCTGCTGGACTTCTGTGCCAGGTGTCTTC 703

Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

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Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180

764 TACTCTGCTATGCCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCTGCC 823

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Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220

884 GGCCGTGCTACCCCTCATCTTCTCCTGCTGCTGAGCAGCCACCTGCTGTGCTGCTGAGG 943

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1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063

Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280

1064 CACCAAGTGTGCTGCGCATGCCCGCACCTGCGCGCGGCTCTCTGTGCTGAGCTGTGC 1123

Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300

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Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

1184 TACCAGGCGTGGCGGAGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1243

Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340

1244 GTTCGGATGGGCGAGCTGGGGCTGTTCCTGAGTGGCGCATCTCCCTGCTCTCTCTG 1303

Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360

1304 GTCATGGACCGCTGGTGCAGCGATTCGCGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363

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Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGTGGCCCCATCCCTGTATATGGCTCCATTTGTCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGCTGTGCCCGCAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 2

US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianqun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-110
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-030-607-110 (1-3410)

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Db 284 ATGGTCCAGAGGCTGTGGGTAGCCGCTGTCTGCGGCACCGGAAAGCCAGCTCTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGCAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAAGTTCATGACCATGGTGTGGCATTTGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTGTCTCCGCTCTAGCTAGCTCAGCCAGTACCCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCGCGGCCCTTCATCTGGGCATCTCTTGGGCATCTCTGTGAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGCGCGATCCAGGCCCTTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGTGGCACTGCTCATCTCGGCGCTGGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 703
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Db 704 ACTCCACTGGAGGCGCTGCTCTCTGACCTCTTCCGGGACCCGAGCACACTGTGCCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATGCTTCATGATCAGTCTTGGGGCTGTGGGGCTTACCTCTGCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGACACAGTGCCTTGGCCCTTACCTGGGACCCAGGAGAGTGCCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGTCTCACCTCATCTCTCCTACCTGGGTAGCAGGCACACTGTGTGCTGAGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAAGGGCTGTGGGCCCTCTCTTGTGCGCCCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCCGGCCCGCTTGGCTTCCGGAACTTGGGGCCCTGCTTCCCGGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCCGATGCCCGCACCCCTGCGCCGCTCTTCTGCTGAGCTGTGC 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
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QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGGCGTCCAGAGCTGAGCGGGCAGCGAGGGCCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGCAGCTGGGGCTGTCTCCAGTGCGGCATCTCCCTGGCTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGCGCGGCTGTGCGAGGATTCGCGACACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
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QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCCCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCTCTACACACGGGAGAGCAGGTGTTCTCGCCCAATACGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGACAGCTGATGACAGCTTCTCCAGGGCCCTAAGCCTGGAGCTCC 1603
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DB 1604 TTTCCCTAATGGACAGCTGGGTGCTGGAGCAGTGGGCTCTCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGGGGGCTCTGCTGCTGATGTCCTCGTACGTGGTGGTGGTGGTGGTGGTGGTGGT 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGTTCGGGGCGGGGATCTGCCGTGGACCTCGCCATCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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DB 1844 ACTGCCTATATGCTGCTGCCAGGCGCTGGTCTGGTGGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCAGCTTGGCCAAATACTCAGCG 1942

RESULT 3

US-09-605-785-110

: Sequence 110, Application US/09605785

: Patent No. 6321716

: GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun

: APPLICANT: Dillon, Davin C.

: APPLICANT: Mitcham, Jennifer L.

: APPLICANT: Harlocker, Susan L.

: APPLICANT: Jiang, Yuqi

: APPLICANT: Henderson, Robert A.

: APPLICANT: Kalos, Michael D.

: APPLICANT: Fanger, Gary R.

: APPLICANT: Retter, Marc W.

: APPLICANT: Stolk, John H.

: APPLICANT: Day, Craig H.

: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C16
: CURRENT APPLICATION NUMBER: US/09/605,785
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 835
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 110
: LENGTH: 3410
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-605-785-110

Alignment Scores:

Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-605-785-110 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGTGTCACAGAGCTGTGGGTGAGCGCCCTGCTGGCGACCGGAAAGCCAGCTCTTGGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
DB 344 GTCAACCTCTAACCCTTTGGCCTGGAGGTGTTTGGCCGAGGCATCACCTATGTGGCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CTCTGCTGCTCGAAGTGGGGGTAGAGAGAGTTTCATCACCCTGGTGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTCTGGCGTGTGTCTGTCGCCGCTCCCTAGGCTCAGCCAGTGCACCTGGGTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACGTCTCTGGGCATCTCTGTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGTCTGCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACTGCTCATCTCTGGCGCTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGGCCCTGCTCTGACCTTTCGGGGACCGGACCCACCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGCTATGCCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCTGCTGGCCCTACCTGGGCACCCAGGAGGAGTCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCGTGTCTACCCCTCATCTCTCCTGCTGAGCAGCCACACTGCTGTGTGGCTGAGGAG 943


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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCGCTGGGCCCCACCAGCAGCAGAGAGGCTGTGCGCCCTCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCCGCTGTGCTTTCGGAAACCTGGGGCCCTGCTCCCGGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCGCCGACCTGCGCGGCTCTTGTGCTGAGCTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGATTTCTGCGGGCAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGCGTCCAGAGCTGAGCGGCGCAGGCGCGGAGACACTATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGGCGAGCTGGGGCTGTTCCTGCGAGTGGCCATCTCCTGTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTTCATGGACCGCTGGTGCAGCGATTCGCGACACTCGAGCAGTCTATTTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCGGGTGCACATGCCGTGCCACAGTGTGGCGGTGGACGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCACCGGAGAGCAGGTGTTCCTGCCCAATACCGAGGGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTACAGTGGAGCAGCCTGATGACCATCTTCCTGCCAGGCGCCPAAGCCTGGAGCTGCC 1603
QY 441 PheProAsnGlyHisValGlyValGlySerGlyLeuLeuProProProProAlaLeu 460
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QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCTCTGCGCTGTGATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuaspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCGCGGCGGGGACATCGCTGGACCTTCGCCATCTCGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCCCATCCCTGTTATGGCTCCATGTGTCACACTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTTGCTGCGCAGCGCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGT 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTACAGAGGACTTGGCCAAATACTCAGCG 1942
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RESULT 4

US-09-439-313-110

; Sequence 110, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-110
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Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-439-313-110 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGGTGAGCGCCTGTGTCGGCACACCGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGTCAACCTTTGGCCTGGAGGTGTGTTGGCCGCGAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTCATGACCATGGTGTCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTCTGGGCTGTGTGTCTGTCCTGCTAGGCTCAGCCAGTGACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CCGTATGGCGCGCGCGCGCGCTTCATCTGGGCACATGCTTGGGCATCCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTACGAGGCTGTGTGCCCGGATCCCGAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGGCTGGGCTGTCTGGGCTCTTCTGTGGCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTCTCTGACCTCTTCGGGGACCCGACCTGCTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGCTTGGGCTACTCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCAAGTGCCTGGCCCCCTTACCTGGGCAACCCAGGAGGAGTGCCTCTTT 883
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Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGCTCACTTCATCTTCTCTCACTCGCTAGCAGCACACACTGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCACGCTGGGCCCCACCGAGGCAGAGAGGGCTGTGGGCCCCCTCTCTGTGCGCCCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATCGCGGGCCGCTTGGCTTTCCGGAACCTGGGGCCCTCTCTCCCGGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGCTCGCGCATGCCCCGCACCCCTGCGCGCGCTCTTGTGGCTGAGCTGTC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACAGGATTTCTGGGGCGAGGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly	320
Db	1184	TACCAGSGCGTGCACAGAGCTGAGCGGCGCACCGAGGGCCCGAGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTGCGATGGGCAGCTGGGGCTGTTCCTGCAGTGGCCCATCTCCCTGGTCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGACCGCGCTGGTGCAGCGATTTCGGCACTTCAGCAGACTCTATTGGCCGACGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380
Db	1364	GCATTTCCTGTGGCTGCGGTGCCACATGCCCTGTCCCACAGTGTGGCGTGGTGACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTCAACGGGTTCACCTTCTCAGCGCTGCAGATCCTCGCCCTACACACTGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCACCGGAGAGCAGGTGTTCCTGCCCAANTACCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTCAGACACGCTGATGACCACTTCCTGCCAGGCGCCTAAGCCTGGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTTAATGGACACGTGGGTGTGGAGCAGTGGCTGTCTCCACCTTCCACCGCGGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCTCTCCCTGTGATGTCCTGACGTGTGTGGTGGGTGAGCCACCGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGCTGGTTCCGGGGCGGGGCATCTGCCTGGACCTTCGCACTCTGGATAGTGCCTTCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTGCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATGTCTCCAGCTCAGCCAGCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCTATATGTGCTGCCCGAGCGCTGGGTCTGGTCGCCATTACTTTGCTTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
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RESULT 5			
US-09-352-616A-110			
; Sequence 110, Application US/09352616A			
; Patent No. 6395278			
; GENERAL INFORMATION:			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Harlocker, Susan Louise			
; APPLICANT: Jiang, Yuqi			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Mitcham, Jennifer Lynn			
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSTICS			
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE			
; FILE REFERENCE: 210121.427C8			
; CURRENT APPLICATION NUMBER: US/09/352,616A			
; CURRENT FILING DATE: 1999-07-13			
; NUMBER OF SEQ ID NOS: 472			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 110			
; LENGTH: 3410			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-352-616A-110			
Alignment Scores:			
Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0
US-09-593-793A-113 (1-553) x US-09-352-616A-110 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuL	
Db	284	ATGCTCCAGAGGCTGTGGGTGAGCGCGCTGCTCGGCACCCGAAAGCCAGCTCTTG	
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValP	
Db	344	GTCACCTGCTTAACCTTTGGCTTGGAGGTGTGTGGCCGACGGCATCACCTATGTG	
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleG	
Db	404	CCCTCGCTGCTGGAGCTGGGGGTAGAGAGAGAGTTTCATGACCATGTGCTGGCCAT	
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgG	
Db	464	CCAGTGTGGCGCTGGTCTGTGTCCCGCTCTTAGGGCTCAGCGACTGACCACTGGCG	
Qy	81	ArgTrpGlyArgArgArgPropheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerL	
Db	524	CGCTATGGCGCGCGCGCGCTTTCATCTGGGCACTGTCTTGGGCATCTCTGTGAGCC	
Qy	101	PheLeuIleProArgAlaGlyITrpLeuAlaGlyLeuLeuCysProAspProArgProL	
Db	584	TTTCTCATCCCAAGGGCGCGCTGGCTAGCAGGCTGCTGTGTCGCCGATCCACGACCC	
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysP	
Db	644	GAGCTGGCACTGCTCATCTCGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCT	
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnA	
Db	704	ACTCCACTGGAGGCCCTTGCTCTGTGACCTCTTCGGGACCCGACCACCTGTGCGCCAG	
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProA	
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QY 201 GlyLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuValAlaGluGlu 220
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHIs 240
Db 944 GCAGCGCTGGGCCACCGAGCAGCAGAGGCTGTCGGCCCTCTCTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATCGCGGCCCTGGCTTCCGGAACCTGGCGCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCATGCCCGCACCCCTGCGCGGCTCTCTGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrLeuPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACCGGATTCGTGGCGGAGGGGTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCTGCCAGAGCTGAGCGGCGACCGAGGCCCGGAGACACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
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QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGTGTGAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTGTGGTGGCGGCGCCACATGCCCTGCCACAGTGGCGGCTGGTGGACGT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGGC 1483
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Db 1664 TCGGGGCTCTGCTGTGATGTCCTGCTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1723
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Db 1724 AGGGTGGTTCGGGGCGGGGCACTGCTGGACCTTCCGACCTCGCCATCTGGATAGTCCCTC 1783
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US-09-602-877A-100
; Sequence 100, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-602-877A-100
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-602-877A-100 (1-3410)

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Db 284 ATGGTCCAGAGGCTGTGGGTGAGCGCCTGCTGCGCGCACCGAAAGCCAGCTTGTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCACACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGCAGGACATCACCTATGTGCGG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CTTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCTATGACCATGGTGGTGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTCTCCCGCTCTAGCTCAGCTCAGCCAGTGACCATGGCTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleThrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTCTCATCCCAAGGCCCGGCTGGCTGAGCAGGCTGTGTGCCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCGGCGCTGGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGCGCTGCTCTCTGACCTCTTCCGGGACCCGAGCACCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCCCTTTCATGATCAGTCTTGGGGGCTGCTGGGGTACCTCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACAGTGCCTTGGCCCTTACCTTGGGCACCCAGGAGGAGTGCCTTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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Db 944 GCAGCGCTGGCGCCACCAGAGCCAGAGAGGCTCTGCGCCCTCTGTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGCGCGCGCTGGCTTTCCGGAACCTGGCGCCCTGTCTCCCGCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
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Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTCTTTTACACGGATTTCTGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1184 TACAGGGCGTGCCAGAGCTGAGCGGGGCGCCAGCGAGCGCCGAGACACTATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGGATGGCAGCTGGGGCTGTCTCCAGTGGCCCATCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGCTGTGCGAGGATTCGCGACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
|||||
Db 1364 GCTTCCCTCTGGCTGCCGCTGCACATGCCTGTCACAGTGTGGCGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCCCTCACCGGTTCACTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1484 TCCTCTACACCGGAGAGAGAGGTTCTCTGCCCAATACGAGGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1544 GCTAGCAGTGAGGACAGCTGTATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuProProProAlaLeu 460
|||||
Db 1604 TTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGGCTGCTCCACCTCCACCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
Db 1664 TGGGGGCGCTCGCTGTGATGTCCTCGTACGTGTGGTGGTGAGCCAGCGAGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGTTCGGGGCGGGGATCTGCCCTGGACCTGCCCATCTGTGATAGTGTCCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCATTTGTCCAGCTCAGCCAGTCTGTG 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCCATATGGTGTCTCCCGAGGCTGGGTCTGGTGGCTGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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RESULT 7

US-09-232-149A-110

; Sequence 110, Application US/09232149A

; Patent No. 6465611

```
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-110
```

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Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-232-149A-110 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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Db 284 ATGGTGCCAGAGGCTGTGGGTGAGCGCCCTGCGCGACCCGGAAGCCAGGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGGCATCACCATTGTGCGC 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGTGTGCTGGGCATTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTGGGCTGTGTCTGTCCGCTCAGCCAGTACGACCTGAGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACACTGTCTTGGGCATCTCTGTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTCTCATCCCAAGGCGCGCTGGGTAGCAGGGCTGTGTGCCCGGATCCCGAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyClnValCysPhe 140
|||||
Db 644 GAGCTGGCACTGCTCATCTGGGCGTGGGGCTGTGGACTTCTGTGGCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCGGGACCCCGAGCACCACCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGTATGCCTTCATGATCATGTCTTGGGGGTGCTGGGCTACCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
Db 824 ATTGATGGGACACCACTGCTGCTGCCCCCTACCTGGGACCCAGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
|||||
Db 884 GGCCTGTCTACCCCTCATCTTCTCCTACCTGCGTAGCAGCCACACTGCTGCTGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
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Db 944 GCAGCGCTGGGCCCCACCCAGAGCCAGAGAGGGCTGTCGGCCCCCTCTCTGTGCGCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGCTTCCGGAACCTGGGGCCCTCTTCCCGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCCGCCACCCCTGCGCCGCTCTTCTGCTGAGCTGTC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGCTTTACACGGATTTCTGGCGGAGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGGGCCAGCCGAGGGCCGGAGACATATGATGAAGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGCGAGCTGGGGCTGTCTCTGCAGTGGCCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGCTGGTGCACGGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTGTGGTCCCGGTGCCACATGCCCTGTCCACAGTGTGGCGTGTGACAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCCTCACCGGCTTCACCTTCTCAGCCCTGCAGATCTTCCCTACACACTGCC 1483
Qy 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCCAGCGGAGAGAGAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGGAGCAGAGCTGATGACACAGCTTCTTCCAGCGCCCTAACCTTGGAGCTCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1604 TTCCCTAATGACACAGCTGGGTGCTGAGGACAGTGGCCCTGCCACCTCCACCCCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCGCTGTGATGTCCTCCGTACGTGTGGTGGGTGAGCCACCCAGGCC 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCGGGGCGGGGATCTGCTCGACCTCGCATCTCTGGATAGTGGCTTCTCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCCAAGTGGGCCCATCTCTGTTATGGCTCCATTTGCCAGCTCAGCCAGCTCTCTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTGCGCGCAGGCTGGGTCTGTGGTCCGATTTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAGAGCAGCTTGGCCAAATACTCAGCG 1942
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RESULT 8

US-09-605-785-704

; Sequence 704, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; DILLON, Davin C.

```
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C16  
; CURRENT APPLICATION NUMBER: US/09/605.785  
; CURRENT FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 835  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 704  
; LENGTH: 4034  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-605-785-704
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Alignment Scores:
Pred. No.: 1,53e-300 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 4

US-09-593-793a-113 (1-553) x US-09-605-785-704 (1-4034)

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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20  
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCGCTCTGCGGACCCGGAAGCCAGCTCTTGCTG 340  
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40  
Db 341 GTCAACCTGCTAACCTTTGGCTGGAGCTGTGTTGGCGCGAGGCATCACCTATGTGCG 400  
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60  
Db 401 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTCAATGACCATGTGCTGGCATTTG 460  
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80  
Db 461 CCAGTGTGGGCTGGTCTGTGTCCTCCGCTCTAGGCTCAGCAGTACCATGTGGCTGGA 520  
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100  
Db 521 CGCTATGSCCGCGCGCCCTTCATCTGGCACCTGTCTTGGGCATCTCTGCTGAGCCTC 580  
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120  
Db 581 TTTCTCATCCCAAGGCGCGCTGCTAGCAGGGCTGTCTGTGCCGGATCCCGAGGCCCTG 640  
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140  
Db 641 GAGCTGGCACCTGCATCTCTGGGCTGGGCTGTCTGGACTTCTGTGGCCAGGTGTGCTTC 700  
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160  
Db 701 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGACCATGTCTGCCAGCC 760  
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180  
Db 761 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCTGCTGCTGCC 820
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QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
Db 821 ATTGACTGGGACACCAAGTGCCTGGCCCTACCTGGGACACCGAGGAGTGCCTCTTT 880
|||||
QY 201 GlyLeuLeuThrLeuPheLeuThrCysValAlaAlaThrLeuValAlaGluGlu 220
|||||
Db 881 GGCTGCTCACCCTCATCTCTCCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
|||||
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGCGCCCCCTCTGTGCGCCCCAC 1000
|||||
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1001 TGTGTCCATGCGCGGCGCGCTTGGCTTTCGGGAACCTGGCGGCCCTGCTTCCCGCGCTG 1060
|||||
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1061 CACCAGCTGTGTGCGCGCATGGCCCGCACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1120
|||||
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
|||||
Db 1121 ACCTGGATGGCACTCATGACCTTCAGCTGTGTTTACACGGATTTCTGTGGCGGAGGCGCTG 1180
|||||
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1181 TACCAGGGCGTGCCAGAGCTGAGCGCGGCACCGAGGCCCGGAGACACTATGATGAAGCT 1240
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RESULT 9
US-09-605-785-702
; Sequence 702, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-702
Alignment Scores:
Pred. No.: 3,67e-245 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-605-785-702 (1-4894)
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QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
|||||
Db 1311 GGCATTGGTCCAGTGTGGGCGCTGGTCTGTGTCCCGCTCTAGGCTCAGCCAGTAGCCAC 1370
|||||
QY 78 TrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
|||||
Db 1371 TGGCGTGGACGCTATGGCCGCCCGCCCTTCATCTGGGCACTGTCTTGGCATCTCG 1430
|||||
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTyrLeuAlaGlyLeuLeuCysProAspPro 117
|||||
Db 1431 CTGAGCCTCTTTCTCATCCAAAGGCGCGCTGCTAGCAGGCTGCTGTGCCGATCCC 1490
|||||
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
|||||
Db 1491 AGGCCCTCGAGCTGGCACTGCTCATCTGCGCTGGGCTGTGGGCTGTCTGTGCCAG 1550
|||||
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
|||||
Db 1551 GTGTGCTTCACCTCCACTGGAGGCGCTGCTCTGTGACCTCTCCGGACCCGACCACTGT 1610
|||||
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
|||||
Db 1611 CGCCAGGCGCTACTCTGCTCTATGCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 1670
|||||
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
|||||
Db 1671 CTGCGCTGCCATTGACTGGGACACCACTGCGCTGGCCCTTACCTGGGCACCCAGGAGGAG 1730
|||||
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
|||||
Db 1731 TGCCCTCTTTGGCGTGTCTACCCCTCATCTTCCTCACCTGCGTAGCACCACTGTCTGGTG 1790
|||||
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
|||||
Db 1791 GCTGAGGAGGAGCGCTGGGCCCCCACCAGCAGCAGAGAGGCTGTCTGGCCCCCTCTTG 1850
|||||
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
|||||
Db 1851 TCGCCCCACTGTGTCCATGCGCGGCCCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTT 1910
|||||
... QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
|||||
Db 1911 CCGCGGCTGCACAGCTGTGCTGCGCGCATGCCCGCACCTGCGCGGCTCTCTCGGGCT 1970
|||||
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
|||||
Db 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGGGCG 2030
|||||
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
|||||
Db 2031 GAGGGCTGTACCAGGGCGTGCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTAT 2090
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QY 318 AspGluGly 320
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Db 2091 GATGAAGT 2099
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RESULT 10
US-09-605-785-705
; Sequence 705, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
```

```
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605/785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-705

Alignment Scores:
Pred. No.: 5,22e-245 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-605-785-705 (1-6976)
QY 58 GlyIleGlyProValLeuLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1202 GGCATTGGTCCAGTGTGGCGCTGTCTGTCTCCCGCTCAGCCAGTACAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1262 TGGCGTGGACGATGGCGCGCGCGCCCTTCATCTGGGCACGTGCTTGGGCATCCTG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
DB 1322 CTGAGCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGTGTGCGCCGATGCC 1381
QY 118 ArgProLeuLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
DB 1382 AGGCCCTCGAGCTGGCACTGCTCATCTCCCTGGCGTGGGCTGCTGAGCTTCTGTGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
DB 1442 GTGTGCTTCACCTCCACTGGAGGCGCTGTCTCTGACCTCTCCGGGACCCGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
DB 1502 CGCCAGGCTACTCTCTATGCTTCATGATCAGTCTTGGGGGTGCTGGGCTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
DB 1562 CTGCGCTGCATTGACTGGACACCACTGCTGCTGCGCTGGCCCTACCTGGGACCCAGGAG 1621
QY 198 CysLeuPheGlyLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
DB 1622 TGCCCTTTGGGCTGTCTACCTCTCATCTTCCTTCCACTGGGTAGCAGCCACACTGCTGGTG 1681
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
DB 1682 GCTGAGGAGCAGCGCTGGGCCCCACCCAGCAGCAGAGGCGCTGTCGGCCCCCTCTTG 1741
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
DB 1742 TCGCCCCACTGTGTCCATGCGCGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
DB 1802 CCGCGGCTGCACCACTGTGTGCGGCATGCGCCCGCACCTGCGCGGCTCTTCGTGGCT 1861
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QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
DB 1862 GAGCTGTGCAGCTGGATGCGCACTCATGACCTCTTACACGAGATTTTCGTGGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
DB 1922 GAGGCGCTTACAGGCGTGGCCAGAGCTGAGCGCGCACCGAGCGCCGAGACACTAT 1981
QY 318 AspGluGly 320
DB 1982 GATGAGGT 1990

RESULT 11
US-09-071-710-16
; Sequence 16, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-16

Alignment Scores:
Pred. No.: 9,36e-238 Length: 2152
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
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DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-16 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGCGTGTACAGGGCGTGGCCAGAGTGGAGCGGCGGACCGGAGAGACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGGGCTTCGGATGGCAGCGTGGGGCTGCTCCAGCGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGTGTATGACCGGCTGGTGGCAGCATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTCCCTGTGGCTGGCGTGGCCATGCTGCCACAGTGTGGCGGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCCGCCCTCAGCGGTTCCACTTCTCAGCCCTGCAGATCTGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCTCCCTCTACCCAGGAGAGAGAGTGTCTGCCAAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTGGAGACAGCCGTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTCCCTAATGGACAGCTGGGTGTGGAGGAGTGGCTGTCCACCTCCACCC 481
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValGlyValValGlyGluProThr 478
Db 482 GCCTCTGCGGGGCTCTGCTGTGTGTCTCGTACGTGTGGTGTGGGTGAGCCACCC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGTGTGTCGGGCGGGGCGATCTGCTCGAGCTCGCCATCTCGGATAGTGC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCTGTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCCTATATGTTGTCTGCGGAGGCTGGGTCTGGTCTGCCCATTTACTTTGCT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACAGAGTAGTATTGACAGAGCGAGTGTGGCCAAATACTCAGCG 766

RESULT 12

US-09-525-397-16
; Sequence 16, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-525-397-16
Alignment Scores:
Pred. No.: 9,36E-238 Length: 2152
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-525-397-16 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGCGTGTACAGGGCGTGGCCAGAGTGGAGCGGCGGACCGGAGAGACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGGGCTTCGGATGGCAGCGTGGGGCTGCTCCAGCGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGTGTATGACCGGCTGGTGGCAGCATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTCCCTGTGGCTGGCGTGGCCATGCTGCCACAGTGTGGCGGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCCGCCCTCAGCGGTTCCACTTCTCAGCCCTGCAGATCTGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCTCCCTCTACCCAGGAGAGAGAGTGTCTGCCAAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438

Db 362 GGAGTGTAGCAGTGAGGACAGCCTGATGACAGCTTCTCCAGGCGCTAAGCCTGGA 421
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuProProPro 458
Db 422 GTCCTCTCCCTAATGAGACAGTGGTGTGGAGGAGTGGCTCTCCACCTCCACCC 481
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 482 GCGCTCTCGGGGCTCTGCTGTGATGCTCCGTACGTGTGGTGGTGGTGGTGGTGGT 541
Qy 479 GluAlaArgValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGACAGGTTGGTTCGGGGCGGGGCGATCTCCCTGGACCTCGCCATCTGGATAGTGC 601
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCCTGCTGTCCAGGTGGCCCACTCCCTGTTATGGGCTCCATGTCCAGCTACGCCAG 661
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCTATATGCTGTCTCCGCGAGGCTGGTCTGGTCCCATTTTACTTTGCT 721
Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 766

RESULT 13
US-09-071-710-15
; Sequence 15, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083-US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623

; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-15
Alignment Scores:
Pred. No.: 7,58e-235 Length: 2143
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
Gaps: 3
US-09-593-793a-113 (1-553) x US-09-071-710-15 (1-2143)
Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaAArgHisTyrAspGluGlyVal 321
Db 3 CAGGCGGTGCCAGAGCTGAGCGGGCAGCCGAGGCGGAGACACTATGATGAAGGCGTT 62
Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCAGCCTGGGGCTGTTCCTGCGAGTGGCGCATCTCCCTGGTCTTCTCTCTGCTC 122
Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTCGGCACCTCAGGAGAGTCTATTTGGCCAGTGTGGCAGCT 182
Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
Db 183 TTCCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 242
Qy 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCC 302
Qy 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyAlaAla 421
Db 303 CTCCTACCGCGGAGAGAGAGGTGTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTC 362
Qy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGGAGGACAGCCTGATGACAGCTTCTGCGGAGCCCTAAGCCTGGAGCTCCCTTC 422
Qy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCys 461
Db 423 CCTAATGGACACGTGGGTGTGGAGGAGTGGCTTCCCTGCTCCCACTCCACCCGCTCTGC 482
Qy 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
Db 483 GGGGCTCTGCTGTGATGCTCCGTAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 542
Qy 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGCGGGGCGCATCTGCTGACCTTCGCGCATCTCTGGATAGTGGCTTCTGCTG 602
Qy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCAGGTGGCCCATCCCTGTTTATGGCTCCATTTGCGAGCTCAGCAGCTCTGCTACT 662
Qy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
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Qy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 14
US-09-525-397-15

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; Sequence 15, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-525-397-15

Alignment Scores:
Pred. No.: 7.58e-235 Length: 2143
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-15 (1-2143)
QY 302 GInGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTCCCGAGAGCTGAGCGGGCAGCGAGCGGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGGAGCGCTGGGGCTGTTCTTCGACAGTGGCCCATCTCCCTGGTCTCTCTGGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTTCGCACTCGCAGCAGCTCTATTGGCCAGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSer 381
Db 183 TTCCCTGTGGTGCCTGCCGTCACATGCTGTCACAGATGTGCCCGTGGTGACAGATTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCGCGCCTCAGCGGGTTACCTTCTCAGCCCTGCAGATCTGCCCCTACACACTGGCCTCC 302
QY 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
Db 303 CTCTACCAACCGGAGAGCAGGTGTTCTTCGCCCAATACCGAGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGAGGACAGCCTGATGACCACTTCCTGCCAGGCCCTAAGCTGGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 423 CCTAATGGACACGTGGTGTCTGGAGGCGAGTGGCTCTCCACCTCCACCGCGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
Db 483 GGGGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGGCGGGGCGCATCTGCTGGACCTCGCCATCTCTGGATAGTGGCTTCCCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCAGGTGGCCCATCTCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGCACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGGTGTCTGCCGAGCGCTGGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 758
RESULT 15
US-09-605-785-703
; Sequence 703, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-703

Alignment Scores:
Pred. No.: 3,19e-218 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-605-785-703 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGGTTCGATGGGAGCCTGGGCTGTCTTCGAGTGGCCATCTCCCTGGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCATGACCGGCTGTGCGAGGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
DB 930 GTGGCAGCTTTCCCTGTGGCTGCCGGTCCACATGCTGTCCACAGTGTGGCCGTGGTG 989
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTGCGCTTACACA 1049
QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1050 CTGGCTCTCCCTTACCACCGGAGAGAGAGGTGTCTTCCGCCAAATACCGAGGGGACACT 1109
QY 419 GlyGlyAlaSerSerGlnAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 1110 GGAGGTGTAGCAGTGAAGACAGCCTGATGACCACTTCTCCCGAGGCCCTAAGCCTGGA 1169
QY 439 AlaProPheProAspGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
DB 1170 GCTCCCTTCCCTAATGGACAGCTGGGTGTGGAGCAGTGGCTGTCCACCTCCACCC 1229
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
DB 1230 CGCCTCTCGGGGCTCTGCCTGTGATGTCCTCGTACGTGTGGTGGTGGAGCCACC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
DB 1290 GAGGCCAGGGTGTTCGGGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
DB 1350 TTCCTGTGTCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
DB 1410 TCTGTCACTGCCTATATGTGTCTCGCGAGGCCCTGGGTCTGGTGCCTATTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1470 ACACAGGTAGTATTGACAAGAGCAGCTTGGCCAAATACTCAGCG 1514

RESULT 16

US-09-020-956-10

; Sequence 10, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-020-956-10

Alignment Scores:
Pred. No.: 3,67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-020-956-10 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
DB 12 GCAGTGTGGCAGCTTTCCTGTGGCTGCCGTCAGATGCTTCCACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
DB 72 GTGGTGACAGCTTCAGCGCCCTCACCGGTTTCACTTCTCAGCCCTGCAGATCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGly 416
DB 132 TACACACTGGCTCCTCTACCCACCGGAGAGCAGGTGTTCCTGCCCAAATACCGAGG 191
QY 417 AspThrGlyGlyAlaSerSerGlnAspSerLeuMetThrSerPheLeuProGlyProLys 436
DB 192 GACACTGGAGGTGTCTAGCAGTGAGGACAGCCTTGATGACAGCTTCTCCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
DB 252 CCTGGAGTCCCTTCCCTAATGGACACCTGGGTGTGGAGGAGTGGCTGCTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
DB 312 CCACCCGCGCTCTGGGGGCGCTCTGCCTGTGATGTCCTCCGTACGTGTGGTGTGGTGTGAG 371
QY 477 ProThr 478
DB 372 CCCACC 377

RESULT 17
US-09-030-607-10
; Sequence 10, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-607-10

Alignment Scores:
Pred. No.: 3.67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-030-607-10 (1-789)

QY	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
DB	12	GCAGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCC	71
QY	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
DB	72	GTGGTGACAGCTTCACGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCTGCC	131
QY	397	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
DB	132	TACACACTGGCTCCCTCTACCAACGGGAGAGCAGGTCTTCTGCCCAATAACGAGGG	191
QY	417	AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
DB	192	GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACACAGCTTCTGCCAGGCCCTAAG	251
QY	437	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro	456
DB	252	CCTGGAGCTCCCTTCCCTAATGGACACAGTGGGTGCTGGAGGAGTGGCTGTCCACCT	311
QY	457	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
DB	312	CCACCCGCCTCTGCGGGGCCCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGAG	371
QY	477	ProThr	478
DB	372	CCACCC	377

RESULT 18
US-09-605-785-10
Sequence 10, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-10

Alignment Scores:
Pred. No.: 3.67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-605-785-10 (1-789)

QY	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
DB	12	GCAGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCC	71
QY	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
DB	72	GTGGTGACAGCTTCACGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCTGCC	131
QY	397	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
DB	132	TACACACTGGCTCCCTCTACCAACGGGAGAGCAGGTGTCTGCCCAATAACGAGGG	191
QY	417	AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
DB	192	GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACACAGCTTCTGCCAGGCCCTAAG	251
QY	437	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro	456
DB	252	CCTGGAGCTCCCTTCCCTAATGGACACAGTGGGTGCTGGAGGAGTGGCTGTCCACCT	311
QY	457	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
DB	312	CCACCCGCCTCTGCGGGGCCCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGAG	371

QY 477 ProThr 478
|||||
Db 372 CCCACC 377

RESULT 19

US-09-439-313-10
; Sequence 10, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(789)
; OTHER INFORMATION: n = A,T,C or G

US-09-439-313-10

Alignment Scores:
Pred. No.: 3.67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-10 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
Db 12 GCCAGTGTGGCAGCTTCCCTGTGGCTGCCGCTGCACATGCTTCCACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 72 GTGGTGACAGCTTACCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCCTCCTCTACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGTAGCAGTGCAGACAGCCTGATGACAGCTTCTCCAGCCCTTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
Db 252 CCTGAGCTCCCTTCCCTAAATGGACAGTGGGTGTGGAGGAGTGGCTGTCTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCCGGCGCTCTGGGGCCCTCTCCCTGTGATGTCCTCCGTACGTGTGGTGGGTGAG 371
QY 477 ProThr 478

|||||
Db 372 CCCACC 377

RESULT 20

US-09-352-616A-10
; Sequence 10, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(789)
; OTHER INFORMATION: n = A,T,C or G

US-09-352-616A-10

Alignment Scores:
Pred. No.: 3.67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-352-616A-10 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
Db 12 GCCAGTGTGGCAGCTTCCCTGTGGCTGCCGCTGCACATGCTTCCACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 72 GTGGTGACAGCTTACCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCCTCCTCTACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGTAGCAGTGCAGACAGCCTGATGACAGCTTCTCCAGCCCTTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
Db 252 CCTGAGCTCCCTTCCCTAAATGGACAGTGGGTGTGGAGGAGTGGCTGTCTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCCGGCGCTCTGGGGCCCTCTCCCTGTGATGTCCTCCGTACGTGTGGTGGGTGAG 371
QY 477 ProThr 478

RESULT 21

US-09-232-149A-10
; Sequence 10, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427G6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-10

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Alignment Scores:		
Pred. No. :	3,678-109	Length:
Score:	122.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	22.06%	Indels:
DB:	4	Gaps:

US-09-593-793A-113 (1-553) x US-09-232-149A-10 (1-789)

357	QY	AlaSerValAlaAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
12	Db	GCCAGGTGTGGCAGCTTTCCTGTGGCTGCGGTGCCACATGCTGTCCACACAGTGTGCC	71
377	QY	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
72	Db	GTGGTGACAGCTTCACGCCCTTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC	131
397	QY	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
132	Db	TACACACTGGCTCCCTCTATCACCGGGAGACAGGTGTCTGCGCCAAATACCGAGGG	191
417	QY	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
192	Db	GACACTGGAGGTCTTAGCAGTAGGACACGCTGTATGACCAGCTTCTCTGCCAGGCCCTAAG	251
437	QY	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyCysSerGlyLeuLeuProPro	456
252	Db	CCTGGAGCTCCCTTCCCTTAATGACACAGTGGGTGCTGGAGGACAGTGGCTGTCCACCT	311
457	QY	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
312	Db	CCACCGCGCTCTGCGGGGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGGTGAG	371

Qy	477	ProThr	478
Db	372	CCCACC	377

RESULT 22
US-09-071-710-1

US 03 071 710 I
; Sequence 1, Application US/09071710
; Patent No. 6130043

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

; APPLICANT: GORDON, JULIAN

; APPLICANT: GRANADOS, EDWARD N.

APPLICANT: HODGES, STEVEN C.

APPLICANT: KLASS, MICHAEL R.

APPLICANT: KRATOCHVIL, JON D.

APPLICANT: RUSSELL, JOHN C. ,
APPLICANT: STROUPE, STEPHEN D. ,
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: ,
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road ,
CITY: Abbott Park ,
STATE: IL ,
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM: ,
MEDIUM TYPE: Diskette ,
COMPUTER: IBM Compatible ,
OPERATING SYSTEM: DOS ,
SOFTWARE: FASTSEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.710'

FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/850,713
 FILING DATE: 02-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 8083-US-P-
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1129
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-1

Alignment Scores:		
Pred. No.:	9,47e-74	
Score:	85.00	Length: 258
Percent Similarity:	100.00%	Matches: 85
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	15.37%	Mismatches: 0
DB:	3	Indels: 0
		Gaps: 0

US-09-593-793A-113 (1-553) X US-09-071-710-1 (1-258)

Qy	299	GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp	318
Db	2	GGCGTGTACACAGGGCGTGGCCAGAGGTAGCCGGGGACCCGAGGCCCGGAGACACTATGAT	61
Qy	319	GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe	338
Db	62	GAAGCGCTTCGATGGCAGCTGGGGCTCTCTCCAGTGGCCCATCTCCCTGGTCTTC	121

[illegible]

Qy	379	ThrAlaSerAlaAla	383
Db	242	ACAGCTTCAGCCGCC	256

RESULT 23
US-09-525-397-1
; Sequence 1, Application US/09525397

Patent No. 6252047
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525.397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071.710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-525-397-1
Alignment Scores:
Pred. No.: 9.47e-74 Length: 258
Score: 85.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.37% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-525-397-1 (1-258)

QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACCGGGCGTGGCCAGAGCTGAGCGGCGCCGAGCGGCAGACATATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGGTTCGATGGGAGCGCTGGGGCTGTCTTCAGTGGCCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGCTGGTGCAGCGATTTCGGCACTTCGAGCAGTCTATTGGCCAGT 181

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCGTGGTG 241
QY 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCGCC 256
RESULT 24
US-09-071-710-4
Sequence 4, Application US/09071710
Patent No. 6130043
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850.713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-4
Alignment Scores:
Pred. No.: 7.38e-71 Length: 247
Score: 82.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.83% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-4 (1-247)

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QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 1 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 60
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 61 GCCTCTGCGGGGCCCTCTGCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACCC 120
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 121 GAGCCAGGTGGTTCGGGGCCGGGCATCTGCTGGACCTCCCATCTCTGGATAGTGCC 180
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 181 TTCCTGCTGCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCAGCTCAGCCAG 240
QY 519 SerVal 520
Db 241 TCTGTC 246
RESULT 26
US-09-525-397-4
; Sequence 4, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
US-09-525-397-4
Alignment Scores:
Pred. No.: 7.38e-71 Length: 247
Score: 82.00 Matches: 82
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.83% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-525-397-4 (1-247)
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 1 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 60
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 61 GCCTCTGCGGGGCCCTCTGCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACCC 120
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 121 GAGCCAGGTGGTTCGGGGCCGGGCATCTGCTGGACCTCCCATCTCTGGATAGTGCC 180
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 181 TTCCTGCTGCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCAGCTCAGCCAG 240
QY 519 SerVal 520
Db 241 TCTGTC 246
RESULT 26
US-09-071-710-2
; Sequence 2, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
```



```
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-710-2

Alignment Scores:
Pred. No.: 3,04e-60 Length: 217
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 3 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-071-710-2 (1-217)
Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTCCAGAGCTGAGCGGGCCAGGCGGAGACACTATGATGAAGCGGT 62
Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGGCGAGCTGGGGCTGTTCCTGCAGTGGCGCATCTCCCTGGTCTCTCTGGTCT 122
Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGCTGGCGGTGCCACATGCCGTGTC 215

RESULT 27
US-09-525-397-2
; Sequence 2, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-525-397-2

Alignment Scores:
Pred. No.: 3,04e-60 Length: 217
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-525-397-2 (1-217)
Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTCCAGAGCTGAGCGGGCCAGGCGGAGACACTATGATGAAGCGGT 62
Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGGCGAGCTGGGGCTGTTCCTGCAGTGGCGCATCTCCCTGGTCTCTCTGGTCT 122
Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGCTGGCGGTGCCACATGCCGTGTC 215

RESULT 28
US-09-071-710-3
; Sequence 3, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
```

```
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-3623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 215
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
US-09-071-710-3

Alignment Scores:
Pred. No.: 3.57e-60 Length: 255
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-3 (1-255)
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 2 ACAGCTTCAGCGCCCTCACCGGGTTCCAGCTTCAGCCCTGCAGATCCTGCCCTACACA 61
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 62 CTGGCTCCCTCTACACCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACT 121
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 122 GGAGGTGCTAGCAGTAGGAGCAGCTGATGACACAGCTTCTGTCCAGGCCCTAAGCCTGGA 181
QY 439 AlaProPheProAsnGlyHisValGlyAlaGly 449
Db 182 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGA 214
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RESULT 29

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US-09-525-397-3
; Sequence 3, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
```

```
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 215
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
US-09-525-397-3

Alignment Scores:
Pred. No.: 3.57e-60 Length: 255
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-3 (1-255)
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 2 ACAGCTTCAGCGCCCTCACCGGGTTCCAGCTTCAGCCCTGCAGATCCTGCCCTACACA 61
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 62 CTGGCTCCCTCTACACCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACT 121
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 122 GGAGGTGCTAGCAGTAGGAGCAGCTGATGACACAGCTTCTGTCCAGGCCCTAAGCCTGGA 181
QY 439 AlaProPheProAsnGlyHisValGlyAlaGly 449
Db 182 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGA 214
```

Db 182 GCTCCCTTCCTTAATGGACACAGGTGGGTGTGGA 214

RESULT 30
US-09-071-710-5
; Sequence 5, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.PI
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-5

Alignment Scores:
Pred. No.: 231 Length: 231
Score: 34.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 6.15% Indels: 1
DB: 3 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-071-710-5 (1-231)

Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515

Db 3 GATAGTGCCTTCTGCTGTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATTGTCCAG 62

Qy 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
|||||

Db 63 CTCAGCCAGTCTGTCACCTGCTATATGGTGTCTGCCGAGG-CTGGGTCTGGTGGCCATT 121

Qy 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||

Db 122 TACTTTGCTACACAGGTAGTATTGACAGAGCGACTTGCCCAATACTCAGCG 175

RESULT 31
US-09-525-397-5
; Sequence 5, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.PI
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-5

Alignment Scores:
Pred. No.: 231 Length: 231
Score: 34.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 6.15% Indels: 1
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-525-397-5 (1-231)

Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515
|||||

```
Db 3 GATAGTGCCTTCTGCTGTCCTCCAGTGCGCCCATCCCTGTTTATGGGCTCCATTGTCCAG 62
QY 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
|||||
Db 63 CTCAGCAGTCTGCTACTGCCTATATGGTGTCTGCGCAGG-CTGGGTCTGGTGCCTT 121
QY 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 122 TACTTTGCTACACAGGTAGTATTGTGACAAGCGGACTTGGCCAAATACTCAGCG 175
RESULT 32
US-09-605-785-488
; Sequence 488, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolx, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 488
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-605-785-488
Alignment Scores:
Pred. No.: 0.658 Length: 33
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-605-785-488 (1-33)
QY 256 LeuLeuProArgLeuHisGlnLeuCys 264
|||||
Db 7 CTTCCTCCCGGCTGCACGAGTGTGC 33
RESULT 33
US-09-397-787-331
; Sequence 331, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-331
Alignment Scores:
Pred. No.: 3.47 Length: 176
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-397-787-331 (1-176)
QY 227 GluProAlaGluGlyLeuSerAlaPro 235
|||||
Db 76 GAACCTGCGGAGGACTGAGTGCCCT 102
RESULT 35
US-08-658-639-11
; Sequence 11, Application US/08658639
; Patent No. 5914238
```

GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..519
US-08-658-639-11

Alignment Scores:
Pred. No.: 12 Length: 613
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 2 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-658-639-11 (1-613)

Qy 227 GluProAlaGluGlyLeuSerAlapro 235
Db 504 GAACCTGCGGAGGACTGAGTGCCT 530

RESULT 36
US-08-944-604-11
Sequence 11, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..519
US-08-944-604-11

Alignment Scores:
Pred. No.: 12 Length: 613
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 2 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-944-604-11 (1-613)

Qy 227 GluProAlaGluGlyLeuSerAlapro 235
Db 504 GAACCTGCGGAGGACTGAGTGCCT 530

RESULT 37
US-08-944-604-15
Sequence 15, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..519
US-08-944-604-11

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..519
US-08-944-604-11

Alignment Scores:
Pred. No.: 12 Length: 613
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-944-604-11 (1-613)

Qy 227 GluProAlaGluGlyLeuSerAlapro 235
Db 504 GAACCTGCGGAGGACTGAGTGCCT 530

RESULT 37
US-08-944-604-15
Sequence 15, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..519
US-08-944-604-11

; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 130..795
; OTHER INFORMATION: /product= "BC-2"
US-08-944-604-15
Alignment Scores:
Pred. No.: 17.7 Length: 903
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-08-944-604-15 (1-903)
QY 227 GluProAlaGluGlyLeuSerAlaPro 235
|||||
Db 780 GAACCTGCGGAGGACTGAGTGCCT 806
RESULT 38
US-09-729-995-3/c
; Sequence 3, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00904
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-3
Alignment Scores:
Pred. No.: 568 Length: 29629
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-729-995-3 (1-29629)
QY 231 GlyLeuSerAlaProSerLeuSerPro 239
|||||
Db 26382 GGTCTCTCAGCCGCCAGTCTCAGCCG 26356
RESULT 39
US-09-785-487/c
; Sequence 487, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-605-785-487
Alignment Scores:
Pred. No.: 6.7 Length: 36
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-605-785-487 (1-36)
QY 318 AspGluGlyValArgMetGlySer 325
|||||
Db 36 GATGAGCGCTCGATGGCAGC 13
RESULT 40
US-09-439-313-487/c
; Sequence 487, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-487
Alignment Scores:

Pred. No.: 36
 Score: 6.7 Length: 36
 Percent Similarity: 100.00% Matches: 8
 Best Local Similarity: 100.00% Conservative: 0
 Query Match: 1.45% Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-487 (1-36)

Qy 318 AspGluGlyValArgMetGlySer 325

Db 36 GATGAGGCGTCTGGATGGCGAC 13

RESULT 41

US-08-673-190A-6

Sequence 6, Application US/08673190A

Patent No. 5985668

GENERAL INFORMATION:

APPLICANT: Mattes, Ralf

APPLICANT: Klein, Kathrin

APPLICANT: Stegmaier, Sabine

TITLE OF INVENTION: Sucrose Metabolism Mutants.

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/673,190A

FILING DATE: 27-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Forman, David S.

REGISTRATION NUMBER: 33,694

REFERENCE/DOCKET NUMBER: 06473.0001-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Enterobacter species

US-08-673-190A-6

Alignment Scores:
 Pred. No.: 65.5 Length: 357
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.45% Indels: 0
 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-673-190A-6 (1-357)

Qy 106 AlaGlyTrpLeuAlaGlyLeuLeu 113

Db 312 GCCGCGTGGCTGGCGGCGCTGCTG 335

RESULT 42

US-09-328-111-46/c

; Sequence 46, Application US/09328111
 ; Patent No. 6262333
 ; GENERAL INFORMATION:
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Steinmann, Kathleen E.
 ; APPLICANT: Astle, Jon H.
 ; APPLICANT: Burgess, Christopher C.
 ; APPLICANT: Bushnell, Steven E.
 ; APPLICANT: Carroll III, Eddie
 ; APPLICANT: Catino, Theodore J.
 ; APPLICANT: Dertli, Adnan
 ; APPLICANT: Ford, Donna M.
 ; APPLICANT: Lewis, Marcia E.
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Schlegel, Robert
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; TITLE OF INVENTION: PRODUCTS
 ; FILE REFERENCE: CCD-257 (US)
 ; CURRENT APPLICATION NUMBER: US/09/328,111
 ; CURRENT FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: US 60/088,801
 ; EARLIER FILING DATE: 1998-06-10
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 46
 ; LENGTH: 633
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(633)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-328-111-46

Alignment Scores:
 Pred. No.: 116 Length: 633
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.45% Indels: 0
 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-328-111-46 (1-633)

Qy 231 GlyLeuSerAlaProSerLeuSer 238

Db 116 GGCCTAAGTGACCGTCTCTGAGC 93

RESULT 43

US-09-345-882-3

Sequence 3, Application US/09345882

Patent No. 6399373

GENERAL INFORMATION:

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-

AND POLYMORPHIC MARKERS) ASSOCIATED WITH SAID NUCLEIC ACID.

FILE REFERENCE: GENSET.031A

CURRENT APPLICATION NUMBER: US/09/345,882

CURRENT FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: US 60/091,315

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/111,909

PRIOR FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patent.pm

SEQ ID NO 3

LENGTH: 999

TYPE: DNA

ORGANISM: Homo sapiens

US-09-345-882-3

Alignment Scores:

Pred. No.: 182 Length: 999

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-345-882-3 (1-999)

QY 93 SerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 484 AGCCTAGGCACTCTTTTAICTTG 507

RESULT 44

US-09-020-956-175/c
; Sequence 175, Application US/09020956
; Patent No. 6261562

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 175:

SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-09-020-956-175

Alignment Scores:
Pred. No.: 213 Length: 1167
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-020-956-175 (1-1167)

QY 447 GlyAlaGlySerGlyLeuLeu 454
|||||
Db 836 GGGGCTGGGGGTCTGGACTCCTG 813

RESULT 45

US-09-030-607-175/c
; Sequence 175, Application US/09030607
; Patent No. 6262245

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 175:

SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-09-030-607-175

Alignment Scores:
Pred. No.: 213 Length: 1167
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-030-607-175 (1-1167)

QY 447 GlyAlaGlySerGlyLeuLeu 454
|||||
Db 836 GGGGCTGGGGGTCTGGACTCCTG 813

Search completed: February 19, 2003, 06:36:44
Job time : 106 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 05:09:05 ; Search time 1653 Seconds
(without alignments)
5418.091 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 553
Sequence: 1 MVQRLWVSRLLRKRAQLL.....AIYEATQVVFVFKSLAKYSA 553

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 16154066 seqs, 8097743376 residues

Word size: 3

Total number of hits satisfying chosen parameters: 32278190

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
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-Q=/cgn2_1/USPRO_pool/US09593793/runat_13022003_161426_21829/app_query.fasta_1.711
-DB=EST -QFMT=fastcap -SUFFIX=olig.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
-DOALIGN=200 -THR_SCORE=quality -THR_MIN=3 -ALIGN=45 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09593793.ecgn_1_1_959_@runat_13022003_161426_21829 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WMAP -LARGESQURY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRGRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_Other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	192	34.7	946	12	BG469889 602533345
2	180	32.5	718	12	BE867241 601442309
3	136	24.6	885	14	BQ948390 AGENCOURT
4	135	24.4	1060	14	BM914562 AGENCOURT
5	108	19.5	959	14	BQ950805 AGENCOURT
6	99	17.9	894	12	BG469520 602532833
7	86	15.6	850	12	BF972601 602243025
8	76	13.7	228	9	AA112574 zm28c12.s
9	76	13.7	482	9	AF109299 AF109299
10	72	13.0	800	12	BG469487 602532993
11	69	12.5	418	12	BF922235 QV2-NT014
12	69	12.5	1035	12	BG828841 602752813
13	63	11.4	342	9	AA112573 zm28c12.r
14	60	10.8	265	12	BF371417 RCO-FN014
15	59	10.7	523	10	AW822644 uq13g05.y
16	59	10.7	537	10	AW87124 120845 MA
17	59	10.7	592	10	AW412402 uo78h02.y
18	59	10.7	630	13	BT145201 602909395
19	59	10.7	650	10	BB627844 BB627844
20	59	10.7	692	10	BB627667 BB627667
21	59	10.7	759	12	BF789072 602104930
22	59	10.7	858	13	BI107873 602901816
23	59	10.7	901	13	BI650119 603296208
24	59	10.7	929	12	BF785813 602112437
25	59	10.7	1116	12	BG242597 602354010
26	57	10.3	348	9	AA984323 am84a12.s
27	51	9.2	934	14	BQ934815 AGENCOURT
28	48	8.7	322	12	BF854825 RCS-FN020
29	48	8.7	412	10	AW175665 RC3-BT004
30	48	8.7	1025	14	BM915082 AGENCOURT
31	47	8.5	1667	14	BM912193 AGENCOURT
32	46	8.3	1063	14	BM915527 AGENCOURT
33	45	8.1	341	13	BI045233 RCS-FN020
34	45	8.1	428	12	BF854834 RCS-FN020
35	44	8.0	242	9	AA647708 vq77h04.s
36	43	7.8	1037	12	BE914848 601667874
37	41	7.4	549	12	BG081576 H3066604
38	41	7.4	700	12	BF581244 602100464
39	41	7.4	969	12	BG173136 602335411
40	39	7.1	786	12	BG174399 602334219
41	37	6.7	317	10	BB707065 BB707065
42	37	6.7	844	12	BG246497 602360526
43	34	6.1	430	9	AF109303 AF109303
44	33	6.0	466	12	BG086547 H3066604
45	33	6.0	564	13	BG964810 602829364
46	33	6.0	578	17	AZ418156 1M0194E12
47	33	6.0	700	10	BB610495 BB610495
48	33	6.0	717	12	BG745565 602723976
49	33	6.0	872	12	BG864609 602798469
50	33	6.0	963	12	BF233285 602023647
51	32	5.8	416	12	BF454698 maa08c03
52	30	5.4	468	10	BB852004 BB852004
53	29	5.2	509	10	BB701488 BB701488
54	28	5.1	748	12	BF232636 602023219
55	27	4.9	363	9	AU023209 AU023209
56	24	4.3	75	17	AZ601104 1M0419A16
57	21	3.8	572	13	BI345407 374221 MA
58	20	3.6	277	10	AW346593 28476 MAR
59	18	3.3	669	10	BB113685 BB113685
60	16	2.9	518	10	BB853288 BB853288
61	16	2.9	906	12	BF680993 602156279
62	15	2.7	414	10	BB850079 BB850079
63	15	2.7	520	12	BG364300 dab86b09
64	15	2.7	946	13	BI144556 602909416

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65 13 2.4 565 13 BM192568
66 13 2.4 865 17 CNS03VME
67 12 2.2 441 10 BB848279
68 12 2.2 744 17 CNS04J4Q
69 10 1.8 262 12 BG221458
70 10 1.8 323 12 BG193546
71 10 1.8 431 10 AW022261
72 10 1.8 450 10 AW022261
73 10 1.8 455 10 BE137141
74 10 1.8 458 10 BE690088
75 10 1.8 549 14 R50985
76 10 1.8 557 9 AL707231
77 10 1.8 622 14 BM725284
78 10 1.8 715 14 BM677725
79 10 1.8 826 12 BG214056
80 10 1.8 989 12 BE893061
81 10 1.8 1220 17 AG044788
82 9 1.6 173 9 AI335878
83 9 1.6 205 9 AI650487
84 9 1.6 219 9 AI753410
85 9 1.6 229 12 BF808211
86 9 1.6 230 17 AO892511
87 9 1.6 259 9 AV162773
88 9 1.6 268 9 AI868949
89 9 1.6 271 9 AI632739
90 9 1.6 272 9 AA036979
91 9 1.6 281 9 AI918017
92 9 1.6 283 9 AI826425
93 9 1.6 284 12 BE762324
94 9 1.6 285 10 AW104168
95 9 1.6 287 14 D24129
96 9 1.6 289 10 BE241795
97 9 1.6 293 12 BE762344
98 9 1.6 293 17 BH867320
99 9 1.6 305 9 AI650794
100 9 1.6 310 13 B1491393

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ALIGNMENTS

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RESULT 1
BG469889 946 bp mRNA linear EST 21-MAR-2001
LOCUS 602533345F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661075 5',
DEFINITION mRNA sequence.
ACCESSION BG469889
VERSION BG469889.1 GI:13402164
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 946)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLCM1459 row: i column: 12
High quality sequence stop: 798.
Location/Qualifiers
1..946
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4661075"
/clone_lib="NIH_MGC_15"
FEATURES
source

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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCACGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 120 a 331 c 296 g 199 t
ORIGIN
Alignment Scores:
Pred. No.: 1.26e-164 Length: 946
Score: 192.00 Matches: 192
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.72% Indels: 0
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BG469889 (1-946)
QY 27 GlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluVal 46
DB 1 GGCCTGGAGGTGTGTTGGCCGAGGCATCATATGTGCCCTCTGCTGCTGGAAGTG 60
QY 47 GlyValGluGluValPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
DB 61 GGGGTAGAGAGGAAGTTCATGACCATTTGGGTGCTGGGCAATTTGGCTGCTGGCCCTGGTC 120
QY 67 CysValProLeuLeuGlySerAlaSerAspHisTyrArgGlyArgTyrGlyArgArg 86
DB 121 TGTGTCCCGCTCCTAGGCTCAGCCAGTACCATGGCGTGGAGCTATGSCGCCGCCCG 180
QY 87 ProPheIleThrAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuLeuProArgAla 106
DB 181 CCCTTCATCTGGGCACCTGCTTGGGCATCTGCTGAGCCTCTTCTCATCCAGGGCC 240
QY 107 GlyThrLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeu 126
DB 241 GGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTGGAGCTGGCAGCTGCATC 300
QY 127 LeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeu 146
DB 301 CTGGGGCTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTCCATCCACCTGGAGGCCCTG 360
QY 147 LeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPhe 166
DB 361 CTCTCTGACCTCTTCGGGACCCGGACCATCTGTCGCGAGGCTACTCTCTATGCTTTC 420
QY 167 MetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspThrAspThrSer 186
DB 421 ATGATCAGCTTTGGGGGCTGCTGGGCTACCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 187 AlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuLeuLeu 206
DB 481 GCCCTGGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATC 540
QY 207 PheLeuThrCysValAlaAlaThrLeuLeuValAla 218
DB 541 TTCTCCTACCTGGGTAGCAGCCACACTGCTGCTGGCT 576
RESULT 2
BE867241
LOCUS 601442309F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846411 5',
DEFINITION mRNA sequence.
ACCESSION BE867241
VERSION BE867241.1 GI:10316017
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9559 row: a column: 04
High quality sequence stop: 693.

FEATURES

Location/Qualifiers
1..718

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3846411"

/clone_lib="NIH_MGC_65"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 112 a 227 c 210 g 168 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 8.18e-154 Length: 718
Score: 180.00 Matches: 180
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 32.55% Indels: 0
DB: 12 Gaps: 0

US-09-593-793a-113 (1-553) x BE867241 (1-718)

Qy 340 LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal 359
|||||
Db 2 CTGGTCATGGACCGCTGGTGCAGGATTCGGCACTCGGACAGTCTATTGGCCAGTGTG 61
Qy 360 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThr 379
|||||
Db 62 GCAGCTTTCCCTGTGGCTGCCGGTCCACATGCCTGTCCACAGTGTGGCGTGTGACA 121
Qy 380 AlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeu 399
|||||
Db 122 GCTTCAGCGCGCTCACCAGGTTACCTTCACGCTTCAGCCCTGCAGATCCTCCCTACACACTG 181
Qy 400 AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly 419
|||||
Db 182 GCCTCCCTCTACACCGGAGAGAGAGCTGTCTCTGCCCAATACCGAGGGACACTGGA 241
Qy 420 GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAla 439
|||||
Db 242 GGTGTAGCAGTGGAGACAGCTGATGACCATGCTTCCTGCCAGGCGCTTAAGCCTGGAGCT 301
Qy 440 ProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAla 459
|||||
Db 302 CCCTTCCTTATGGACAGTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCCCGG 361
Qy 460 LeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGlu 479
|||||
Db 362 CTCCTGGGGGCTCTGCTCTGTGATCTCCGTACGTGTGGTGGTGGAGCCACCCAG 421
Qy 480 AlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPhe 499
|||||
Db 422 GCCAGGGTGGTTCGGGGCGGGGATCTGCCTGGACCTTCGCCATCTCGCATCTGATAGTGCCTTC 481

Qy 500 LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer 519
|||||
Db 482 CTGCTGTCCAGGTGGCCCATCCTCTGTTATGGGCTCCATTGCTCCAGCTCAGCAGTCT 541

RESULT 3

BQ948390

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 885)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13611 row: b column: 08

High quality sequence stop: 615.

FEATURES

Location/Qualifiers

1..885

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6198823"

/clone_lib="Lupski_sciatic_nerve"

/sex="male"

/tissue_type="sciatic nerve"

/dev_stage="adult, 70 yr"

/lab_host="DH10B"

/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCATGATCGGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 129 a 286 c 294 g 176 t

ORIGIN

Alignment Scores:

Pred. No.: 1.72e-113 Length: 885

Score: 136.00 Matches: 136

Percent Similarity: 100.00% Conservativeness: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 24.59% Indels: 0

DB: 14 Gaps: 0

US-09-593-793a-113 (1-553) x BQ948390 (1-885)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

Db 259 ATGTCACAGAGGCTGGGTGAGCGCTGCTGCGGACCGACCGAAGCCAGCTTGTCTG 318

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40

Db 319 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGCGCAGGCATCACCTATGTGCG 378

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QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 379 CCTCTGCTGCTGAAGTGGGGTAGAGAGAGATTTCATGACCATGGTGTGGGCTTGGT 438
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 439 CCAGTCTGGGCTGCTGTGTGTCGGCTCCAGGCTCAGGCTGAGGCTGAGGCTGGA 498
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 499 CGCATGGCCGGCCGGCCCTTCATCTGGGCACTGCTTGGGATCCTGCTGAGCCCTC 558
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 559 TTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTG 618
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGly 136
Db 619 GAGCTGGCACTGCTATCCTGGGCGTGGGCTGCTGGACTTCTGTGGC 666

RESULT 4
BM914562 1060 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT_6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
5', mRNA sequence.
ACCESSION BM914562
VERSION BM914562.1 GI:19364941
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 1060)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: m column: 14
High quality sequence stop: 485.
FEATURES
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1..1060
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480245"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 282 a 294 c 314 g 169 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.78e-112 Length: 1060
Score: 135.00 Matches: 135
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.41% Indels: 0
DB: 14 Gaps: 0

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```

US-09-593-793a-113 (1-553) x BM914562 (1-1060)
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 3 GGAGGTGTAGCAGTGAGGACAGCCTGATGACACGCTTCTGCCAGGCCCTAAGCCTGGA 62
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 63 GCTCCCTCCCTTAATGGACACGCTGGTGGTGGGAGGAGGCTGCTCCACCTCCACCC 122
QY 459 AlaLeuCysGlyAlaSerAlaCysaspValSerValArgValValValGlyGluProThr 478
Db 123 GCGCTCTGCGGGGCTCTGCTGCTGATGCTCCGTACGTGTGTGTGGTGGGTGAGGCCACC 182
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 183 GAGGCCAGGTGTGTCGCGGCGGGGCACTGCTGGACCTGCCATCTGCTGATAGTGCC 242
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 243 TCTCTGCTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTCAGCTCAGCCAG 302
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 303 TCTGTCACTGCTATATGTGTGTCGCCGAGGCCCTGGGTCTGTCGCCATTTACTTTGCT 362
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 363 ACACAGGTAGTATTGTACAGGCGACTTGGCCAAATACTCAGCG 407

RESULT 5
BM950805 959 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204253 5', mRNA sequence.
ACCESSION BM950805
VERSION BM950805.1 GI:22366283
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 959)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health; Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13625 row: d column: 14
High quality sequence start: 2
High quality sequence stop: 490.
FEATURES
source
1..959
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6204253"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="vector: pCMV-Sport6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGAGCCCACTGAGTCCG-3' and
5'-GACTAGTCTTAGTCGCGAGCGGCCCT(15)-3'. Size selected >

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1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT 139 a 312 c 308 g 200 t
ORIGIN

Alignment Scores:

Pred. No.: 7.34e-88 Length: 959
Score: 108.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.53% Indels: 0
DB: 14 Gaps: 0

US-09-593-793A-113 (1-553) x BQ950805 (1-959)

Qy 446 ValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAla 465
Db 8 GTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCGCGCTCTGGCGGCTCTGCC 67
Qy 466 CysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGly 485
Db 68 TGTGATGCTCCGTACGTGTGGTGGTGAGCCACCGAGCGAGGTGGTTCCGGGC 127
Qy 486 ArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAla 505
Db 128 CGGGCATCTCGCTGGACCTCGCCATCTGGATAGTGGCTTCTGCTGCCAGGTGCC 187
Qy 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
Db 188 CCATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTCTACCTATATGGT 247
Qy 526 SerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
Db 248 TCTCCCGAGGCGTGGGTCTGGTGGCCATTTACTTTGTGTACACAGGTAGTATTGACAAG 307
Qy 546 SerAspLeuAlaLysTyrSerAla 553
Db 308 ACCGACTTGGCCAAATACTACGCG 331

RESULT 6
BG469520 894 bp mRNA linear EST 21-MAR-2001
LOCUS 602532833F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660496 5',
DEFINITION mRNA sequence.

ACCESSION BG469520
VERSION BG469520.1 GI:13401795
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 894)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLCM1458 row: a column: 09
High quality sequence stop: 671.
Location/Qualifiers

FEATURES

source

1. .894
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IMAGE:4660496"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 173 a 272 c 264 g 185 t
ORIGIN

Alignment Scores:

Pred. No.: 1.12e-79 Length: 894
Score: 99.00 Matches: 163
Percent Similarity: 97.60% Conservative: 0
Best Local Similarity: 97.60% Mismatches: 1
Query Match: 17.90% Indels: 4
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG469520 (1-894)

Qy 390 SerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal 409
Db 3 TCAGCCCTGACAGATCCCTCCCTACACTGGCCCTCCCTACACCGGGGAGACAGGTG 62
Qy 410 PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThr 429
Db 63 TTCCTGCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACC 122
Qy 430 SerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGly 449
Db 123 AGCTTCCTGCCAGGCCCTTAAGCCTGGAGCTCCCTTAATGGACAGCGTGGTCTGGA 182
Qy 450 GlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSer 469
Db 183 GCGAGTGGGCTGCTCCACCTCCACCGCGCTCTGCGGGGCTCTGCTGTGATGCTCC 242
Qy 470 ValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyLeuCys 489
Db 243 GTACGTGTGGTGGTGGGTGAGCCACCGAGCGGCGGTTCGCGGGCGGCATCTC- 301
Qy 490 --LeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuP 509
Db 302 GCCTGGACCTCGCCATCTGGATAGTGCCTTCCCTGCTGCCAGGTGGCCCATCCCTGT 361
Qy 509 heMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla- 528
Db 362 TTATGGGCTCCATGTTCAGCTCAGCTCAGCAGTGTGCTATGCTATGCTGCTCCGCGAG 421
Qy 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
Db 422 GGCCTGGTCTGTGGTGGCCATTTACTTTGCTACACAGGTAGTATTGACAGAGGCGACTTG 481
Qy 549 AlaLysTyrSerAla 553
Db 482 GCCAAATACTCAGCG 496

RESULT 7

BF972601

LOCUS

DEFINITION

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BF972601 850 bp mRNA linear EST 22-JAN-2001
LOCUS 602243025F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4331407 5',
DEFINITION mRNA sequence.

ACCESION BF972601

VERSION BF972601.1

KEYWORDS GI:12339816

SOURCE EST.

human.

```

REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcgaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1196 row: a column: 08
High quality sequence stop: 675.
FEATURES
Location/Qualifiers
1..850
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:431407"
/clone_lib="NIH_MGC_46"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 128 a 266 c 261 g 195 t
ORIGIN
Alignment Scores:
Pred. No.: 7,96e-68 Length: 850
Score: 86.00 Matches: 157
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 1
Query Match: 15.55% Indels: 1
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BF972601 (1-850)
Qy 396 ProTyThrLeuAlaSerLeuTyHisArgGluLysGlnValPheLeuProLysTyArg 415
Db 3 CCTACACACTGGCTCCCTCTACACCGGAGAGCAGGTGTTCTGCCCAATACCGA 62
Qy 416 GlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPro 435
Db 63 GGGGACACTGGAGTGCTAGCAGTGACGACAGCCTGATGACAGCTTCTCGCAGGCCCT 122
Qy 436 LysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPro 455
Db 123 AAGCTTGGAGTCCCTTCCCTAATGGACACGCTGGGTGTGGAGGAGTGCGCTGCCA 182
Qy 456 ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGly 475
Db 183 CTTCCACCGCGCTCTCGGGGCCCTCTGCCGTGATGTCCTCGTACGTGTGGTGGGT 242
Qy 476 GluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeu 495
Db 243 GAGCCACCGAGGCCAG-GTGGTTCGGGGCGGGCATCTGCTGGACCTCGCCATCTG 301
Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerSerLeuPheMetClySerIleValGln 515
Db 302 GATAGTGGCTTCTCTCTGCCAGGTGCCCATCCCTGTTTATGGGTCCATGTCCAG 361
Qy 516 LeuSerGlnSerValThrAlaTyMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
Db 362 CTCACCCAGTCTGTCTACTGTATATGTTGTTCTGCCGAGGCCCTGGGTCTGGTCCCAT 421

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Qy 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTySerAla 553
Db 422 TACTTTGTACACAGGTAGTATTTTGACAAGAGCGACTTGGCCAAATACTACGCG 475
RESULT 8
RA112574
LOCUS AAL12574 228 bp mRNA linear EST 23-DEC-1997
DEFINITION zm28c12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:526966 3', mRNA sequence.
ACCESSION AAL12574
VERSION AAL12574.1 GI:1665121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 228)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissole, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Plante, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box, 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.
FEATURES
Location/Qualifiers
1..228
/organism="Homo sapiens"
/db_xref="GDB:3918395"
/db_xref="taxon:9606"
/clone="IMAGE:526966"
/clone_lib="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGCGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTCTTTTCTTTTCTTTT 3'"
BASE COUNT 40 a 81 c 62 g 45 t
ORIGIN
Alignment Scores:
Pred. No.: 2.02e-59 Length: 228
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.74% Indels: 0
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x AAL12574 (1-228)
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1 GCTTTCCCTGTGGCTGCGGTGCCACATGCTGTCCCACAGTGTGGCGGTGGTACAGT 60
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyThrLeuAla 400

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Db 61 TCAGCGCCCTCACCAGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 120
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 121 TCCCTCTACCAACCGGAGAGCAGGTTCCTTGCCCAATACCGAGGGGACACTGGAGT 180
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 181 GCTAGCAGTGAGGACACGCTGATGACCACTTCCTGCCAGGCCCTAAG 228

RESULT 9
AF109299 AF109299 Homo sapiens prostate adult Homo sapiens cDNA clone IPCA-2
LOCUS AF109299 , mRNA sequence. 482 bp mRNA linear EST 28-JAN-2000
DEFINITION AF109299
ACCESSION AF109299
VERSION AF109299.1 GI:6782692
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 482)
JOURNAL Walker M.G., VolkMuth, W., Sprinzak, E., Hodgson, D. and Klingler, T.
MEDLINE Prediction of gene function by genome-scale expression analysis:
COMMENT prostate cancer-associated genes
Genome Res. 9 (12), 1198-1203 (1999)
20082966
Contact: Walker MG
Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304, USA
co-expressed with known prostate-cancer genes.
Location/Qualifiers
1..482
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IPCA-2"
/clone_lib="Homo sapiens prostate adult"
/tissue_type="prostate"
/dev_stage="adult"
/note="multiple clone assembly from multiple libraries and
donors"
BASE COUNT 57 a 179 c 141 g 105 t
ORIGIN
Alignment Scores:
Pred. No.: 5.28e-59 Length: 482
Score: 76.00 Matches: 151
Percent Similarity: 98.69% Conservative: 0
Best Local Similarity: 98.69% Mismatches: 1
Query Match: 13.74% Indels: 2
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x AF109299 (1-482)
Qy 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 26 GCCCAGGTGTGTTTACCTCCATCGAGGCCCTGCTCTGTGACCTCTTCGGGACCGGAC 85
Qy 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGly 175
Db 86 CACTGTGCGCAGCGCTACTCTGCTATGCTTCATGATTAGTCTTGGGGCTGCTGGGC 145
Qy 176 TyrLeuLeuProAlaIleAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 146 TACCTCTCCCTGCCATTCAGTGGGACACCACTGCCCTGGCCCTTACCTGGGGACCCAG 205
Qy 196 GluGluCysLeuPheGlyLeuLeuThrIlePheLeuThrCysValAlaAla-ThrIle 215
Db 206 GAGGAGTGCCTTTTGGCTGTCTACCCCTCATCTTCTCCTCACCTGGCTAGA-CCCCACACT 264
Qy 215 uLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPr 235
Db 3 AGCCTGATGACCACTCTCTGCGAGGCCCTAAGCCTGAGCTCCCTTCCTTAATGACAC 62
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Db 265 GCTGTGGCTGAGGAGCGAGCGCTGGGCCCCACCGAGCAGAGGCGCTGTGCGCCCC 324
Qy 235 oSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAl 255
Db 325 CTCCTTGTGCCCCACTGCTGTCCATGCGGGCGCGCTTGGCTTCCGGAACCTGGCGC 384
Qy 255 aLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgLeuPh 275
Db 385 CCTGTCTCCCGGCTGCACCACTGTGCTGCCGATGCCCGCACCTGCGCGGCTCTT 444
Qy 275 eValAlaGluLeuCysSerTrpMetAlaLeuMetThr 287
Db 445 CGTGGCTGAGCTGTGACGTGGATGGCACTCATGACC 481

RESULT 10
BG469487 BG469487 800 bp mRNA linear EST 21-MAR-2001
LOCUS BG469487
DEFINITION 602532993F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660703 5',
mRNA sequence.
ACCESSION BG469487
VERSION BG469487.1 GI:13401762
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 800)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1458 row: i column: 24
High quality sequence stop: 741.
Location/Qualifiers
1..800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4660703"
/clone_lib="NIH_MGC_15"
/lab_host="DH10B (phage-resistant)"
/tissue_type="adenocarcinoma cell line"
/note="Organ: colon; Vector: pGB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 135 a 245 c 239 g 181 t
ORIGIN
Alignment Scores:
Pred. No.: 4.57e-55 Length: 800
Score: 72.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 13.02% Indels: 1
DB: 12 Gaps: 0

US-09-593-793a-113 (1-553) x BG469487 (1-800)
Qy 426 SerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHis 445
Db 3 AGCCTGATGACCACTCTCTGCGAGGCCCTAAGCCTGAGCTCCCTTCCTTAATGACAC 62
```


BASE COUNT 227 a 273 c 341 g 194 t
ORIGIN

Alignment Scores:
Pred. No.: 3.51e-52 Length: 1035
Score: 69.00 Matches: 69
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.48% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG828841 (1-1035)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 279 ATGGTCCAGAGCTGTGGGTGAGCCGCTGCCGACCCGGAAGCCAGCTCTTGCG 338
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 339 GTCAACCTGCTAACTTTGGCCTGGAGGTGTGTTGGCGCAGGCATCACCATTGTGCGG 398
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 399 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGCTGCTGGCATTTGGT 458
QY 61 ProValLeuGlyLeuValCysValPro 69
|||||
Db 459 CCAGTGTGGGCTGTGTGTGTGCTCCG 485

RESULT 13
AA112573/c 342 bp mRNA linear EST 23-DEC-1997
LOCUS
DEFINITION zm28c12 r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:526966 5', mRNA sequence.

ACCESSION
AA112573
VERSION
AA112573.1 GI:1665120

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Wilson, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 307.

FEATURES

Location/Qualifiers

1..342

/organism="Homo sapiens"

/db_xref="GDB:3918395"

/db_xref="taxon:9606"

/clone="IMAGE:526966"

/clone_lib="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTGTGTGTGTGTGTGTGTGT 3' "

BASE COUNT 67 a 100 c 115 g 59 t
ORIGIN

Alignment Scores:
Pred. No.: 2.57e-47 Length: 342
Score: 63.00 Matches: 98
Percent Similarity: 98.00% Conservat: 0
Best Local Similarity: 98.00% Mismatches: 1
Query Match: 11.39% Indels: 2
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x AA112573 (1-342)

QY 383 AlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeu 402
|||||
Db 303 GCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGCCCTCCCTC 244
QY 403 TyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSer 422
|||||
Db 243 TACCACCGGGAGACAGAGGTGTCTGCCCAATACCAGGGGACACTGGAGGTGCTAGC 184
QY 423 SerGluAspSerLeuMetThrSerPhe-LeuProGlyProLysProGlyAlaProPhePr 442
|||||
Db 183 AGTGAGGACAGCTGATGACACAGTTCCTTGCAGGCGCTAAGCCTGGAGCTCCCTTCC 124
QY 442 OlanGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGl 462
|||||
Db 123 TAATGGACACGTGGGTGTGGAGCAGTGGCTGTCCACCTCCACCGCN-CTCTGCGG 65
QY 462 yAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481
|||||
Db 64 GGCCCTGCTGT 7

RESULT 14

BF371417/c

LOCUS

BF371417

DEFINITION

RCO-FN0140-040800-023-H03 FN0140 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF371417

VERSION

BF371417.1 GI:11333442

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 265)

Dias Neto, E., Garcia Correa, R., Vertovski-Almeida, S., Briones, M. R.,

Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. P.,

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,

Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare

, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and

Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC0&t2=RC0-FN0140-040800-023-h03&t3=2000-08-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 265.

FEATURES
source

1..265
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0140"
/dev_stage="Adult"
/note="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 68 a 72 c 94 g 31 t

ORIGIN

Alignment Scores:
Pred. No.: 1.02e-44 Length: 265
Score: 60.00 Matches: 60
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.85% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF371417 (1-265)

QY 124 LeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeu 143
|||||
Db 255 CTGCTCATCTGGCGTGGGCTGGACTTCTGTGGCCAGGTGTCTCACTCCACTA 196
|||||
QY 144 GluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerVal 163
|||||
Db 195 GAGGCCCTGCTCTGACCTCTTCGGGGACCGGACCACTGCGCCAGCCCTACTCTGTC 136
|||||
QY 164 TyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTyr 183
|||||
Db 135 TATGCCCTTCATGATCAGTCTTGGGGCTGCTGGGTACTCTCTGCTGCCATTGACTGG 76
|||||

RESULT 15
AW822644 523 bp mRNA linear EST 17-MAY-2000
LOCUS
DEFINITION
IMAGE:2803292 5', mRNA sequence.

ACCESSION
AW822644

VERSION
GI:7915661

KEYWORDS
EST.

SOURCE
house mouse.

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 523)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other ESTs: uq13q05.x1

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4441 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.

MGI:1041916

Seq primer: Primer name ambiguous
High quality sequence stop: 474.

Location/Qualifiers

1..523

/organism="Mus musculus"

/strain="C3H"

/db_xref="taxon:10090"

/clone="IMAGE:2803292"

/clone_lib="Ren Stubbs mouse thymus"

/sex="mixed"

/dev_stage="3 weeks"

/lab_host="DH10B"

/note="Organ: thymus; Vector: pT7T3D-Pac; Site_1: NotI;
Site_2: PacI; 1st strand cDNA was primed with an oligo(dT)
primer; double-stranded cDNA was ligated using 5' linker
ggcgctat and 3' linker aactggaagcttaatt. Library is
size-selected >2.5 kb and average insert size is 3.5 kb.
Clones were arrayed from primary plating; non-amplified.
Library constructed by X. Ren and L. Stubbs (Lawrence
Livermore National Laboratory and DOE Joint Genome
Institute, 7000 East Ave, L-453, Livermore, CA 94550)."

BASE COUNT 102 a 146 c 170 g 105 t

ORIGIN

Alignment Scores:
Pred. No.: 2.01e-43 Length: 523
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW822644 (1-523)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||

Db 294 AGCCCTGCTGCTAGCGACCGGAAAGCTCAGCTCCTGCTGCTCAACTGCTCACCCTTGGC 353
|||||

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuGluValGly 47
|||||

Db 354 CTGGAGGTGTGCTGCTGGTGGCGGCATTACCTATGTGCGCACCCCTCTCTGCTGGAAGTCGGG 413
|||||

QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||

Db 414 GTGGAGGAGAAATTCATGACCATGCTGTGGGCAITGGCCAGCTAGTCCCTGGTT 470
|||||

RESULT 16
AW878124 537 bp mRNA linear EST 09-JUL-2000
LOCUS
DEFINITION
IMAGE:120845 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.

ACCESSION
AW878124

VERSION
GI:7843900

KEYWORDS
EST.

SOURCE
pig.

ORGANISM
Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 537)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

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PCR Primers
FORWARD: AGGAACACGATGACCAT
BACKWARD: GTTTCCAGCTCAGCAGC
Plate: 45 row: C column: 12
Seq primer: ATTTAGCTGACACTATAG.
Location/Qualifiers
source
1. .593
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lpiG"
/tissue_type="pooled"
/lab_host="DH10B"
/Note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 96 a 161 c 186 g 94 t
ORIGIN
Alignment Scores: 2.07e-43 Length: 537
Pred. No.: 59.00 Matches: 59
Score: 59.00 Conservat: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 10.67% Mismatches: 0
DB: 10 Indels: 0
Gaps: 0
US-09-593-793a-113 (1-553) x AW787124 (1-537)
QY 8 SerArgLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
Db 297 AGCCGCTCTCGGGCATCGGAAGCCAGCTCCTGCTGTTAACCTGCTGACGTTCCGC 356
QY 28 LeuGluValCysLeuAlaGlyIleThrTyrrValProProLeuLeuGluValGly 47
Db 357 CTGGAGGTGCTGCGCCAGCATCCTACGTGCCACCCCTGCTGTGAAGTGGG 416
QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
Db 417 GTAGAGGAGAGTTCATGACCATGCTGTGGCATCGGTCCAGTGGCTGGGCTGGTC 473
RESULT 17
LOCUS AW412402 592 bp mRNA linear EST 08-FEB-2000
DEFINITION u078h02.y1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2648691 5',
similar to TR:Q39231 Q39231 SUCROSE-PROTON SYMPORTER. [1] ;, mRNA
sequence.
ACCESSION AW412402
VERSION AW412402.1 GI:6938274
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 592)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other_ESTs: u078h02.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov/image.html
MGI:1029143
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
source
1. .592
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:2648691"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 91 a 193 c 168 g 140 t
ORIGIN
Alignment Scores: 2.35e-43 Length: 592
Pred. No.: 59.00 Matches: 59
Score: 59.00 Conservat: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 10.67% Mismatches: 0
DB: 10 Indels: 0
Gaps: 0
US-09-593-793a-113 (1-553) x AW412402 (1-592)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
Db 341 CAGCTGTGCTGCGCATGCTCGACCCCTACGCCACACTCTTTGTGGCTGAGCTGTGCAGC 400
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrrThrAspPheValGlyGlyLeuTyr 301
Db 401 TGGATGGCACTTATGACTTTCACACTGTCTACACGGACTTCGTGGGAGAGGGGTGTAC 460
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrrAspGluGly 320
Db 461 CAGGTTGTACCCAGAGCCGAGCCAGCCAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCC 517
RESULT 18
LOCUS BI145201 630 bp mRNA linear EST 05-JUL-2001
DEFINITION 602909395F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5050583 5',
mRNA sequence.
ACCESSION BI145201
VERSION BI145201.1 GI:14605202
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 630)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11137 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 630.
Location/Qualifiers
source
1. .630
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:5050583"
/clone_lib="NCI_CGAP_Li9"
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI-CGP Library."
BASE COUNT 114 a 180 c 199 g 137 t
ORIGIN
Alignment Scores:
Pred. No.: 2,55e-43 Length: 630
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 13 Gaps: 0
US-09-593-793A-113 (1-553) x BI145201 (1-630)
QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 272 AGCGGTCTGCTACGGCACCAGCAAGCTCAGCTCTGCTGTCACACCTGCTCAGCTTTGGC 331
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluValGly 47
|||||
Db 332 CTGGAGGTGTGCTGCTGCTGCCGCATTACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 391
QY 48 ValGluGlyPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 392 GTGAGGAGAAATTCATGACCATGCTGGTGGGCAATTTGGCCAGTGTAGCCCTGGTT 448
RESULT 19
BB627844
LOCUS BB627844 650 bp mRNA linear EST 26-OCT-2001
DEFINITION musculus cDNA clone 9530042D02 5', mRNA sequence.
VERSION BB627844.1 GI:16465416
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 650)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Kouda
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
Tagami,M., Tagawa,A., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1..650
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9530042D02"
/clone_lib="RIKEN full-length enriched, adult male urinary
bladder"
/sex="male"
/tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTGAGTTAAATTAATTCCTCCCTCCCTCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from
Lambda FLC I."
BASE COUNT 120 a 182 c 214 g 134 t
ORIGIN
Alignment Scores:
Pred. No.: 2,65e-43 Length: 650
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x BB627844 (1-650)
QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 333 AGCGGTCTGCTACGGCACCAGCAAGCTCAGCTCTGCTGTCACACCTGCTCAGCTTTGGC 392
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluValGly 47
|||||
Db 393 CTGGAGGTGTGCTGCTGCTGCCGCATTACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 452
QY 48 ValGluGlyPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 453 GTGAGGAGAAATTCATGACCATGCTGGTGGGCAATTTGGCCAGTGTAGCCCTGGTT 509
RESULT 20
BB627667
LOCUS BB627667 692 bp mRNA linear EST 26-OCT-2001
DEFINITION BB627667 RIKEN full-length enriched, adult male urinary bladder Mus
musculus cDNA clone 9530024M01 5', mRNA sequence.
ACCESSION BB627667
VERSION BB627667.1 GI:16465271

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Pred. No.: 3.23e-43 Length: 759
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27

|||||
Db 303 AGCGGCTGTCAGGCACCGGAAGCTCAGCTCCTGCTGCTCAACCTGCTCAGCTTTGGC 362

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47

|||||
Db 363 CTGAGGTGCTGCTGCTGCCGCGCATACCTATGTGCCACCCCTTCTGCTGGAAGTCGG 422

QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66

|||||
Db 423 GTGGAGGAGAAATTCATGACCATGTGTGGGCGATTGGCCAGTGTGCTAGCGCTGGTT 479

RESULT 22

BI107873 858 bp mRNA linear EST 26-JUN-2001
LOCUS 602901816F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5031771 5',
DEFINITION mRNA sequence.

ACCESSION BI107873

VERSION BI107873.1 GI:14558766

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 858)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1088 row: 0 column: 04

High quality sequence stop: 810.

Location/Qualifiers

1. .858

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5031771"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH108"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

Alignment Scores:

Pred. No.: 3.79e-43

Score: 59.00 Length: 858

Percent Similarity: 100.00% Matches: 59

Best Local Similarity: 100.00% Conservative: 0

Query Match: 10.67% Mismatches: 0

Indels: 0

Gaps: 0

DB:

US-09-593-793A-113 (1-553) x BI107873 (1-858)

QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281

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Db 433 CAGCTGTGCTGCGCATGCTGCACCTACGCCGACTCTTTGTGGCTGAGCTGCAGC 492

QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301

|||||

Db 493 TGGATGGCACTATGACTTTACACGCTTCTACACGCACTTCTGGCAGAGGGCTGTAC 552

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

|||||

Db 553 CAGGGTGTACCCAGAGCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 609

RESULT 23

BI650119

LOCUS 603296208F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5337073 5',

DEFINITION mRNA sequence.

ACCESSION BI650119

VERSION BI650119.1 GI:15564355

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 901)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1855 row: p column: 02

High quality sequence stop: 778.

Location/Qualifiers

1. .901

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5337073"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH108"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

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22, 37-43 (1999)."

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22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

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Db 339 AGCCGTCGTACGGACCCGGAAGCTCAGCTCCTGCTGGTCAACCTGCTCACCTTTGGC 398
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QY 28 LeuGluValCysLeuAlaAGlyLeThrTyrValProLeuLeuLeuGluValGly 47
|||||
Db 399 CTGGAGTGTGCTGCTGGTCCGCCATCTACCTATGTGCCACCCCTCTGCTGGAAGTCGGG 458
|||||
QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 459 GTGGAGGAGAAATTCATGACCATGTGTGGGCAATTGGCCAGTGTAGGCTGGTT 515
|||||
RESULT 24
BF785813 929 bp mRNA linear EST 12-JAN-2001
LOCUS 602112437F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240617
DEFINITION 5', mRNA sequence.
ACCESSION BF785813
VERSION BF785813.1 GI:12090849
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9855 row: j column: 10
High quality sequence stop: 610.
Location/Qualifiers
1..929
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 190 a 275 c 262 g 202 t
ORIGIN
Alignment Scores:
Pred. No.: 4.19e-43 Length: 929
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BF785813 (1-929)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
|||||
Db 267 CAGCTGTGTCGGCATGCTCGCACCCCTACCGGACTCTTTGTGGCTCAGCTGTGCAGC 326
|||||
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
|||||
Db 327 TGGATGGCACTTATGACTTTTCACACTGTCTACACGCACTTCGTGGCAGAGGGGCTGTAC 386
|||||
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
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Db 387 CAGGGTGTACCCAGAGCCGAGCCAGCACCAGGCCCCGGAGACACTATGATGAAGC 443
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RESULT 25
BG242597 1116 bp mRNA linear EST 13-FEB-2001
LOCUS 602354010F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4482362 5',
DEFINITION mRNA sequence.
ACCESSION BG242597
VERSION BG242597.1 GI:12752412
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1116)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10319 row: c column: 03
High quality sequence stop: 666.
Location/Qualifiers
1..1116
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 209 a 349 c 314 g 244 t
ORIGIN
Alignment Scores:
Pred. No.: 5.3e-43 Length: 1116
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BG242597 (1-1116)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
|||||
Db 53 CAGCTGTGTCGGCATGCTCGCACCCCTACCGGACTCTTTGTGGCTGAGCTGTGCAGC 112
|||||
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
|||||
Db 113 TGGATGGCACTTATGACTTTTCACACTGTCTACACGCACTTCGTGGGAGGGGCTGTAC 172
|||||
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 173 CAGGGTGTACCCAGAGCCGAGCCAGCACCAGGCCCCGGAGACACTATGATGAAGC 229
|||||
RESULT 26
AA984323 348 bp mRNA linear EST 27-MAY-1998
LOCUS am84a12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
DEFINITION IMAGE:1629790 3', mRNA sequence.
```

```

ACCESSION      AA984323
VERSION        AA984323.1  GI:3162848
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 348)
AUTHORS        Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
                Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
                J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                White,Y., Wylie,T., Waterston,R. and Wilson,R.
                WashU-NCI human EST Project
TITLE          Unpublished (1997)
JOURNAL        Contact: Wilton RK
COMMENT        Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                This clone is available royalty-free through LML; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                Possible reversed clone: polyT not found
                Seq primer: -40ml3 fwd. ET from Amersham
                High quality sequence stop: 348.
                Location/Qualifiers
FEATURES       source
               1..348
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:1629790"
                /clone_lib="Stratagene schizo brain S11"
                /sex="male"
                /tissue_type="schizophrenic brain S-11 frontal lobe"
                /dev_stage="34 years old"
                /lab_host="SOLR (kanamycin resistant)"
                /notes="Vector: Bluescript SK-; Site_1: EcoRI; Library
                constructed from S-11 frontal lobe, male, 34 years old,
                50% caucasian, 50% Aleutian. Schizophrenic suicide.
                Random primed into EcoRI site of ZAP II Vector. Mass
                excised. Custom library. Avg insert length 1.4kb.
                Material obtained by Johnston N., Torrey, E.F., Yolken R.,
                and the Stanley Neuropathology Consortium. Analysis of
                RNAs from the brains of individuals with psychiatric
                Diseases (Unpublished) Stanley Neurovirology Laboratory,
                Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT     78 a 99 c 118 g 53 t
ORIGIN
Alignment Scores:
Pred. No.:      7.99e-42      Length:      348
Score:          57.00      Matches:      95
Percent Similarity: 97.94%      Conservative: 0
Best Local Similarity: 97.94%      Mismatches: 1
Query Match:    10.31%      Indels:    2
DB:             9      Gaps:          0

US-09-593-793a-113 (1-553) x AA984323 (1-348)
QY 326 LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 348 CTGGGGCTGTCTCGAGTGCAGCATCTCCCTGGTCTTCTCTGTGTCATGGACCGGCTG 289
QY 346 ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365
Db 288 GTCCAGGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCTGTGGCT 229
QY 366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAla-Leuth 385
Db 228 GCCGGTGCACATGCTGCTCCACAGTGTGGCGTGGTGCAGCTTCAGCCGA-CCTCAC 170
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisar 405
Db 169 CGGGTTACCTTCTCAGCCCTGCAGATCTGCGCCTACACACTGGCCTCCTCTACACCG 110

QY 405 gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
Db 109 GGAGAAGCAGGTCTCTCTGCCAAATACCGAGGGGAGTGGAGGTCT 61

RESULT 27
LOCUS      BQ934815
DEFINITION AGENCOURT_8881033 NCI_CGAP_Co24 Mus musculus cDNA clone
ACCESSION  BQ934815
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 934)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13892 row: i column: 05
            High quality sequence stop: 634.
            Location/Qualifiers
FEATURES     source
            1..934
            /organism="Mus musculus"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="IMAGE:6396364"
            /clone_lib="NCI_CGAP_Co24"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.6 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT   164 a 278 c 273 g 219 t
ORIGIN

Alignment Scores:
Pred. No.:      8.62e-36      Length:      934
Score:          51.00      Matches:      51
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     9.22%      Indels:    0
DB:             14      Gaps:          0

US-09-593-793A-113 (1-553) x BQ934815 (1-934)
QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
Db 267 AGCCGTCGTCTACGGCAGCCGGAAGCTCAGCTCTCTGTCAACCTGCTCACCCTTGGC 326
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrIleThrValProLeuLeuLeuGluValGly 47
Db 327 CTGGAGGTGCTGCTGCTGCCGCAATACCTATGTGCCACCCCTTCTGTGGAAGTCGG 386
... QY 48 ValGluGluLysPheMetThrMetValLeuGly 58
Db 387 GTGGAGGAGAAATTCATGACCATGGTGGTGGGC 419
RESULT 28
LOCUS      BF854825/c
DEFINITION RC6-FN0202-271000-011-A03 FN0202 Homo sapiens cDNA, mRNA sequence.

```



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ACCESSION   BF854825
VERSION     BF854825.1  GI:12242569
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 322)
AUTHORS    Dias Neto,E., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Nagai,M.A., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
            Goldman,G.H., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            Brunstein,A., de Oliveira,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
            271000-011-A03&t3=2000-10-27&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 12
            High quality sequence stop: 321.
FEATURES    Location/Qualifiers
             source
               1..322
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="FN0202"
               /dev_stage="Adult"
               /note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
               : Site_2: SmaI; A mini-library was made by cloning
               products derived from ORESTES PCR (U.S. Letters Patent
               application No. 196,716 - Ludwig Institute for Cancer
               Research) profiles into the puc 18 vector. Reverse
               transcription of tissue mRNA and cDNA amplification were
               performed under low stringency conditions."
BASE COUNT  64 a 101 c 112 g 45 t
ORIGIN
Alignment Scores:
Pred. No.: 1.21e-33 Length: 322
Score: 48.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.68% Indels: 0
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BF854825 (1-322)
Qy 430 SerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGly 449
|||||
Db 242 AGCTTCCTGCCAGGCCCTAAGCGCTCCCTCCCTAATGGACACGGTGGTCTCGGA 183
Qy 450 GlySerGlyLeuLeuProProProAlaLeuGlyAlaSerAlaCysAspValSer 469
|||||
Db 182 GCGAGTGGCGCTGCCACCTCCACCGCGCTCTCGGGGGCTCTGCGTGTGATGCTCC 123
Qy 470 ValArqValValValGlyGluPro 477
|||||
Db 122 GTACGTGTGGTGGTGGTGAGCCC 99
RESULT 29
AW175665/c

LOCUS       AW175665
DEFINITION  RC3-BT0046-310899-002-F07 BT0046 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW175665
VERSION     AW175665.1  GI:6441806
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 412)
AUTHORS    HCGP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
JOURNAL
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0046-
            310899-002-F07&t3=1999-08-31&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 411.
FEATURES    Location/Qualifiers
             source
               1..412
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="BT0046"
               /dev_stage="Adult"
               /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
               SmaI; A mini-library was made by cloning products derived
               from ORESTES PCR (U.S. Letters Patent application No. 196
               716 - Ludwig Institute for Cancer Research) profiles
               into the puc 18 vector. Reverse transcription of tissue
               mRNA and cDNA amplification were performed under low
               stringency conditions."
BASE COUNT  106 a 117 c 128 g 61 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-33 Length: 412
Score: 48.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.68% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x AW175665 (1-412)
Qy 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
|||||
Db 401 CCTTCCCTGTTTATGGGCTCCATTGTCAGCTCAGCCAGTCTGTCACGTATATGCTG 342
Qy 526 SerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
|||||
Db 341 TCTGCCGAGCGCTGGGTCTGTCGCCATTTACTTTGTACACAGGTAGTATTTGACAAG 282
Qy 546 SerAspLeuAlaLysTyrSerAla 553
|||||
Db 281 ACCGACTTGGCCAAATACTACGCG 258
RESULT 30
BW915082
LOCUS       BW915082
DEFINITION  AGENCOURT_6702317 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481218
            5', mRNA sequence.
ACCESSION   BW915082
VERSION     BW915082.1  GI:19365461
KEYWORDS    EST.

```

SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1025)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2005 row: f column: 03 High quality sequence start: 35 High quality sequence stop: 657.
FEATURES	<p>Location/Qualifiers</p> <p>1..1025</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:5481218"</p> <p>/clone_lib="NIH_MGC_41"</p> <p>/tissue_type="amelanotic melanoma, cell line"</p> <p>/lab_host="DH10B (phage-resistant)"</p> <p>/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."</p>
BASE COUNT	237 a 273 c 252 g 263 t
ORIGIN	
Alignment Scores:	
Pred. No.:	5.35e-33
Score:	48.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	8.68%
DB:	14
US-09-593-793A-113 (1-553) x BM915082 (1-1025)	
QY 506	ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
Db 12	CCATCCCTGTTTATGGCTCCATTGTCACCTAGCCAGTCTGTCACTGCCTATATGGTG 71
QY 526	SerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
Db 72	TCCTGCCGACGCCCTGGCTCTGGTCGCCATTCTTTCTACACAGGTAGTATTGTACAAG 131
QY 546	SerAspLeuAlaLysTyrSerAla 553
Db 132	AGGACTTGGCCAAATACTCAGCG 155
RESULT 31	
BM912193	
LOCUS	BM912193 1667 bp mRNA linear EST 12-MAR-2002
DEFINITION	AGENCOURT_5613122 NIH_MGC_41 Homo sapiens cdna clone IMAGE:5473696
ACCESSION	5', mRNA sequence.
VERSION	BM912193
KEYWORDS	EST.
SOURCE	BM912193.1 GI:19362572
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1667)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov ;
Tissue Procurement: DCTD/DTP ;
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI985 row: 1 column: 17
High quality sequence stop: 448.
Location/Qualifiers :
1..1667
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5473696"
/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 310 a 665 c 258 g 418 t 16 others
ORIGIN

Alignment Scores: 1
Pred. No.: 8.2e-32 Length: 1667
Score: 47.00 Matches: 47
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.50% Indels: 0
DB: 14 Gaps: 0

US-09-593-793A-113 (1-553) x BM912193 (1-1667)

QY 507 SerLeuPheMetGlySerIleValGlnLeuSerClnSerValThrAlaTyrMetValSer 526
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Db 1 TCCTGTGTTATGGGCTCCATTGTCCAGCTCAGGCAGTCTGTCACTGGCTATATGGTGCT 60
|||||

QY 527 AlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSer 546
|||||
Db 61 GCGCAGGCCCTGGTCTGGTTCGCATTACTTTGCTACACAGGTAGTATTGTGACAAAGC 120
|||||

QY 547 AspLeuAlaLysTyrSerAla 553
|||||
Db 121 GACTTGGCCAAATACTCAGCG 141
|||||

RESULT 32
BM915527
LOCUS
DEFINITION

BM915527 1063 bp mRNA linear EST 12-MAR-2002
5', mRNA sequence. NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481717

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM915527
BM915527.1 GI:19365906
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1063)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/Drp
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2006 row: j column: 22
High quality sequence start: 131
High quality sequence stop: 308.
Location/Qualifiers
1..1063
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5481717"
/tissue_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 246 a 283 c 261 g 272 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 3.77e-31 Length: 1063
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.32% Indels: 0
DB: 14 Gaps: 0
US-09-593-793A-113 (1-553) x BW915527 (1-1063)
QY 507 SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSer 526
|||||
Db 1 TCCCTGTTATGGGCTCCATTGTCAGCTCAGCCAGCTGTGCTACCTATATGCTGTCT 60
QY 527 AlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSer 546
|||||
Db 61 GCCGCGCCCTGGGTCTGCTGCCATTACTTTGCTACACAGGTAGTATTTGACAAGAGC 120
QY 547 AspLeuAlaLysTyrSer 552
|||||
Db 121 GACTTGGCCAAATACTCA 138
RESULT 33
BI045233 341 bp mRNA linear EST 14-JUN-2001
LOCUS RC6-FN0202-080101-014-F01 FN0202 Homo sapiens cDNA, mRNA sequence.
DEFINITION BI045233
ACCESSION BI045233.1 GI:14451855
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 341)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
COMMENT
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
080101-014-F01&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 279.
Location/Qualifiers
1..341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0202"
/dev_stage="Adult"
/note="Organ: prostate, normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 56 a 105 c 84 g 95 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 7.19e-31 Length: 341
Score: 45.00 Matches: 45
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.14% Indels: 0
DB: 13 Gaps: 0
US-09-593-793A-113 (1-553) x BI045233 (1-341)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
|||||
Db 206 GCATTGGTCCAGTGTGGGCTGTGCTGTGCTCCGCTCTAGGCTCAGCCAGTCACCAC 265
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTyrPheAlaLeuSerLeuGlyIleLeu 97
|||||
Db 266 TGGCGTGGACGCTATGGCGCGGCGGCTTCATCTGGCAGCTGCTTGGGCATCCTG 325
QY 98 LeuSerLeuPheLeu 102
|||||
Db 326 CTGAGCCCTCTTCTC 340
RESULT 34
BF854834 428 bp mRNA linear EST 16-JAN-2001
LOCUS RC6-FN0202-271000-011-E04 FN0202 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF854834
ACCESSION BF854834
VERSION BF854834.1 GI:12242578
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 428)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

```

```
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&tl2=RC6-FN0202-
271000-011-E04&tl3=2000-10-27&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 423.
FEATURES
Location/Qualifiers
1..428
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0202"
/dev_stage="Adult"
/note="organ: prostate_normal; Vector: puc18; Site_1: Smai
; Site_2: Smai; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector; Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 111 a 111 c 137 g 68 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 9,62e-31 Length: 428
Score: 45.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.14% Indels: 0
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BF854834 (1-428)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 218 GGCATTGGTCCAGTGTGGCCCTGGTCTGTCCGCTCCTAGGCTACCGAGTGACCAC 159
QY 78 TrpArgGlyArgTyGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 158 TGGCGTGGAGCGTATGGCGCGCGCGCCCTTCATCTGGGCACCTGTCCTTGGGCATCCTG 99
QY 98 LeuSerLeuPheLeu 102
DB 98 CTGAGCCTCTTCTC 84
RESULT 35
AA647708 242 bp mRNA linear EST 28-OCT-1997
LOCUS vq77h04.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
DEFINITION IMAGE:1108375 5', mRNA sequence.
ACCESSION AA647708
VERSION AA647708.1 GI:2574137
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 242)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box #501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:606543
High quality sequence stop: 213.
FEATURES
Location/Qualifiers
1..242
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:1108375"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="organ: embryo; Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTGACCGTCGACCGTGTGTGTTT-3', CDNAS
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
BASE COUNT 42 a 68 c 75 g 57 t
ORIGIN
Alignment Scores:
Pred. No.: 3,79e-30 Length: 242
Score: 44.00 Matches: 44
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.96% Indels: 0
DB: 9 Gaps: 0
US-09-593-793a-113 (1-553) x AA647708 (1-242)
QY 16 AlaGlnLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGly 35
DB 109 GCTAGCTCCTGCTGGTCAACCTGCTACCTTGGCTGGAGTGTCCTGGCGCG 168
QY 36 IleThrTyValProLeuLeuGluValGlyValGluLysPheMetThrMet 55
DB 169 ATTACTATGTCCACCCCTTCTGCTGGAAGTGGGGTGGAGAGAAATTCATGACCATG 228
QY 56 ValLeuGlyIle 59
DB 229 GTGTTGGGCATT 240
RESULT 36
BE914848 1037 bp mRNA linear EST 29-
LOCUS BE914848
DEFINITION 601667874F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3967,
mRNA sequence.
ACCESSION BE914848
VERSION BE914848.1 GI:10413891
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1037)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```


REFERENCE 1 (bases 1 to 700)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM9803 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 680.
Features Location/Qualifiers
1..700
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4220415"
/clone_lib="NCI_CGAP_C024"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 110 a 227 c 197 g 166 t
ORIGIN
Alignment Scores:
Pred. No.: 8.17e-27 Length: 700
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.41% Indels: 0
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BF581244 (1-700)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
Db 254 CAGCTGTGCTGCCGATGCTCGCACCTACGCCGACTTTTGTGGCTGAGCTGCAGC 313
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
Db 314 TGGATGGCATTATGACTTTCACACTGTTCTACAGGACTTCGTGGAGAGGGGCTGTAC 373
QY 302 Gln 302
Db 374 CAG 376
RESULT 39
BG173136
LOCUS
DEFINITION BG173136 969 bp mRNA linear EST 06-FEB-2001
mRNA sequence.
ACCESSION BG173136
VERSION BG173136.1 GI:12679748
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 969)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10257 row: e column: 03
High quality sequence stop: 608.
Features Location/Qualifiers
1..969
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4458602"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 199 a 289 c 287 g 194 t
ORIGIN
Alignment Scores:
Pred. No.: 1.24e-26 Length: 969
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.41% Indels: 0
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BG173136 (1-969)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
Db 229 CAGCTGTGCTGCCGATGCTCGCACCTACGCCGACTTTTGTGGCTGAGCTGCAGC 288
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
Db 289 TGGATGGCATTATGACTTTCACACTGTTCTACAGGACTTCGTGGAGAGGGGCTGTAC 348
QY 302 Gln 302
Db 349 CAG 351
RESULT 40
BG174399
LOCUS
DEFINITION BG174399 786 bp mRNA linear EST 06-FEB-2001
mRNA sequence.
ACCESSION BG174399
VERSION BG174399.1 GI:12681102
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 786)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10254 row: e column: 05
High quality sequence stop: 666.


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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 844)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10336 row: c column: 08
High quality sequence stop: 655.
FEATURES
    source
    1..844
        Location/Qualifiers
            /organism="Mus musculus"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="IMAGE:488895"
            /tissue_type="tumor, biopsy sample"
            /dev_stage="10 months, virgin"
            /lab_host="DH10B"
            /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Library constructed by Life Technologies. Investigator
            providing samples: Gilbert Smith, NIH"
BASE COUNT 152 a 251 c 262 g 179 t
ORIGIN
Alignment Scores:
Pred. No.: 4.7e-23 Length: 844
Score: 37.00 Matches: 37
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.69% Indels: 0
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BG246497 (1-844)
QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
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Db 336 AGCGGTGCTGACGGCACCAGCGAAGCTCAGCTCTGCTGTCACCTTGGC 395
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeu 44
|||||
Db 396 CTGGAGGTGCTGCTGCTGCCGCATTACTATGTGCCACCCCTTCTGCTG 446
RESULT 43
AF109303
LOCUS AF109303 430 bp mRNA linear EST 28-JAN-2000
DEFINITION AF109303 Homo sapiens prostate adult Homo sapiens cDNA clone IPCA-8
mRNA sequence.
ACCESSION AF109303
VERSION AF109303.1 GI:6782698
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 430)
AUTHORS Walker,M.G., Volkmut,W., Sprinzak,E., Hodgson,D. and Klingler,T.
TITLE Prediction of gene function by genome-scale expression analysis:
prostate cancer-associated genes
JOURNAL Genome Res. 9 (12), 1198-1203 (1999)
MEDLINE 20082966
COMMENT Contact: Walker MG
Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304, USA
co-expressed with known prostate-cancer genes.
FEATURES
    source
    1..430
        Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IPCA-8"
            /tissue_type="prostate"
            /dev_stage="adult"
            /note="multiple clone assembly from multiple libraries and
            donors"
BASE COUNT 81 a 119 c 150 g 80 t
ORIGIN
Alignment Scores:
Pred. No.: 1.09e-20 Length: 430
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.15% Indels: 0
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x AF109303 (1-430)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||
Db 252 ATGTTCACAGGCTGTGGGTGAGCGCCCTGTCGGCACCAGGAGCTCTTGTGCTG 311
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAla 34
|||||
Db 312 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCA 353
RESULT 44
BG068547/c
LOCUS BG068547 466 bp mRNA linear EST 26-JAN-2001
DEFINITION H3066G04-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3066G04 3', mRNA sequence.
ACCESSION BG068547
VERSION BG068547.1 GI:12551116
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 466)
AUTHORS Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
,T.S., Carter,M.G. and Ko,M.S.H.
TITLE Verification and initial annotation of NIA mouse 15K cDNA clone set
JOURNAL Unpublished (2001)
COMMENT Other ESTs: H3066G04-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://igsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3066 row: G column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 466
POLYA=Yes.
FEATURES
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    1..466
        Location/Qualifiers
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="niaEST:H3066G04-3"
            /db_xref="taxon:10090"
            /clone="H3066G04"
            /clone_lib="NIA Mouse 15K cDNA Clone Set"
            /sex="Clones arrayed from a variety of cDNA libraries"
            /dev_stage="Clones arrayed from a variety of cDNA
            libraries"
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/lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 121 a 138 c 126 g 81 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9.9e-20 Length: 466
 Score: 33.00 Matches: 60
 Percent Similarity: 96.77% Conservative: 0
 Best Local Similarity: 96.77% Mismatches: 1
 Query Match: 5.97% Indels: 2
 DB: 12 Gaps: 0

US-09-593-793a-113 (1-553) x BG068547 (1-466)

QY 485 GlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnVal 504
 |||||
 Db 363 GGACGGGGCATTTGCTGGACCTGGCCATTCTGGACAGTGCCCTTTCTGCTGCCAGGTG 304
 |||||
 QY 505 AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
 |||||
 Db 303 GCTCCGTCCTGTTTCATGGCTCCATTGCCAGTGAGCCA-CTCTGTCTACATGCTATAT 245
 |||||
 QY 524 tValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAs 544
 |||||
 Db 244 GGTATCAGTCGAGGCTGGGTCTGGTGCCTTACTTTGTCTACACAGGTAGTGTGTA 185
 |||||
 QY 544 pLys 545
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 Db 184 CAAG 181

RESULT 45
 BG964810
 LOCUS 602829364F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4984191 5',
 DEFINITION mRNA sequence.
 ACCESSION BG964810
 VERSION BG964810.1 GI:14352447
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM10989 row: p column: 16
 High quality sequence stop: 563.
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 /clone_lib="NCI_CGAP_Co24"
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 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 95 a 156 c 168 g 143 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.27e-19 Length: 564
 Score: 33.00 Matches: 60
 Percent Similarity: 96.77% Conservative: 0
 Best Local Similarity: 96.77% Mismatches: 1
 Query Match: 5.97% Indels: 2
 DB: 13 Gaps: 0

US-09-593-793a-113 (1-553) x BG964810 (1-564)

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 QY 505 AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
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 Db 308 CAAG 311

Search completed: February 19, 2003, 06:34:54
 Job time : 1672 secs

Seq 16

2-7760

→ encodes 254 AA

AA 299-553

553

~~299~~
254

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 05:16:55 ; Search time 71 Seconds
(without alignments)
3966.986 Million cell updates/sec

Title: US-09-593-793a-113

Perfect score: 553

Sequence: 1 MVQRLMWSRLLRHKAQLL.....AIYPATQVDFKSLAKYSA 553

Scoring table:

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 424239 seqs, 254661826 residues

Word size: 3

Total number of hits: 3
Parameters: 785189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Database :

Published Applications NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	553	100.0	3410	9	US-10-012-896-110
4	553	100.0	3410	9	US-09-895-793-110

5	553	100.0	3410	9	US-09-895-814-110	Sequence 110, App
6	553	100.0	3410	10	US-09-745-288-100	Sequence 100, App
7	553	100.0	3410	10	US-09-759-143-110	Sequence 110, App
8	553	100.0	3410	10	US-09-780-669-110	Sequence 110, App
9	553	100.0	3410	10	US-09-030-606-110	Sequence 110, App
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13	320	57.9	4034	9	US-09-895-793-704	Sequence 704, App
14	320	57.9	4034	9	US-09-895-814-704	Sequence 704, App
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ALIGNMENTS

RESULT 1
US-09-838-785-1
; Sequence 1, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
; APPLICANT: Lau, Ted
; APPLICANT: Lin, Rick
; APPLICANT: Parkes, Debbie
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; APPLICANT: Van Heult, Pam T
; APPLICANT: Wu, John
; TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
; FILE REFERENCE: 51831AUSM1
; CURRENT APPLICATION NUMBER: US/09/838,785
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/200,065
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(1943)
US-09-838-785-1

Alignment Scores:
Pred. No.: 0 Length: 3320
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-838-785-1 (1-3320)

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Db 1362 GCTTTCCTGTGGCTGCCGTCACATGCCAGTGTCCACAGTGTGGCGGTGTGACAGCT 1421
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
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QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
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QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1902 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1940
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RESULT 2

US-09-232-880-110
; Sequence 110, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-232-880-110 (1-3410)

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Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCGGACCATGTGCGCAGGCC 763
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QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 823
|||||
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluLysLeuPhe 200
|||||
Db 824 ATTTAGTGGGACACAGTGGCTGGCCCTTACCTGGGCACCGAGGAGTGCCTCTTT 883
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QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
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Db 884 GGCCTGCTCACCTCATCTTCTCCTACCTGCGTAGCAGCCACACTGCTGTGGCTGAGGAG 943
|||||
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGCTGTGGGCCCTCTCTTGTGCGCCAC 1003
|||||
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCCGGAACCTGGGCGCTGCTTCTCCCGGCTG 1063
|||||
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgAlaGlyLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGTCGCGCATGCGCCGACCCCTGCGCGGCTCTTGTGTGGCTGAGTGTGC 1123
|||||
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
|||||
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGGAGGGCTG 1183
|||||
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGGCGTCCCGAGCTGAGCGGGCACCGGAGGCCCGGAGACACTATATGAAGGC 1243
|||||
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGTCAGTGGGCATCTCCCTGCTCTCTCTG 1303
|||||
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGCTGCTGCAGCGATTTCGGCACTCAGCAGAGTCTATTGCGCCAGTGTGGCA 1363
|||||
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
|||||
Db 1364 GCTTTTCCCTGTGGCTGCCGTGCCACATGCTGTCTCCACAGTGTGGCGCTGGTGCAGACT 1423
|||||
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCGCCTCACCAGGTTTCACTTCTCAGCCCTGCGAGATCCTGCCCTACACACTGGCC 1483
|||||
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||

Db	1484	TCCCTCTACCACCGGAGAGCAGGTGTTCTCTGCCCAATAACCGAGGGGACACHTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTCAGGACACGCCTGATGACCACTCTCTGCCAGGCCCTAAGCCTTGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACGCTGGGTGTCGGAGCAGCTGGCTCTCCACCTCCACCCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCCCTCTGCCCTGTGATGTCCTCGTACGTGTGGTGGTGGAGCCACCCAGGCCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTGGTTCGGGGCGGGGCATCTGCCTGGACCTGCCATCTCTGGATGTCCTTCTCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCACAGGTGGCCGCATCCCTGTTATTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCATATATGTGTCTGCCCGAGCCCTGGGTCTGGTGCATTTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaIleTyrSerAla	553
Db	1904	GTAGTATTTCACAGACGCACTTGGCCAAATACTCAGCG	1942

RESULT 3

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US-10-012-896-110
: Sequence 110, Application US/1012896
: Publication No. US20020183251A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqiu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/012.896
: CURRENT FILING DATE: 2001-12-10
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 110
: LENGTH: 3410
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-012-896-110
Alignment Scores:

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Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
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Db 1244 GTTCGGATGGCAGCCTGGGGCTGTCTCGAGTCGCCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGCTGGTCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCTTTCCTGTGGCTGGCGGTGCCACATGCCCTGCCACAGTGGCCGTGGTACAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCGCCCTCACCGGCTTCACCTTCTCAGCCCTGCAGATCTTCGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1484 TCCCTCTACCCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1544 GCTAGCAGTAGGACAGCCTGATGACCACTTCCTGCCAGGCCCTTAAGCCTGGAGCTCCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
|||||
Db 1604 TTCCCTATGACAGCTGGGTGCTGGAGCAGTGGCTTCCACCTCCACCCCGGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
Db 1664 TCGGGGGCTCTGCTGTGATCTCTCCAGTGTGTGGTGGTGGTGGAGCCACCCAGGCC 1723
Qy 481 ArgValValProGlyArgGlyGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGTGGTTCGGGGCGGGGATCTGCTGGACCTCGGCATCTCGATGGATGGCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCCAAGTGGCCCATCCCTGTTTATGGCTCCATTGTCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCTATATATGGTGTCTGCGCGCAGGCCTGGGTCTGGTGGCATTTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1904 GTAGTATTTGACAGAGCGACTTGGCCAAATACTACAGCG 1942

RESULT 4
US-09-895-793-110
: Sequence 110, Application US/09895793
: Publication No. US20020192763A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
```

```
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.534C2
: CURRENT APPLICATION NUMBER: US/09/895.793
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 110
: LENGTH: 3410
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-895-793-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-110 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
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Db 284 ATGGTCCAGAGCTGTGGGTGAGCGCCTGCTGCGGCGACCGGAAAGCCAGCTTGTCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCACCTGCTAACCTTTGGCTGGAGCTGTGTTGGCGCGAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAAGTAGAGGAGAGTTCATGACCATGGTCTGGGCATTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTGGGCTGGTCTGTGCTCCGCTCTAGGCTCAGCCAGTGACCATGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCCGCGCGGCCCTTCATCTGGGCACCTGTCTTGGGCATCTGCTGAGCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTCTCATCCCAAGGGCGGCTGCTAGCAGGGCTGTGTGCCCGGATCCCAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 644 GAGCTGGCAGCTGCTCATCTCGGGCTGGGGCTGTGGAGCTTCTGTGGCAGGTGTCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGGGGACCCGACCACTGTCCGAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGTCTATGGCTTCATGATCAGTCTTGGGGCTGCCTGGGCTACCTCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
Db 824 ATTGACTGGGACACAGTGGCCCTGGCCCCCTACCTGGGCGACCCAGGAGGTGCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
|||||
Db 884 GGCCTGCTCACCTTCATCTTCCCTCACCTGCTAGCAGGCACACACTGCTGGTGGCTGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Db 944 GCAGCGCTGGGGCCACCGAGCCAGAGAGGGGTGTGGGCCCTCTCTTGTGCGCCCAAC 1003
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QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGCGCGCTGGCTTTCCGGAACCTGGGCGCCCTGCTCCCGCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCTTGCGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPhePheThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGCCACTCATGACCTTCACGCTGTTTACACGGAATTCGTGGCGGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGTGCCAGAGCTGAGCGGGCACCGAGCGCGGAGACACATGATGAAGCG 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGCAGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGCTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCTGGACCGCTGGTGCGAGCATTCGCGCACTCGAGCAGTCTATTGGCCAGTGTGGA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCGCTGGTGACGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACACCGGAGAGCAGGTGTCTCGCCAAATCCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCCTGATGACCACTTCCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
QY 441 PheProAspGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTTAATGGACAGCTGGGTGCTGGAGGAGTGGCGCTGCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCTCTGCTGTGATCTCCGTACCTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCCGGGCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCAATCCCTGTTTATGGCTCCATTTGTCAGCTCAGCCAGCTGTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGCTGTGCCCGCAGGCTGGGTCTGGTGGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGGCACTTGCCAAATACTCAGCG 1942
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RESULT 5

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US-09-895-814-110
; Sequence 110, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

```
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: POSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-814-110 (1-3410)
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.. QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGGTGAGCCCTGCTGCGGCACCGAAAGCCAGCTCTTGGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGCGAGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGCTAGAGGAGAAGTTTCATCACCATGCTGTGGCATTTGCT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTCTCCCGCTCCTAGGCTCAGCCAGTACACCATGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CCCTATGGCCCGCGCGCCCTTCATCTGGGCACATGCTCTTGGGCATCTCTGTGACCTTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCAGCTGCTCATCTGGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGAGCACCTGTGCCAGGCC 763
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QY 121 GluLeuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCTGGGCGTGGGCTGCTGACTTCTGTGGCCAGGTGCTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGAGCCGACCACTGTGCCAGGCG 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTCAATGATCACTGTGGGGCTGCTGGGCTTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 884 GGCTGCTCACCCTCATCTTCTCACTGCTGCTAGCAGCCACACTGCTGCTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCACCGAGCGAGGAGGCTGCTGGCCCCCTCTCTGTGCGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATCGCGGCGCTGCTGCTTCCGGAACCTGGGCGCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCGCATGCGCCGACCCCTGCGCGGCTCTTCTGCTGCTGAGCTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrLeuAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTATGACCTTACGCTGTTTTACACGGATTCGTGGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCGGGCGTGCCAGAGCTGAGCGGCGACCGAGGCGCGAGCACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGAGCGCTGGGCGTGTCTCTGCACTGCGCCATCTCCTGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGCTGTGTGCGCGATTCGGCACTCGAGCACTATTGCGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCGCGTGCACATGCTTCCACAGTGTGGCGGTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGAGAGGAGGTGTCTTCCGCCAAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCTGATGACCACTTCTTCCAGCGGCCCTTAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTTAATGGACAGCTGGGTGCTGAGGCACTGCTTCCCACTCCACCCCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCTGCTGATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGT 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500

Db 1724 AGGGTGGTTCGGGCGGGCGCATCTGCTGGACCTGCGCATCTGATAGTCCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGTGGGCGCCATCCCTGTTTATGGGCTCCATTTGGCAGTCAAGCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGCTGCTGCTGCCGAGGCTGGTCTGGTGGCTTACTTTCTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 8
US-09-780-669-110
; Sequence 110, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-110
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-780-669-110 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGTGAGCGCTGCTGCGGACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

Db 404 CCTCTGCTGTGAAGTGGGGTAGAGGAAGTTTCATGACCATTGCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGCGCTGGTCTGTGTCGCCGCTCTAGGCTCAGCCAGTAGCCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGTATATGGCGCGCGCGCTTTCATCTGGGCACCTGTCTTGGGCATCTCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCAGGCGCGCTGCTAGCAGGGCTGTGTGCCCGGATCCAGGCCCTTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGSCACTGTCTCATCTTGGCGTGGGCTGCTGGACTTCTGTGCCAGGTTGCTTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGTCTCTGTGACTTCTCCGGGACCCGGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 764 TACTGTCTATGCCCTTCATGATCAGTCTTGGGGGCTGTGGGCTACCTCTGCCCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCTTCCCTGCCCCCTACCTGGGCACCCAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGGCTGCTCACCTCATCTTCTCCTCAGCTGCGTAGCAGCCACACTGTGCTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGTGGGCCCCACCGAGCAGCAGAGGGCTGTGGGCCCCCTTGTGTGCCCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGTGTCCATGCGCGCGCTGGCTTTCGGGAACCTGGGCGCCCTGTCTCCCGCGCTG 1063
QY 261 HisGlnLeuCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCGGCATGCCCCCACCACCTCGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCAGCTGTTTTACACGGATTTCTGGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCCAAGAGCTGAGCGCGGCACCGAGCGCGGAGACACATATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGCAGCTGGGGCTGTTCCTCCTCAGTGGCCACTCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGACCGGCTGGTGAGCGGATTCGGGCACFCGAGCAGTCTATTTGGCCAGTGGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCITTTCCCTGTGCTGCCGTGCCATGCTGTGCCAGAGTGTGGCGGTGGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCATCCCGGGTTACCTTCTCAGCCCTGCAGATCTGTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACACCGGGAAGAGGTTTCTTCCGCCAAATACCGAGGGGACACTGGAGGT 1543

Alignment Scores:

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGACAGCCTGATGACCACTTCTTCCAGGCCCTTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTCTAATGGACACGTGGTGTCTGGAGCAGTGGCTGTCTCCACGCTCCACCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGGCGGGCTCTGCCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGG 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGTTCGGGCGCGGGCATCTGCTGGACCTGCCCATCTCTGGATAGTGTCTCTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCCAAGTGGCGCCCATCTCCCTGTTTATGGGTCTCCATTTGCCAGCTCAGCCAGTGTCT 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTGTCTGCCGAGCGCTGGTCTGTCTGCCATTACTTGTCTGTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTACAAAGAGCAGCTTGGCCAAATACTCAGCG 1942

RESULT 9

US-09-030-606-110
; Sequence 110, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; ATTORNEY: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-110

Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-09-593-793A-113 (1-553) x US-09-030-606-110 (1-3410)			
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DB	284	ATGGTCCAGAGCTGTGGGTGAGCCCTGCTGGCGCACCCGGAAGCCAGACTCTTGCTG	343
QY	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
DB	344	GTCAACCTGCTAACCTTTGGCCGTGGAGGTGTGTTGGCCGCGAGGCATACCTATGTGCGG	403
QY	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
DB	404	CCCTGCTGCTGGAAGTGGGGGTAGAGGAGAAAGTTTCATGACCATGGTGTGGGCATTGGT	463
QY	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
DB	464	CCAGTCTGGGCTGTGCTGTGCTCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGA	523
QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
DB	524	CGCTATGGCGCGCGCGCCCTTCATCTGGGCACGTGCTTGGGCATCTCTGAGCCCTC	583
QY	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
DB	584	TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGCTGTGCGCGATCCAGGCCCTG	643
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
DB	644	GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTTC	703
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
DB	704	ACTCCACTGGAGCCCTGCTCTGACCTCTCCGGGACCCGACCACTGTGCGCAGGCC	763
QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
DB	764	TACTCTGTATGCCCTTCATGATCATGCTTGGGGGCTGCTGGGCTACCTCTGCTGCC	823
QY	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
DB	824	ATTGACTGGGACCACTGGCCCTGGCCCTACCTGGGCACCCAGAGGAGTGCCCTTTT	883
QY	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
DB	884	GCCCTGCTCACCTTCATCTTCCTACCTGCGTAGCAGCCACACTGCTGTGGCTGAGGAG	943
QY	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
DB	944	GCAGCGCTGGGCCCCCACCAGCAGCAGAGGGCTGTGCGGCCCTCTCTGTGCGCCCCAC	1003
QY	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
DB	1004	TGCTGTCCATGCCGGCCCGCTTGGCTTTCGGAACTCTGGGCGCCCTGCTTCCCGGCTG	1063
QY	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
DB	1064	CACCAGCTGTGTCGCGCATGCCCCGACCCCTGCGCGGCTCTTCGTGGCTGAGGTGTC	1123
QY	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
DB	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTGCTGGCGAGGGCTG	1183
QY	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
DB	1184	TACCAGGGCGTGCCAGAGCTAGCGCGGACCCGAGGGCCCGAGACACTATGATGAAGGC	1243

QY	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
DB	1244	GTTCGATGGCAGCGCTGGGCTGTTCCTGCGAGTGGCCATCCCTGCTCTCTCTG	1303
QY	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
DB	1304	GTCAATGGACCGCTGGTGCAGCGATTTCGGCACTTCGAGCAGTCTATTTGGCCAGTGGCA	1363
QY	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
DB	1364	GCTTTCCTGCTGGCTGGCGTCCCATGCTGTCACAGTGTGGCGTGGTGGAGCT	1423
QY	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
DB	1424	TCAGCGCCCTCACCGGTTCACTTCTCAGCCCTGCAGATCTGCGCTTACACACTGGCC	1483
QY	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
DB	1484	TCCTCTACCCCGGAGAGAGGTTTCCTGCCCAATAACCGAGGGGACACTGGAGGT	1543
QY	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
DB	1544	GCTACGATGAGCAGCAGCTGATGACCACTTCCTGCCAGGCCCTAAGCCTGGAGCTCC	1603
QY	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu	460
DB	1604	TTCCCTAATGGACACGTTGGTGTGAGGACAGTGCCTCCACCTCCACCCGCGCTC	1663
QY	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
DB	1664	TCGGGGGCTCTGCTGTGTATGCTCCGCTACGTGTGGTGGTGGTGGAGCCACCAGGCC	1723
QY	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
DB	1724	AGGTGTGTTCCGGCGCGGGGCACTGCGCTGGACCTGCGCATCTCGATGATGCTCTCTG	1783
QY	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
DB	1784	CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGCTGTC	1843
QY	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
DB	1844	ACTGCTATATGTTGTCTGCCGAGCGCTGGTCTGGTGGCATTTACTTTGCTACACAG	1903
QY	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
DB	1904	GTAGTATTGACAGAGGACTTGGCCAAATACTCAGCG	1942
RESULT 10			
US-09-822-827-110			
; Sequence 110, Application US/09822827			
; Patent No. US20020081680A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121.534C1			
; CURRENT APPLICATION NUMBER: US/09/822,827			
; NUMBER OF SEQ ID NOS: 982			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 110			
; LENGTH: 3410			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-822-827-110			
Alignment Scores:			
Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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DB: 10 Gaps: 0
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QY 1 MetValClnArgLeuValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCAGAGGCTGGGGAGCCGCTGCTCGCGACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlaGlyLeuThrValPro 40
DB 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGCATCATCTATGTGCCG 403
QY 41 ProLeuLeuLeuValGlyValGluGluLysPheMetThrMetValLeuGlyLleGly 60
DB 404 CCTCTGCTGCTGAAGTGGGGGTAGAGGAGAGTTTCATGACCATGTGTGCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlyLysSerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGGCTGGTGTGTGCCGCTCCTTAGGCTCAGCCAGTACCACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyLleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTGCTGAGCCCTC 593
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCAAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCGGATCCAGCGCCCTG 643
QY 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGACCTGCTCATCTCGGGCGTGGGCTGCTGGACTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGAGGCGCTGCTCTCTGACCTCTCCGGGACCCGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
DB 824 ATTGATGGGACACCACTAGTGCCTTGGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCTGCTCACCTCATCTCTCTACCTGCTGCTAGCAGCCACACTGCTGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAAGGCTGCTGGCCCCCTCTTGTGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGTGTCCTATGCGCGGCGCGCTTGGCTTTCGGAACCTGGCGGCGCTGCTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCACCTGTGCTGCCGATGCCCGCCGACCTGCGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
DB 1124 AGCTGGATGGCATCATGACCTTCACGCTGTTTACACGGATTTCTGGCGGAGGGGCTG 1183
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DB 1184 TACCAGGGCGTGGCCAGACTGAGCGGGCACCGAGCGCGGAGACACTATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGAGCCTGGGGCTGTTCCTGCAGTGGCCCATCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
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DB 1304 GTCATGACCGGCTGCTGCGCATTCGCGACATTCGAGCAGTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGCTGCCGTTGCCATGCTGCTCCACAGTGTGCCGCTGGGTGAGAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCCGCTCACCAGGTTACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCTCTACACCGGAGAGCAGGTGTTCTGCCAAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCTGGAGTCCC 1603
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RESULT 11
US-09-115-453-110
; Sequence 110, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-115-453-110 (1-3410)
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; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-10-012-896-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCAGAGGCTGTGGGTGAGCGCCCTGCTGCGGCACCGGAAAGCCAGCTCTTGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGCGAGGCATCATCTATGTGCGG 400
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGTAAGTGGGTGAGGAGAGAGTTTATGACCATGTGCTGGCATTTGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGTCTGTGTCGCCCTCTAGGCTCAGGCAGTGACCACTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGTCTTGGGCATCTGCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTATCCCAAGGCCGGCTGGTAGCAGGGCTGTGTGCCGGATCCCGAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGTCTATCTGGCGTGGGCTGTCTGGACTTCTGTGGCCAGGTGTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGTCTGTGACCTTTCCGGGACCCCGGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATGCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGACACCACTGCTGCCCTTACCTGGGCACCCAGGAGGAGTCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCTGCTCACCCTCATCTTCTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGCCCCCACCAGCCAGCAGAGGGCTGTGCGCCCCCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTTCATGCGCGCGCTTGGCTTTCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTCGCGCATGCCCGCACCTTCCGCGCGCTCTCTGCTGCTGAGCTGTGC 1120

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGATTTCTGTCGGCGAGGCGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTrpAspGluGly 320
Db 1181 TACCAGGGCGTCCCGAGAGCTGAGCGGCGCACCGAGGCCGAGACACTATGATGAAGGT 1240

RESULT 13
US-09-895-793-704
; Sequence 704, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCAGAGGCTGTGGGTGAGCGCCCTGCTGCGGCACCGGAAAGCCAGCTCTTGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGCGAGGCATCATCTATGTGCGG 400
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGTAAGTGGGTGAGGAGAGAGTTTATGACCATGTGCTGGCATTTGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGTCTGTGTCGCCCTCTAGGCTCAGGCAGTGACCACTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGTCTTGGGCATCTGCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTATCCCAAGGCCGGCTGGTAGCAGGGCTGTGTGCCGGATCCCGAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGTCTATCTGGCGTGGGCTGTCTGGACTTCTGTGGCCAGGTGTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGTCTGTGACCTTTCCGGGACCCCGGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATGCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGACACCACTGCTGCCCTTACCTGGGCACCCAGGAGGAGTCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCTGCTCACCCTCATCTTCTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGCCCCCACCAGCCAGCAGAGGGCTGTGCGCCCCCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTTCATGCGCGCGCTTGGCTTTCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTCGCGCATGCCCGCACCTTCCGCGCGCTCTCTGCTGCTGAGCTGTGC 1120
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Db 461 CCAAGTGGCGCTGCTGTGTGTCGGCTCTAGGCTCAGCCAGTGACCACCTGGCGCTGA 520
QY 81 ArqTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCCCTTCATCTGGGCACTGCTCTGGGCATCTGCTGAGCCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGCTGCTGGCCGATCCAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGGCCAGGTGCTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCCCTCATGATGATCAGTCTTGGGGCTGCTGGCTTACCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCAAGTGCCTGGCCCTACCTGGGCACCCAGGAGGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCCTCATCTCTCACCCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAAGGCTCTCGGCCCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTGTCATGGCGGCGCTGGCTTTCCGGAACTGGCGGCCCTGCTTCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTCGCGCATGCCCGCACCCCTGGCGGCTCTCTGCTGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTACCGCTTTTACACGATTTCGTGGCGAGGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCGTGGCCAGAGCTGAGCGGCGCACCGAGGCCCGGAGACACTATGATGAAGT 1240

RESULT 14

US-09-895-814-704
; Sequence 704, Application US/09895814
; Publication NO. US20020193296A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: DIAGNOSIS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-704

Alignment Scores:

Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-814-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTGCCAGAGCTGTGGGTGAGCCGCTGCTGGCGCACCCGAAAGCCAGCTCTTGC 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCACCTGCTAACCTTTGGCCTGGAGGTGCTTTGGCGCAGGCATCACCTATGTGCG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGGCATTGGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGTGTGTCTCCGCTCCTAGGCTCAGCCAGTACCCAGTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCCCTTCATCTGGGCACATGCTCTGGGCATCTGCTGAGCCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGCTGCTGGCCGATCCAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGGCAGGTGCTTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCCCTTCATGATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCAAGTGCCTGGCCCTACCTGGGCACCCAGGAGGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCCTCATCTTCTCACCCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||

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Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGAGGCGCTGTGCGCCCCCTCTTGTCTGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTCCATGCCGGGCCCCCTGGCTTCCGGAACCTGGGCGCCCTGTCTCCCGGCGTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCCGCATGCCCGACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCAGAGGCCCGGAGACACTATGATGAAGGT 1240

RESULT 15
US-09-759-143-704
; Sequence 704, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGTCACAGAGGCTGTGGGTGACCCCGCTGCTCGGCACCCGGAACCCAGCTCTTGGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCGG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 401 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATCACCATTGCTGTGGCATTTGGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAAGTCTGGGCCCTGGTCTGTGTCCCGCTCTTAGGCTCAGCCAGTACCACCTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCTTGGGCATCTCTGCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTCTGGCGGTGGGCTGCTGGACTTCTGTGCCAGGTGTGCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGAGCCACTGTGCGCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGGCTTCATGATCAGTCTTGGGGGTGGCTGGGCTACCTCTGCTGCTG 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 821 ATTGACTGGACACCACTGCTGCGGCCCTCTCTGCGGCACCCAGGAGGAGTGCTCTCTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCGCTGCTCACCCTCATCTTCTCCTACCTGGTAGCAGCCACACTGCTGGTGGCTGAGG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGGCTGTCGCCCCCTCTTCTGCGCCGCTG 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTCCATGCGCGGCGCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGGCGCATGCCCGCACCCCTGCGCGGCTCTTCTGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCAGGAGGCCCGGAGACACTATGATGAAGGT 1240

RESULT 16
US-09-780-669-704
; Sequence 704, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
```

```
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-780-669-704 (1-4034)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGTGTAGCGGCTGTGGCGCACCGAAAGCCAGCTCTTGCTG 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACTTTGGCTGTGGGTGTGTTGGCGCAGGCATCACCTATGTGCGG 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGlyPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGGAAGTGGGGCTAGAGGAGAGTTCATCTGGGCATCTGCTGAGCCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGTGTAGAGGCTGTGTGCGCGATCCAGGCCCCCTG 640
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyInValCysPhe 140
Db 641 GAGCTGGCAGCTGCTCATCTGGCGTGGGCTGTGGACTTCTGNGCCAGGTGTGCTTC 700
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCGCTCTCTCATCTCTCCGGACCGGACCACTGTGCGCAGGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATAGCCCTCATGATCATGCTTGGGGCTGCCCTGGGCTACCTCTGCGCTGCC 820
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGGACACAGTGGCCCTGCCCCCTACCTGGGACCCAGGAGAGTGCCTCTTT 880
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCCTGCTCACCTCATCTCTCATCTGCTAGCAGCCACACACTGCTGGTGGTGAGGAG 940
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Qy 221 AlaAlaLeuLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGGGCCCTCTCTGTGCGCCAC 1000
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATCGCGGCGGCTGTGGCTTTCGGAAACCTGGGCGCCTCTCTCCCGGGCTG 1060
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCCGATGCCCGCACCTGGCGCGCTCTGCTGGCTGAGCTGTGC 1120
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTTGCTGGCGAGGGCTG 1180
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCGGAGCGGAGACACTATGATGAAGGT 1240

RESULT 17
US-09-822-827-704
; Sequence 704, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-704
```

```
Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 10 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-822-827-704 (1-4034)

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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGGCTGTGGCGCACCGAAAGCCAGCTCTTGCTG 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACTTTGGCTGTGGGTGTGTTGGCGCAGGCATCACCTATGTGCGG 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGlyPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGGAAGTGGGGCTAGAGGAGAGTTCATGACCATGCTGCTGGCATTTGGT 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCATGTCTGGGCGCTGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGGCTCTTATCTGCGGCACTGTCTTGGGCACTCTCTGCTGAGCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
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Db 1192 GTGGGCGAG 1200
RESULT 19
US-09-895-793-851
; Sequence 851, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-851
Alignment Scores:
Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservativeness: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-895-793-851 (1-1203)
QY 36 IleThrTyrValProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMet 55
Db 412 ATCATCTATGTCCCGCTCTGTGTGGAAGTGGGGTAGAGAGAAGTTTCATGACCATG 471.
QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCGATGTTCAGTGTGGCCCTGGTCTGTGTCCTCTCTGAGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCGTGGAGCTATGCGCGCGCGCCCTTCATCTGGGCATGTCTTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCTCTGTGAGCTCTTTCTCATCCCAAGGCGCGGTGGCTAGCAGGGCTGCTGCGCG 651
QY 116 AspProArgProLeuLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCCCTGGAGCTGGCACTGTCTATCCCTGGGGCTGGGCTGCTGACTTCTGT 711
QY 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGCCAGGCCCTACTCTGTCTATGCTTCATCATCTTGGGGGCTGCCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACCTCTGCTGCCATTGACTGGGACACCATGGCCCTGGCCCCCTACCTGGGCACCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
Db 892 GAGGAGTGTCTCTTTGGCCCTGCTCACCCCTCATCTTCTCCTCACCTGCGTAGCAGCACACTG 951
QY 216 LeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluLeuSerAlaPro 235
Db 952 CTGGTGGCTGGAGGAGGACGCTGGGCCCGCCAGCAGCAGAGGGCTGTGGGCCCGCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCTTGTGCCCGCCACTGCTGTCCATGCGCGGCCCGCTTGGCTTTCGGGAACCTGGCGGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGCGCTGCACACGCTGTCTGCCGATGCTCCCGCACCTGCGCGGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGGCGAG 1200
... RESULT 20
US-09-895-814-851
; Sequence 851, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-895-814-851

Alignment Scores:

Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-814-851 (1-1203)

QY 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGlyValGluGluLysPheMetThrMet 55
|||||
Db 412 ATCACCTATGTGGCGCTCTGCTGTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCAGT 471
QY 56 ValLeuGlyIleGlyProValLeuLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
|||||
Db 472 GTGCTGGGCATTGGTCCAGTGTGGGCTGGTCTGTCTCCCGCTCTAGGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
|||||
Db 532 GACCACTGGCGTGGACGTATGGCGCGCGCGCTTCATCTGGGCACTGTCTTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
|||||
Db 592 ATCCTGTGAGCCTCTTCTCATCCCAAGGCGGGCTGGCTAGCAGGGCTGTCTGCCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuLeuIleGlyValGlyLeuLeuAspPheCys 135
|||||
Db 652 GATCCAGGCGCTGGAGCTGGACATGCTCATCTGGGCGTGGGCTGTGGACTTCTGT 711
QY 136 GlyGlnValCysPheTrpProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
|||||
Db 712 GCCAGGTGTCTACTCCACTGGAGCGCTCTCTCTGACCTCTTCCGGACCCGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
|||||
Db 772 CACTGTGCCAGGCTACTCTGTATGCGCTTCATGATCATGCTTGGGGCTGCCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
|||||
Db 832 TACCTCTGCTGCCATTACTGGGACACAGTGGCCCTTCCAGCTTCCGGACCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
|||||
Db 892 GAGGAGTGCTCTTGGCGTGTACCCCTCATCTTCTCACCTGGCTAGCAGCCACATG 951
QY 216 LeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
|||||
Db 952 CTGGTGGCTGAGGAGCAGCGCTGGGCGCCACCGAGCCAGCAGAGGGCTGTCCGGCCCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
|||||
Db 1012 TCTTGTGCGCCCACTGTGTCTCATGCGGGCGCGCTTGGCTTTCGGGAACCTTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
|||||
Db 1072 CTGCTTCCCGGCTGACCAAGCTGTGCTGCCGATGCCCGCGACCTTGGCCCGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe 295
|||||
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCACTCATGACCTTACAGCTGTTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
|||||
Db 1192 GTGGGCGAG 1200

RESULT 21

US-09-759-143-851

; Sequence 851, Application US/09759143

; Patent No. US2002022248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-851

Alignment Scores:
Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-851 (1-1203)

QY 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGlyValGluGluLysPheMetThrMet 55
|||||
Db 412 ATCACCTATGTGGCGCTCTGCTGTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCAGT 471
QY 56 ValLeuGlyIleGlyProValLeuLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
|||||
Db 472 GTGCTGGGCATTGGTCCAGTGTGGGCTGGTCTGTGTCCTCTAGGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
|||||
Db 532 GACCACTGGCGTGGACGTATGGCGCGCGCGCTTCATCTGGGCACTGTCTTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
|||||
Db 592 ATCCTGTGAGCCTCTTCTCATCCCAAGGCGGGCTGGCTAGCAGGGCTGTCTGCCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuLeuIleGlyValGlyLeuLeuAspPheCys 135
|||||
Db 1012 TCTTGTGCGCCCACTGTGTCTCATGCGGGCGCGCTTGGCTTTCGGGAACCTTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
|||||
Db 1072 CTGCTTCCCGGCTGACCAAGCTGTGCTGCCGATGCCCGCGACCTTGGCCCGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe 295
|||||
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCACTCATGACCTTACAGCTGTTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
|||||
Db 1192 GTGGGCGAG 1200

|||||
Db 892 GAGGAGTGGCTCTTTGGCGCTGCTCACCCATCTTCTCACCTGGCTAGCAGCCACACTG 951
QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGAGGACGCGCTGGGCCCCACCGAGCCAGCAGAGGGGTGTCGGCCCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCCTGTGCCCCCACTGTCTCCATGCGCGGCCGCTTGCGCTTCCGGAACTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGGCTGCACCGCTGTGCTGCCGATGCTGCCCGCCAGCCCGCGGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGACTCATGACCTTCACGCTGTTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGCGGAG 1200

RESULT 22
US-09-780-669-851
; Sequence 851, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-851

Alignment Scores:
Pred. No.: 6, 29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-780-669-851 (1-1203)

QY 36 IleThrTyrValProLeuLeuGluValGlyValGluGluLysPheMetThrMet 55
|||||

Db 412 ATCACCTATGTGCCGCTCTGCTGCTGGAAGTGGGGTAGAGAGAAGTTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCATTGGTCCAGTGTGGGCCGTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCGTGGAGCTATATGCCCGCGCCCTTCATCTGGGCACACTGCTCTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCTCTGCTGAGCTCTTCTCATCCAGGGCGGTGGCTAGCAGGGGTGTGTGCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCCCTGGAGCTGGCACTGCTCATCTCTGGGGCTGGGCTGGTGGACTTCTGT 711
QY 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GCCAGGTGTCTTCACTCCACTGGAGGCCCTGCTCTGACCTTCTCCGGGACCCGGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGCCAGGCTTACTCTGTATGCTTTCATGATCAGTCTTGGGGCTGCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACCTCTGCTGCTTGGCCCTGCTCACCTCATCTTCTTCCCTGCTGAGTGGGACCCAG 891
QY 196 GluGlyCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
Db 892 GAGGAGTGGCTCTTGGCCCTGCTCACCTCATCTTCTTCCCTGCTGAGTGGGACCCAG 951
QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGGAGGAGCGCTGGGCCCCACCGAGCCAGCAGAGGGGTGTGCGGCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCCTGTGCCCCACTGCTGCTCCATGCGGGGCCCTTGGCTTCCGGAACTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGGCTGCACCGCTGTGCTGCCGATGCTCCCGCACCTGCGCGGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGCGGAG 1200

RESULT 23
US-09-822-827-851
; Sequence 851, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-851

Alignment Scores:
Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-822-827-851 (1-1203)

QY 36 IleThrTyrValProLeuLeuValGlyValGluGluLysPheMetThrMet 55
Db 412 ATACCTATTGGCGCTCTGCTGGAAGTGGGGTAGAGAGAAGTTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCATTGGTCAGTGTGGGCTGTGTGTCTCCGCTCTAGGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCGTGGAGCGTATGGCCGCGCGCGCTTTCATCTGGGCACTGTCTTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCTGCTGAGCCTCTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGCCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCGCTGGAGTGGCACTGTCTATCTCTGGCGTGGGGCTGTGGACTTCTGT 711
QY 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GGCCAGGTGTCTACTCCACTGGAGGCGCTCTCTCTGACCTCTCCGGGACCCGGAC 771
QY 156 HisCysArgGlnAlaTrpSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGGCGAGCCCTACTGTCTATGCTTTCATGCTCAGTCTTGGGGCTGCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACTCTGCTGCCATTGACTGGGACACAGTGGCCCTGGCCCGCCCTACCTGGGCACTCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
Db 892 GAGGAGTGGCTCTTGGCTGTCTCAGCCCTCATCTCTCCTCAGTGTAGCAGCCACTGT 951
QY 216 LeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGGAGGAGCGCTGGGGCCCGACCGAGCCAGCAAGGGCTGTGGCCCGCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCTTGTGCGCCCACTGTCTCATCGCGGGCCGCTTGGCTTTCGGGAACCTGGCGGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGCGGTGACACAGCTGTCTGCGCATGCCCGCACCTGGCGCGGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGACGTGGATGGCACTCATGACCTTACCGTGTGTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGGCGAG 1200

RESULT 24

US-10-012-896-702
; Sequence 702, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 702
LENGTH: 4894
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-702

Alignment Scores:
Pred. No.: 2,39e-240 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Query Match: 47.56% Gaps: 0
DB: 9

US-09-593-793A-113 (1-553) x US-10-012-896-702 (1-4894)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1311 GCATTGGTCCAGTGTGGGCTGTGTGTCTGTCTAGCTCCTAGGCTCAGCCAGTGACCAC 1370
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1371 TGGCGTGGAGCGTATGGCCCGCGCGCTTCATCTGGGCACTGTCTTGGCATCTCTG 1430
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1431 CTGAGCCTCTTCTCATCCAAAGGCGCGCTGGCTAGCAGGCGTGTGTCCCGGATCCG 1490
QY 118 ArgProLeuLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1491 AGGCCCTCGAGTGGCACTGTCTCATCTGGGCGTGGGCTGTGTGGCTCTGTGTGGCCAG 1550
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1551 GTGTGCTTCACTCCACTGGAGGCGCTGTCTGTGACCTCTTCCGGACCCGGACCACTGT 1610
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1611 CGCCAGGCGCTACTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGTGTGGGCTACCTC 1670
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
Db 1671 CTGCTTGGCATTGACTGGGACACCACTGTGGCCCTTACCTTGGGCACTTGTGGGAGGAG 1730


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; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY, AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-702

Alignment Scores:
Pred. No.: 2,39e-240 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-814-702 (1-4894)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1311 GGCATTGGTCCAGTGTGGCCCTGGTCTGTGTCCTCTAGGCTCAGCCAGTGACCAC 1370

QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1371 TGGCGTGGAGCGTATGGCGCGCGCCCTCATCTGGGCACTGTCTTGGGCATCCG 1430

QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
DB 1431 CTGAGCCTCTTTCTCATCCAGGCGCGGCTGGCTAGCAGGGCTGTGTGCCGGATCCC 1490

QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuAspPheCysGlyGln 137
DB 1491 AGCCCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGCTGTGGACTTCTGTGGCCAG 1550

QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
DB 1551 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGACCTCTTCGGGACCCGGACCACTGT 1610

QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
DB 1611 CGCCAGCGCTACTCTCTATGCTTTCATGATCATGATGCTTTGGGGGCTGCTGGGCTACCTC 1670

QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
DB 1671 CTGCTGTGCATTGACTGGACACCACTGGCCCTGGCCCTTACTTGGGCACCCAGGAGGAG 1730

QY 198 CysLeuPheCysLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuVal 217
DB 1731 TGCCCTCTTTGGCTGCTCACCTCATCTTCTCACCTGCTAGCAGCCACCACTGCTGGTG 1790

QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
DB 1791 GCTAGGAGGACGCGCTGGGGCCCCACCGAGCCAGCAAGAGGGCTGTGCGGCCCTCTCTTG 1850
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QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
DB 1851 TCGCCCCCACTGCTGTCATGCGGGCCGCTTGGCTTTCGGAACCTGGCGCCCTGCTT 1910

QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
DB 1911 CCGCGGCTGCACAGCTGTGCTGCCGATGCCCGCACCTGCGCGGCTCTTCGTGGCT 1970

QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
DB 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTTCACACGATTTTCGTGGGC 2030

QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
DB 2031 GAGGGGCTGTACAGGGCGTGGCCAGAGCTGAGCCGGGACCGAGGCCCGGAGACTAT 2090

QY 318 AspGluGly 320
DB 2091 GATGAAGGT 2099

RESULT 27
US-09-759-143-702
; Sequence 702, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-702

Alignment Scores:
Pred. No.: 2,39e-240 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-759-143-702 (1-4894)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1311 GGCATTGGTCCAGTGTGGCGCTGGTCTGTGTCCTCTAGGCTCAGCCAGTGACCAC 1370

QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1371 TGGCGTGGAGCGTATGGCGCGCGCCCTCATCTGGGCACTGTCTTGGGCATCCG 1430
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Qy	98	LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro	117
Db	1431	CTGAGCCTCTTTCTCATCCAAAGGCCGGCTGGCTAGCAGGGCTGCTGTGCCGAGATCCC	1490
Qy	118	ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln	137
Db	1491	AGGCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGGCTCTGGACATCTCTGTGGCCAG	1550
Qy	138	ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys	157
Db	1551	GTGTGTTTCACTCCACTGGAGGCCCTGTCTCTGACCTCTTCCGGGACCCGAGCACTGT	1610
Qy	158	ArgGluAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu	177
Db	1611	CGCAGGCTTACTCTCTATGCTTCAATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC	1670
Qy	178	LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu	197
Db	1671	CTGCCTGCCATTGACTGGGACACCACTGCCCTGGGCCCCCTACCTGGGACCCAGAGGAG	1730
Qy	198	CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal	217
Db	1731	TGCCTCTTTGGCGTGTCAACCCTCATCTTCTCACTGCGTAGCAGCCACACTGCTGGTG	1790
Qy	218	AlaGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu	237
Db	1791	GCTGAGGAGGACGCGTGGGGCCCCACCGAGCCAGCAGAAAGGCTGTGCGGCCCTCTCTG	1850
Qy	238	SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu	257
Db	1851	TCGCCCACTGCTGTCATCCGGGCCCGCTTGGCTTTCCGGAACTTGGGGCCCTCGCTT	1910
Qy	258	ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla	277
Db	1911	CCCCGGCTGCACCAGCTGTGCTGCCCATGCCGCCACCCCTGCGCCGCTCTTCTCGTGGCT	1970
Qy	278	GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly	297
Db	1971	GAGCTGTGCAGCTGGATGGCATCTAATGACCTTCAGCTGTGTTTTACACGGATTTGTTGGGC	2030
Qy	298	GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr	317
Db	2031	GAGGGCTGTACCAGGCGTGCACAGACTGAGCGGGGACCCGAGGCCCGGAGNACTAT	2090
Qy	318	AspGluGly 320	
Db	2091	GATCAAGGT 2099	

RESULT 28

US-09-780-669-702
; Sequence 702, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

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Db 2031 GAGGGGCTGTACAGGCGCTGCCAGAGCTGAGCGGACCGAGGCGCGGAGACACTAT 2090
      |||
QY 318 AspGluGly 320
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Db 2091 GATGAAGGT 2099
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RESULT 29
US-09-822-827-702
; Sequence 702, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-702
Alignment Scores:
Pred. No.: 2,39e-240 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-822-827-702 (1-4894)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
      |||
Db 1311 GGCATTGGTCCAGTGTGGCGCTGGTCTGTGTCGCCCTCTAGGCTCAGCCAGTACCAC 1370
      |||
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
      |||
Db 1371 TGGCGTGGAGCGCTATGGCGCGCGCGCTTCATCTGGGCACTGTCTTGGGCATCTCG 1430
      |||
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
      |||
Db 1431 CTGAGCCTCTTCTCATCCAGGGCGGCTGGCTAGCAGGCTGTGTGCCGGATCCC 1490
      |||
QY 118 ArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
      |||
Db 1491 AGGCCCTGGAGCTGGCACTGTCTCATCTCTGGGCTGGGCTGTGTGGCCAG 1550
      |||
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
      |||
Db 1551 GTGTGCTTCACTCCACTGAGGCGCGCTCTCTGACCTCTTCGGGACCGGACCACTGT 1610
      |||
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
      |||
Db 1611 CGCCAGCGCTACTCTCTCTATGCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTC 1670
      |||
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
      |||
Db 1671 CTGCTTGCCATTGACTGGGACACCACTGCTGCGCCCTTACCTGGGCACTGGGAGGAGG 1730
      |||
QY 198 CysLeuPheGlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
      |||
Db 1731 TGCCCTTTGGGCTGCTACCTCCATCTCTCTCACCTGCTGAGCAGCCACACTGTGTGTG 1790
      |||
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
      |||
Db 1791 GCTGAGAGCGCAGCGTGGGCGCCCGCCAGGACGAGAGGCTGTGCGGCCCTCTCTTG 1850
      |||
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
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Db 1851 TCGCCCACTGTGTCCATGCGGGCGCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTT 1910
      |||
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
      |||
Db 1911 CCCCCGCTGCACGAGCTGTGCTGCCGATGCCCGCACCTGCGCGGCTCTTCGTGGCT 1970
      |||
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
      |||
Db 1971 GAGCTGTGCAGCTGGATGCACCTCATGACCTTCACGCTGTTTACACGATTTCTGTGGC 2030
      |||
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
      |||
Db 2031 GAGGGCTGTACAGGCGCTGCCAGAGCTGAGCGCGGACCGAGGCGCGGAGACACTAT 2090
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QY 318 AspGluGly 320
      |||
Db 2091 GATGAAGGT 2099
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RESULT 30
US-10-012-896-705
; Sequence 705, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meadner, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-705
Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0
US-09-593-793a-113 (1-553) x US-10-012-896-705 (1-6976)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
      |||
```

GENERAL INFORMATION:	
APPLICANT:	Xu, Jiangchun
APPLICANT:	Dillon, Davin C.
APPLICANT:	Mitcham, Jennifer L.
APPLICANT:	Harlocker, Susan L.
APPLICANT:	Jiang, Yugu
APPLICANT:	Kalos, Michael D.
APPLICANT:	Retter, Marc W.
APPLICANT:	Stolk, John A.
APPLICANT:	Day, Craig H.
APPLICANT:	Vedwick, Thomas S.
APPLICANT:	Carter, Darrick
APPLICANT:	Li, Samuel X.
APPLICANT:	Wang, Aijun
APPLICANT:	Skeiky, Yassir A.W.

```
Db 1802 CCCGGCTGCACGAGTGTCTGCCGATGCCCGCCACCCCTGCGCGGCTCTTCGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGCAGCTGGATGGCACTCATGACCTTACGCTGTTTTACACGGATTTCGTGGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGCTGTACAGGGCGTGGCCAGAGCTGAGCGCGGACCGAGGCGCGGACACTAT 1981
QY 318 AspGluGly 320
Db 1982 GATGAAGGT 1990

RESULT 32
US-09-895-814-705
; Sequence 705, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-705

Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-814-705 (1-6976)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GCATTGGTCCAGTGTGGCGCTGGTCTGTGCCGCTCCTAGGCTACGCCAGTACCAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGCGTGGAGCTATGCGCGCGCGCCCTTCATCTGGGCACTGTCTTGGCATCTCG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
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Db 1322 CTGAGGCTCTTCTCATCCAAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTCGAGCTGGCACTGCTCATCTTGGCGTGGGCTGCTGTGACACTTCTGTGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCACTCCACTGGAGGCCCTGTCTGTGACCTTTCGGGACCGCGGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCTTACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGCCCTGGGCTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
Db 1562 CTGCCCTGCCATTGACTGGGACACCACTGCGCTGGCCCCCTACTGGGACACCGAGGAG 1621
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1622 TGCCCTTTGGCTGCTCACCCCTCATCTTCCACCTGCTAGCAGCCACACTGTGTGGTG 1681
QY 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1682 GCTGAGGAGGCGCGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGCGCCCCCTCCTTG 1741
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1742 TCGCCCCACTGCTGTCCATGCGCGGCCCTGTTGGCTTCCGGAACCTGGCGGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1802 CCGCGGCTGCACAGCTGTGCTGCCGCATGCCCGCACCTGCGCGGCTCTTCGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGCAGCTGGATGGCACTCATGACCTTTCACGCTGTTTTACACGGATTTCGTGGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGCTGTACAGGGCGTGGCCAGAGCTGAGCGCGGACCGAGGCGCGGAGACACTAT 1981
QY 318 AspGluGly 320
Db 1982 GATGAAGGT 1990

RESULT 33
US-09-759-143-705
; Sequence 705, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
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;
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-705

Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-705 (1-6976)

Qy 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGTCTGGGCGCTGGTCTGTGTCGGCTCTAGGCTCAGCCAGTGACCAC 1261
Qy 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCGTGGACGCTATGGCGCGCGCGCTTCATCTGGGCACCTGCTCTGGGCATCCTG 1321
Qy 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1322 CTGAGCCCTTTTCTCATCCCAAGGCGCGCTGGTAGCAGGGCTGCTGTGCCCGGATCCC 1381
Qy 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTTGGAGCTGGCACTGCTCATCTTGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1441
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCACTCCACCTGGAGCCCTTGTCTGTACCTCTTCCGGGACCCGACCACTGT 1501
Qy 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
Db 1502 GCCCAGGCGCTACTGTCTATGCCCTTCATGATCATGTCTGGGGCTGCTGGGTACCTC 1561
Qy 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
Db 1562 CTGCCTGCCATTGACTGGGACACCACTGCCCTGGCCCTTACCTGGGACCCAGGAGGAG 1621
Qy 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1622 TGCCTCTTTGGCGCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 1681
Qy 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1682 GCTGAGGAGGAGCGCTGGGGCCCCACCGAGCCAGCAGAGGGCTGTCCGGCCCCCTCCCTTG 1741
Qy 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1742 TCGCCCCACTGCTGTCCATGCGGGCCCGCTTGGCTTTCCGGAACCTGGGGCGCCCTGCT 1801
Qy 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1802 CCCCAGCTGCACAGCTGCTGTCGGCATGCCCCGACCCCTGCGCGCGCTCTTCTGCGCT 1861
Qy 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGAGCTGGATGGCACTCATGACCTTCAGCTGCTTTTACACGATTTTGTGGGCG 1921
Qy 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGGCTGTACAGGGGCTGCCACAGAGCTGAGCGGGGACCCAGGGCCCGGAGACATAT 1981
Qy 318 AspGluGly 320
|||||

Db 1982 GATGAAGCT 1990
RESULT 34
US-09-780-669-705
; Sequence 705, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-705

Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-780-669-705 (1-6976)

Qy 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGTCTGGGCGCTGGTCTGTGTCGGCTCTAGGCTCAGCCAGTGACCAC 1261
Qy 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCGTGGACGCTATGGCGCGCGCGCTTCATCTGGGCACCTGCTCTGGGCATCCTG 1321
Qy 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1322 CTGAGCCCTTTTCTCATCCCAAGGCGCGCTGGTAGCAGGGCTGCTGTGCCCGGATCCC 1381
Qy 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTTGGAGCTGGCACTGCTCATCTTGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1441
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCACTCCACCTGGAGCCCTTGTCTGTACCTCTTCCGGGACCCGACCACTGT 1501
Qy 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCGCTACTGTCTATGCTTCATGATCATGTCTTGGGGCTGCTGGGTACCTC 1561


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; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-703

Alignment Scores:
Pred. No.: 6.32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-10-012-896-703 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGTTCGGATGGGCGAGCTGGGGCTGTTCTCGCAGTGGCCATCTCCCTGGTCTTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTTCATGGAGCGGCTGGTCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTTCCCTGTGGCTGCCGTCACATGCTCCACAGTGTGGCGGTGGTG 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCCCTCCATACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACACCGGAGAGCAGGTGTTCTTCGCCCAATACCGAGGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGTGCTACGATGAGGACAGCTGATGACCAAGCTTCTTCCAGGCGCCCTAAGCCTTGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1170 GCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGACGTGGCTTCCCTCCACCTCCACCC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 CGGCTCTCGGGGGCTCTCGCTGTGATGTCCTCCGTACGTGTGGTGGTGAGGCCACC 1289
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGGTGTTCGGGGCGGGGATCTGCCCTGGACCTCGGCATCTCGGATAGTGCC 1349
Qy 499 PheLeuLeuSerGlnValAlaProSerSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCCTGTCTCCAGGTGGCCCATCCTGTTTATGGGCTCCATGTGCCAGCTCAGCCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGGTGTCTCGCGCAGGCCCTGGGTCTGGTCGCCATTACTTTGCT 1469
Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGTGACAAGGAGGACTTGGCCAAATACTCAGCG 1514

RESULT 37
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US-09-895-793-703
; Sequence 703, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-703

Alignment Scores:
Pred. No.: 6.32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-703 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGTTCGGATGGGCGAGCTGGGGCTGTTCTCGCAGTGGCCATCTCCCTGGTCTTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTTCATGGAGCGGCTGGTCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTTCCCTGTGGCTGCCGTCACATGCTCCACAGTGTGGCGGTGGTG 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCCCTCCATACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACACCGGAGAGCAGGTGTTCTTCGCCCAATACCGAGGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGTGCTACGATGAGGACAGCTGATGACCAAGCTTCTTCCAGGCGCCCTAAGCCTTGA 1169
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QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1170 GCTCCCTTCCCTTAATGGACACAGCTGGTGTGGAGGACAGTGGCTGCTCCACCTCCACCC 1229
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValAtqValValGlyGluProThr 478
Db 1230 GCGCTCTCGGGGCGCTCTGCCCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACCC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGTGTTCCGGCGCGGGGCATCTCCCTGGACCTGCCATCCTGGATAGTGC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTGCTCTCCAGTGCGCCCATCTCCCTGTTATGGGCTCCATGTCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTACATGCTATATGCTGTGCGGAGGCGCTGGGTCTGGTCCCATTTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTACAGCG 1514

RESULT 38

US-09-895-814-703
; Sequence 703, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-814-703 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGTTCGATGGCAGCGCTGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTCATGACCGCGCTGGTCAGCGATTCGCGACTCGAGCTCTATTTGGCCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCCGTGGTG 989
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCCTGCCTACACA 1049
QY 399 LeuAlaSerLeuTyrHisArgGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGGCTCCCTCTACACCGGAGAGCAGGTGTTCTGCCAAATACCGAGGGACACT 1109
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGTGTCTAGCAGTGAGCAGCCTGATGACCCAGCTTCTGCCAGGCCCTAAGCCTGGA 1169
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 1170 GCTCCCTCCCTAATGGACACGTGGTGTGGAGGACAGTGGCTGCTCCACCTCCACCC 1229
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTCGGGGCGCTCTCCCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACCC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGTGGTTCGGGGCGGGGCATCTGCTGGACCTGCCATCCTGGATAGTGC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTGCTGTCCAGGTGGCCCATCTCCCTGTTATGGGCTCCATGTCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCTATATGCTGTGCGGAGGCGCTGGGTCTGGTCCCATTTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTACAGCG 1514

RESULT 39

US-09-759-143-703
; Sequence 703, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER

```
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-703 (1-2904)

QY 319 GluGlyValArgMetCysSerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGGTTCGGATGGGAGCGCTGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTC 869

QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
DB 930 GTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCCTTCTCCACAGTGTGCCCGTGGTG 989

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCTCGCCCTACACA 1049

QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1050 CTGGCCTCCCTCTACACCGGAGAGGAGGTTCTCTGCCAATACCGAGGGACACT 1109

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 1110 GGAGGTGCTAGCAGTGAGGACAGCGCTGATGACCACTGTCCAGCAGTCTCCCTGA 1169

QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
DB 1170 GCTCCCTTCCCTTAATGGACAGTGGGTGTGGAGGAGTGGCGCTGCCACCTCCACCC 1229

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
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; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-780-669-703 (1-2904)

QY 319 GluGlyValArgMetCysSerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGGTTCGGATGGGAGCGCTGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTC 869

QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
DB 930 GTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCCTTCTCCACAGTGTGCCCGTGGTG 989

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCTCGCCCTACACA 1049

QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1050 CTGGCCTCCCTCTACACCGGAGAGGAGGTTCTCTGCCAATACCGAGGGACACT 1109

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 1110 GGAGGTGCTAGCAGTGAGGACAGCGCTGATGACCACTGTCCAGCAGTCTCCCTGA 1169

QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
DB 1170 GCTCCCTTCCCTTAATGGACAGTGGGTGTGGAGGAGTGGCGCTGCCACCTCCACCC 1229

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478

; RESULT 40
; Sequence 703, Application US/09780669
; Patent No. US20020051977A1
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Db 1230 GCGCTCGGGGCCCTCCCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACC 1289
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGTGTCCGGCGGGGCATCTCGCTGGACCTCGCCATCTCGATAGTGCC 1349
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTCTGCTGCCAGGTGGCCCATCCCTGTTTATGGGTCCATTGTCAGCTCAGCCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTTGTGCGCAGGCGCTGGTCTGGTCGCCATTTACTTTGCT 1469
Qy 539 ThrGlnValValPheAspLysSerAlaAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1514

RESULT 41
US-09-822-827-703
; Sequence 703, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-822-827-703 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGGCGTTTCGGATGGGCGAGCGCTGGGCTGTTCTCGAGTGGCCATCTCCCTGGTCTTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTCTATGACCGGCTGGTGGCAGGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCGGTGGT 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCCCTCACCGGGTTTCACCTTCTCAGCCCTGCAGATCTCGCCCTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCCCTCCCTTACACCGGAGAGAGCGGTGTTCTCTCCCAAAATACCGAGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGGTGCTAGCAGTGGAGACAGCCTGATGACACAGCTTCTCGCAGGCGCTAAGCCCTGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
```

```
Db 1170 GTCTCCCTTCCCTAAATGGACACGCTGGGTGCTGGAGGAGTGGCTTCTCCACCTCCACC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTCGCGGGCCCTCTCCCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACC 1289
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGTGTCCGGCGGGGCATCTGCTGGACCTCGCCATCTCGGATAGTGCC 1349
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTCTGCTGCCAGGTGGCCCATCCCTGTTTATGGGTCCATTGTCAGCTCAGCCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTTGTGCGCAGGCGCTGGTCTGGTCGCCATTTACTTTGCT 1469
Qy 539 ThrGlnValValPheAspLysSerAlaAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1514

RESULT 42
US-10-012-896-1010
; Sequence 1010, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Hitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1010
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-1010

Alignment Scores:
Pred. No.: 1.13e-168 Length: 1065
Score: 187.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.82% Indels: 0
DB: 9 Gaps: 0
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US-09-593-793A-113 (1-553) x US-10-012-896-1010 (1-1065)

Qy	342	Meta	SpArg	LeuVal	GlnArg	PheGly	ThrArg	AlaVal	TyrLeu	AlaSer	ValAla	Ala	361
Db	478	ATG	ACC	GGT	TGT	GTG	CAG	GAT	TCC	GCA	CTC	GAG	537
Qy	362	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	381
Db	538	TTT	CC	TGT	GG	CT	CCG	GGT	CC	AC	TGT	CC	597
Qy	382	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	401
Db	598	GCC	G	CC	CT	CAC	GGT	TT	CAC	CT	TCT	CAG	657
Qy	402	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	421
Db	658	CTC	TAC	ACC	CGG	GAG	AAG	CAG	G	TGT	TCT	TGC	717
Qy	422	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	441
Db	718	AGC	AGT	GAG	GAC	AGC	CTG	ATG	ACC	AGT	TCT	TGC	777
Qy	442	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Ser	Gly	Leu	461
Db	778	CCT	AAT	GAG	AC	CTG	GGT	GCT	GG	AGC	AGT	GCC	837
Qy	462	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser	Val	Arg	Val	481
Db	838	GGG	GC	CT	CTG	CTG	ATG	CTC	CGT	TAC	GTG	TGGT	897
Qy	482	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	501
Db	898	GTG	GT	TCC	GGG	CGG	GGC	ATC	TGC	TGG	ACCT	TCG	957
Qy	502	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	521
Db	958	TCC	AGG	TGG	CC	CCAT	CC	CTG	TTT	ATG	GGC	TCC	1017
Qy	522	Ala	Tyr	Met	Val	Ser	Ala	Ala					
Db	1018	GC	TAT	ATG	GTG	TCT	GC	GGCC					

DB:	9	Gaps:	0
US-09-593-793A-113 (1-553) x US-09-232-880-10 (1-789)			
Qy	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
Db	12	CCAGTGTGGCAGTTTCCCTGTGGCTGCCGGTCCACATGCCCTGCCACAGTGGGCC	71
Qy	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
Db	72	GTGGTGACAGTTCAGCGCGCCTCACCGGGTTCACCTTCTCAGCGCTGCAGATCCTGCC	131
Qy	397	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
Db	132	TACACATGGGCTCCCTCTACACCGGGGAAGCAGGTGTCTCGGCCAAATACCGAGGG	191
Qy	417	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
Db	192	GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACACAGTTCCTCGCCAGGCCCTAAG	251
Qy	437	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro	456
Db	252	CCTGGAGTCCTCTCCCTTAATGGACAGCTGGGTGCTGGAGGCAGTGGCCCTGCCACCT	311
Qy	457	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
Db	312	CCACCGGGCTCGCGGGGCTCTGCCCTGTGATGTCCTCCGTACGTGTGGTGGGTGAG	371
Qy	477	ProThr	478
Db	372	CCCAACC	377

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RES001 44
US-10-012-896-10
: Sequence 10, Application US/10012896
: Publication No. US20020183251A1
:
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/012,896
: CURRENT FILING DATE: 2001-12-10
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 10
: LENGTH: 789
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:

```

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; NAME/KEY: misc_feature
; LOCATION: 9, 380, 451, 565, 582, 716, 718, 758, 762, 765, 768, 771,
; LOCATION: 779, 783
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-10

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Alignment Scores:		
Pred. No.:	5.84e-107	Length:
Score:	122.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	22.06%	Indels:
DB:	9	Gaps:

US-09-593-793A-113 (1-553) x US-10-012-896-10 (1-789)

357	QY	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
12	Db	GCCAGTGTGCAGCTTCCCTGTGGCTGCCGGTGCCACATGCTGTCCACAGTGTGGCC	71
377	QY	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
72	Db	GTGGTGACAGCTTCAGCGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCGGCC	131
397	QY	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
132	Db	TACACACTGGCCTCCCTCTACCAACCGGGAGACAGGTGTTCTGCCCAAAATACCGAGGG	191
417	QY	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
192	Db	GACACTGGAGGTGCTAGCAGTAGGACACGCTGTATCACCAGCTTCTGTCGACGGCCCTAAG	251
437	QY	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro	456
252	Db	CCTTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCCTGCCACCT	311
457	QY	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
312	Db	CCACCGCGGCTCTGCGGGGCGCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTGAG	371
477	QY	ProThr	478
372	Db	CCCAACC	377

RESULT 45

US-09-895-793-10
; Sequence 10, Application US/09895793
; Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT:	Xu, Jiangchun
APPLICANT:	Dillon, Jennif C.
APPLICANT:	Mitcham, Jennifer L.
APPLICANT:	Harlockner, Susan L.
APPLICANT:	Jiang, Yuqiu
APPLICANT:	Kalos, Michael D.
APPLICANT:	Rettler, Marc W.
APPLICANT:	Stolk, John A.
APPLICANT:	Day, Craig H.
APPLICANT:	Vedvick, Thomas S.
APPLICANT:	Carter, Darrick
APPLICANT:	Li, Samuel X.
APPLICANT:	Wang, Aijun
APPLICANT:	Seelky, Yasir A.W.
APPLICANT:	Hepler, William T.
APPLICANT:	Henderson, Robert A.
APPLICANT:	Hural, John
APPLICANT:	McNeill, Patricia D.
APPLICANT:	Houghton, Raymond L.
APPLICANT:	Vinals de Bassolis, C
APPLICANT:	Foy, Teresa
APPLICANT:	Fanger, Gary R.

1	INVENTOR:	WILLIAM R. HANLEY
2	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE THERAPY AND
3	TITLE OF INVENTION:	DIAGNOSIS OF PROSTATE CANCER

```

; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10

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LENGTH: 789

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; LENGTH: 793
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(789)
; OTHER INFORMATION: n =
US-09-895-793-10

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Alignment Scores:

Pred. No.:	5.84e-107	Length:	789
Score:	122.00%	Matches:	122
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	22.06%	Indels:	0
DB:	9	Gaps:	0

US-09-593-793A-113 (1-553) x US-09-895-793-10 (1-789)

357	Qy	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
12	Db	GCCAGTGTGCAGCTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCACACAGTGTGGCC	71
377	Qy	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
72	Db	GTGGTGACAGCTTCAGCGGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGGCCC	131
397	Qy	TyrThrLeuAlaSerLeuTyrHisArgLulysGlnValPheLeuProLysTyrArgGly	416
132	Db	TACACACTGGCCCTCCCTCTACACACCGGGAGAACACAGGTGTTCTGGCCCAATACACAGGG	191
417	Qy	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
192	Db	GACACTGGAGGTGCTAGCAGTGAAGACAGCCTCATCACCAGCTTCCTGCCACGGCCCTAAG	251
437	Qy	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro	456
252	Db	CCTGGAGACTCCCTTCCCTAATGACACAGTGGGTGGAGGCAGTGGCTGTCTCCACCT	311
457	Qy	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGlu	476
312	Db	CCACCGCGCTCTGCGGGGCTCTGGCTGTGTATGTCTCCGTACGTGTGGTGGGTGGAG	371
477	Qy	ProThr	478
372	Db	CCACCC	377

Search completed: February 19, 2003, 06:38:49
Job time : 155 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 04:50:30 ; Search time 2882 Seconds
(without alignments)
5584.265 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 553
Sequence: 1 MVQRLWVSRLLRRKQAQLL.....AIYFATQVVFVFKSLAKYSA 553

Scoring table:
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size 3 amino acids = 9 nucleotides

Total number of hits: 3872064

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09593793/runat_13022003_161426_21820/app_query.fasta.1.711
-DB=GenEmbl -OFMT=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=3 -ALIGN=45 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09593793@cgn.1.1.1724. @runat_13022003_161426_21820 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_mu.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vi.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgt_mus.*
34: em_hgt_pln.*
35: em_hgt_rod.*
36: em_hgt_mam.*
37: em_hgt_vrt.*
38: em_sy.*
39: em_hgtgo_hum.*
40: em_hgtgo_mus.*
41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

length of match

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	3320	6	AX327336 Sequence
2	553	100.0	3410	6	AX106329 Sequence
3	553	100.0	3410	6	AX140620 Sequence
4	553	100.0	3410	6	AX200480 Sequence
5	553	100.0	3410	6	AX267136 Sequence
6	553	100.0	3410	6	AX429961 Sequence
7	553	100.0	3410	9	AY033593 Homo sapi
8	501	90.6	2133	6	AX343857 Sequence
9	320	57.9	1593	6	AX343860 Sequence
10	320	57.9	4034	6	AX200995 Sequence
11	320	57.9	4034	6	AX267730 Sequence
12	263	47.6	1203	6	AX201078 Sequence
13	263	47.6	1203	6	AX267877 Sequence
14	263	47.6	4894	6	AX200993 Sequence
15	263	47.6	4894	6	AX267728 Sequence
16	263	47.6	6976	6	AX200996 Sequence
17	263	47.6	6976	6	AX267731 Sequence
18	263	47.6	157988	2	AC096533 Homo sapi
19	255	46.1	2152	6	AR112295 Sequence
20	252	45.6	2143	6	AR112294 Sequence
21	235	42.5	2477	9	AL832933 Homo sapi
22	235	42.5	2904	6	AX200994 Sequence
23	235	42.5	2904	6	AX267729 Sequence
24	158	28.6	3514	9	AB060851 Macaca fa
25	131	23.7	2917	9	AB062977 Macaca fa
26	122	22.1	789	6	AX106229 Sequence
27	122	22.1	789	6	AX140520 Sequence
28	122	22.1	789	6	AX200380 Sequence
29	122	22.1	789	6	AX267036 Sequence
30	85	15.4	258	6	AR112280 Sequence
31	82	14.8	247	6	AR112283 Sequence
32	71	12.8	217	6	AR112281 Sequence
33	71	12.8	255	6	AR112282 Sequence
34	69	12.5	406	11	HSPE54C06
35	63	11.4	198037	2	AC126523
36	59	10.7	2611	10	BC034084 Mus muscu
37	59	10.7	3354	10	BC031381 Mus muscu
38	59	10.7	178567	2	AC107837 Mus muscu
39	34	6.1	231	6	AR112284 Sequence
40	33	6.0	1593	10	BC024519 Mus muscu
41	33	6.0	198037	2	AC126523 Rattus no
42	20	3.6	60	6	AX201081 Sequence
43	20	3.6	60	6	AX267880 Sequence
44	12	2.2	57	6	AX201091 Sequence
45	12	2.2	57	6	AX267890 Sequence
46	11	2.0	149430	2	AC119299 Rattus no
47	11	2.0	162209	9	CNS01R1H Human chr
48	11	2.0	184361	2	AC098929 Rattus no
49	10	1.8	30	6	AX201083 Sequence
50	10	1.8	30	6	AX267882 Sequence

51	10	1.8	1980	9	AF511533	Homo sapi
52	10	1.8	1980	9	AF512951	Homo sapi
53	10	1.8	2285	9	AF010233	Homo sapi
54	10	1.8	66029	2	AC127863	Rattus no
55	10	1.8	68577	2	AC128149	Rattus no
56	10	1.8	72974	2	AC013841	Drosophil
57	10	1.8	127456	2	AC119380	Rattus no
58	10	1.8	130935	2	AF004192	Oryza sat
59	10	1.8	143702	2	AC128427	Rattus no
60	10	1.8	153727	10	AC093449	Mus muscu
61	10	1.8	159331	9	AL589741	Human DNA
62	10	1.8	160154	2	AL391066	Homo sapi
63	10	1.8	170499	2	AC104360	Homo sapi
64	10	1.8	172854	3	AC023706	Drosophil
65	10	1.8	176233	2	AC027737	Homo sapi
66	10	1.8	177814	2	AC009858	Homo sapi
67	10	1.8	179779	2	AP005315	Oryza sat
68	10	1.8	183152	2	AL732371	Homo sapi
69	10	1.8	191601	2	AC105598	Rattus no
70	10	1.8	197632	10	AL672039	Mouse DNA
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ALIGNMENTS

RESULT 1	AX327336	3320 bp	DNA	linear	PAT 07-JAN-2002
LOCUS	AX327336	Sequence 1 from Patent WO0181577.			
DEFINITION	AX327336				
ACCESSION	AX327336				
VERSION	AX327336.1	GI:18097882			
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Lau, T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W., Steinbrecher, R., van Heut, P.T. and Wu, J.				
TITLE	Dna encoding the prost 03 polypeptide				
JOURNAL	Patent: WO 0181577-A 1 01-NOV-2001;				
FEATURES	SCHERING AKTIENSELLSCHAFT (DE)				
source	Location/Qualifiers				
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Best Local Similarity:	100.00% Mismatches: 0
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Qy	1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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Qy	21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
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Qy	41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db	402 CCTCTGCTGCTGGAAGTGGGGTAGAGAGAGATTCATGACCATGTGCTGGGCATTGT 461
Qy	61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db	462 CCAGTGTGGGCTGTGTGTGCTCCCTCCTTAGGCTCAGCCAGTGACCACTGGCGTGA 521
Qy	81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db	522 CGCTATGGCCGCGCGCCCTTCATCTGGGCACGTGCTTGGGCATCCTGCTGAGCCCTC 581
Qy	101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuCysProAspProArgProLeu 120
Db	582 TTTCATCTCCCAAGGCGCGCTGGCTAGCAGGCTGTGTGCCCCGATCCAGGCCCTTG 641
Qy	121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db	642 GAGCTGGCACTGCTCATCTCCGGGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 701
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Qy	161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db	762 TACTCTGCTATGCCCTTCATGATCACTTGTGGGGCTGCTGGGGTACTCTCTGCTGCC 821
Qy	181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
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Qy	201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db	882 GGCTGTGCTACCCCTCATCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 941

QY	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
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QY	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1002	TGCTGTCCATGCGGGCGCGCTGGCTTTCCGGAACCTGGGCGCTGCTCCCGCGTG	1061
QY	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1062	CACCACTGTGTCGCCGATGCCCCCAGCTGCGCGCGCTCTTCGTGGCTGAGCTGTC	1121
QY	281	SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu	300
Db	1122	AGCTGGATGGCACTCATGACCTTCAGCTGTTTACACGGATTCGTGGCGAGGGCTG	1181
QY	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1182	TACCAAGGCGTGCCACAGCTGAGCGGGCACCAGCGCCGAGACACTATGATGAAGC	1241
QY	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1242	GTTGGATGGGAGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGTCTCTCTCTG	1301
QY	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1302	GTCATGGACCGCTGGTGACGATTCGGCACTCGAGCAGTCTATTGGCCAGTGGCA	1361
QY	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380
Db	1362	GCTTTCCCTGTGCTGCCGTGCCACATGCTGTCCACAGTGTGCCGTGGTACAGCT	1421
QY	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProThrThrLeuAla	400
Db	1422	TGACCGCCCTCACCGGTTCACCTTCTCAGCCCTGCAGATCTCGCCCTACACACTGGCC	1481
QY	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1482	TCCCTCTACCCAGGAGAGCAGGTGTTCTTCCCAATACCGAGGGGACACTGGAGT	1541
QY	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1542	GCTACAGTGGAGACAGCTGATGACCACTTCCTGCCAGGCCCTAAGCCTGGAGCTCC	1601
QY	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuLeuProProAlaLeu	460
Db	1602	TTCCTTAATGGACAGTGGGTGCTGAGGACGTGGCTGCTCCACCTCCACCCGCGCTC	1661
QY	461	CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla	480
Db	1662	TGCGGGCTCTGCTGTGATGTCCTGTCCTGTCGTGGTGGTGGTGGTGGTGGTGGT	1721
QY	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1722	AGGGTGGTTCGGGGCGGATCTGCTGGACCTGCGCATCTCGATCTGATGCTGCTG	1781
QY	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1782	CTGTCCCAAGTGGCCCCAFCCTGTTATGGGCTCCATGTCAGCTCAGCCAGTCTGTC	1841
QY	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1842	ACTGCTATATGTTCTGCCCGAGCCCTGGTCTGGTGGTGGTGGTGGTGGTGGTGG	1901
QY	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1902	GTAGTATTGACAAGAGGCACTTGGCCAAATACTCAGCG	1940
RESULT 2			
AX106329			
LOCUS			
DEFINITION			

Sequence 110 from Patent WO0125272. DNA linear PAT 30-APR-2001

ACCESSION	AX106329		
VERSION	AX106329.1	GI:13922014	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.		
TITLE	Compositions and methods for therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0125272-A 110 12-APR-2001;		
FEATURES	CORIXA CORPORATION (US)		
Source	1. 3410		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
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Alignment Scores:			
Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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QY	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCACACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGACGATCACCTATGTGCG	403
QY	41	ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGCTGGAAGTGGGGTAGAGGAAGTTCTATGACCATGGTGCTGGGCATTTG	463
QY	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
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QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGCCCTTCATCTCTGGCACATGCTCTTGGGCATCTGCTGAGCCTC	583
QY	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTATCCCCAAGGCGCGCTGCTGCTAGCAGGCTGCTGTGCCCGGATCCCCAGGCCCTG	643
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCGGCGTGGGGCTGCTGACTTCTGTGGCAGGTGCTTC	703
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
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QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGCTATGCTTATGATCAGTCTTGGGGGCTGCTTGGGCTTACCTCTGCTGCTGCC	823
QY	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe	200
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QY	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGTCTCACCTCATCTCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	943

QY	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
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QY	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCGCGGCCCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCGCGCTG	1063
QY	261	HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys	280
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QY	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
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Db	1184	TACAGGGCTGCCAGAGCTGAGCGGGCAGCAGAGCGCGGAGACACTATGATGAAGGC	1243
QY	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCCGATGGCAGCGCTGGGCTGTCTCCAGTGGCCATCTCCCTGGTCTCTCTCTG	1303
QY	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGACCGGCTGGTCAGCGATTCCGCACTCGAGCAGTCTATTTGGCCAGTGGCA	1363
QY	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380
Db	1364	GCCTTCCCTGTGCTGCCGTGCCATGCTGCTCCACAGTGTGGCGCTGGTGACAGCT	1423
QY	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC	1483
QY	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCTCTACACCGGAGAGCAGGGTTCTTCCGCCAATACCGAGGGCAGCTGGAGT	1543
QY	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCC	1603
QY	441	PheProAsnGlyHisValGlyAlaGlyLysSerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACGTGGGTGCTGGAGCAGTGGCTCTCCACCTCCACCGCGCTC	1663
QY	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCTCTGCCCTGTGATGTCCTGTCGTGGTGGTGGTGGAGCCCGAGGCC	1723
QY	481	ArgValValProGlyArgGlyLysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGGTGGTTCCGGCGCGGGCATCTGCCCTGGACCTGCCCATCTGGATAGTCCCTCTG	1783
QY	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTC	1843
QY	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCATATGGTCTCGCGCAGCGCTGGGTCTGGTGGTGGTGGTGGTGGTGGTGGT	1903
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ACCESSION	AX140620		
VERSION	AX140620.1	GI:14280737	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3410)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0134802-A 110 17-MAY-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	1..3410		
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ORIGIN	1 others		
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Db	344	GTCACCTGCTAACCTTTGGCGTGGAGGTGTGTTGGCCGAGGCATCATCTATGTGCG	403
QY	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CTCTGCTGCTGGAAGTGGGTGAGGAGAGTTCATGACCATGCTGGGCATTTGCT	463
QY	61	ProValLeuGlyLeuValCysValProLeuLeuGlyLysSerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTGTGGGCGCTGGTGTGTCCTCCGCTCTAGGCTCAGCCAGTACACCTGGCGTGA	523
QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGCGGCTTCATCTGGGCACGTCTCTGGGCATCTCTGTGAGCCCTC	583
QY	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGCGCGGCTGGCTAGAGGGCTGCTGTGCCGATCCAGGCCCTTG	643
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCGGGCGTGGGCGTGGTGGCTTCTGGCCAGGTGTGCTTC	703
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGCGCTGCTCTGACCTTTCGGGACCCCGGACCACTGTGCCAGGCC	763
QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGTCTATGCTTCATGATCAGTCTGTGGGCGTGGCTGGGTACCTCTGCTGCC	823
QY	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
Db	824	ATTGACTGGACACCACTGCTCCCTGCGCCCTACCTACCTGGGCGCACCCAGGAGGTGCTCT	883
QY	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220

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Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240	DEFINITION	Sequence 110 from Patent WO0151633.				
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Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280	ORGANISM	Homo sapiens				
Db	1064	CACCAGCTGTGTCGCATGCCCCGACCCCTGCGCGCTCTTCTGCTGAGCTGTGC	1123	REFERENCE	1 (bases 1 to 3410)				
Qy	281	SerTyrMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu	300	AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,				
Db	1124	AGCTGATGGCACTCATGACCTTCAGCTGTGTTTACACGGATTTCGTGGCGAGGGCTG	1183	REED,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,					
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320	STOLK,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.					
Db	1184	TACCAGGGCGTGCCACAGAGCTGAGCGGCGACCGAGGCCGAGACACTATGATGAAGC	1243	TITLE	Compositions and methods for the therapy and diagnosis of prostate				
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340	JOURNAL	Patent: WO 0151633-A 110 19-JUL-2001;				
Db	1244	GTTCCGATGGCGAGCTGGGGCTGTCTCTGCAGTGCAGTCTCCCTGGCTTCTCTCTG	1303	FEATURES	CORIXA CORPORATION (US)				
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360	source	1. 3410				
Db	1304	GTCATGGACCGCTGGTGACGGATTCGGCACTCGCAGCTATTTGGCCAGTGTGGCA	1363	BASE COUNT	667 a 1014 c 945 g 783 t			1 others	
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380	ORIGIN					
Db	1364	GCTTTCCCTGTGCTGCCGCTGCCACATGCTTCCACAGTGTGCCGTGGTGACAGT	1423	Alignment Scores:					
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400	Pred. No.:	0	Length:	3410		
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvik, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 110 04-OCT-2001;
CORIXA CORPORATION (US)
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VERSION AX429961.1 GI:21541123
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AUTHORS Reed,S.G., Xu,J., Dillon,D.C., Retter,M.W. and Harlocker,S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: WO 0198339-A 100 27-DEC-2001;
CORIXA CORPORATION (US)
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REFERENCE 1 (bases 1 to 3410)
AUTHORS Xu, J., Kalos, M., Stolk, J. A., Zasloff, E. J., Zhang, X., Houghton, R. L.,
Filho, A. M., Nolasco, M., Badaro, R. and Reed, S. G.
IDENTIFICATION and characterization of prostate, a novel
prostate-specific protein
Cancer Res. 61 (4), 1563-1568 (2001)
JOURNAL MEDLINE 21139094
PUBMED 11245466
REFERENCE 2 (bases 1 to 3410)
AUTHORS Xu, J., Kalos, M., Stolk, J. A., Zasloff, E. J., Zhang, X., Houghton, R. L.,
Filho, A. M., Nolasco, M., Badaro, R. and Reed, S. G.
DIRECT SUBMISSION
TITLE Submitted (27-APR-2001) Antigen Discovery, Corixa Corporation, 1124
JOURNAL Columbia Street, Seattle, WA 98104, USA
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LOCUS Sequence 3 from Patent WO0200892.
ACCESSION AX343857
VERSION AX343857.1 GI:18491926
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS cabezon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between
thioredoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 3 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
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DEFINITION Sequence 6 from Patent WO0200892.
ACCESSION AX343860
VERSION AX343860.1 GI:18491927
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS cabazon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between thiorodoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 6 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
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AUTHORS		Mammalia; Eutheraia; Primates; Catarrhini; Homnidae; Homo.	
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		Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,	
		Red,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,	
		Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.	
TITLE		Compositions and methods for the therapy and diagnosis of prostate	
JOURNAL		cancer	
		Patent: WO 0151633-A 625 19-JUL-2001;	
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Db	401	CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGCTGGCAT	460
QY	61	ProValLeuLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
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QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
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AX267730
LOCUS AX267730 4034 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 704 from Patent WO0173032.
ACCESSION AX267730
VERSION AX267730.1 GI:16516402
KEYWORDS
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 704 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
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QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 641 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGCCAGGTGTGCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 701 ACTCCACTGGAGCCCTGCTCTGTACCTCTTCCGGGACCGGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 761 TACTCTGTCTATGCCCTTCATGATCACTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 820
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DB 821 ATTGACTGGACACCACTAGTGCCTTGGCCCTTACCTGGCACCCAGGAGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 881 GGCTGTCTCACCCTCATCTTCCTCACCTAGCAGCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 941 GCAGCGCTGGCCCCACCAGCAGCCAGCAGAGGGCTCTCGGCCCTCTCTTGTGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1001 TGTGTCTCATGCGCGCGCTTGGCTTTCGCGAAGCTGGCGCCCTGCTTCCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
DB 1061 CACCAGCTGTCTGCGCATGCCCCCGCACCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
DB 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTG 1180
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AX201078
LOCUS AX201078 1203 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 708 from Patent WO0151633.
ACCESSION AX201078
VERSION AX201078.1 GI:15390883
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1203)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 708 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1 .1203
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/db_xref="taxon:9606"
BASE COUNT 175 a 415 c 368 g 245 t
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Alignment Scores:
Pred. No.: 1.82e-271 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 6 Gaps: 0
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QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
DB 472 GTGTGGGGATTGGTCCAGTGTGGGCTGGTCTGTGTCCTCCGCTCTAGGCTCAGCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95

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Qy	96	IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro	115
Db	592	ATCTGTGTGAGCCCTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTCTGTGCCCCG	651
Qy	116	AspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys	135
Db	652	GATCCCAAGGCCCTGGAGCTGGCACTGCTCATCTCGGGCGTGGGGCTCTGGACTTCTGT	711
Qy	136	GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp	155
Db	712	GGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGACCTTTCGGGGACCCGGAC	771
Qy	156	HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly	175
Db	772	CACGTGCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGCTGCCTGGGC	831
Qy	176	TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln	195
Db	832	TACCTCTGCTGCGCATTTGACTGGGACACCACTGCGCCCTGGCCCTACTCTGGGACCCAG	891
Qy	196	GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu	215
Db	892	GAGAGTGGCCCTTTGGCCTCTCACCTCATCTTCCTCACTGGTAGCAGCACACTG	951
Qy	216	LeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro	235
Db	952	CTGTGGCTGAGGAGGAGCGCTGGGCCCCACCAGCCAGCAGGAAGGGCTGTCTGGCCCCC	1011
Qy	236	SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla	255
Db	1012	TCCTTGTGCGCCCCACTGTGTTCATGCGGGCGCGCTGGCTTTCGCGAACCTGGGGCC	1071
Qy	256	LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe	275
Db	1072	CTGCTTCCCCGGCTGACACAGCTGTGTGCGCGCATGCCCGCACCCCTGGCGGCTCTTC	1131
Qy	276	ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe	295
Db	1132	GTGGCTGAGCTGCGAGCTGGATGGCACTCATGACCTTCAGCGTGTTCACACGGATTTC	1191
Qy	296	ValGlyGlu 298	
Db	1192	GTGGCGCAG 1200	
RESULT	13		
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LOCUS		1203 bp	DNA linear PAT 26-OCT-2001
DEFINITION	Sequence 851 from Patent WO017032.		
ACCESSION	AX267877		
VERSION	AX267877.1	GI:16516515	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvik, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T., and Henderson, R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0173032-A 851 04-OCT-2001;		
FEATURES	CORIXA CORPORATION (US)		
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BASE COUNT	175 a 415 c 368 g	245 t	
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A., and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 623 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..4894
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 928 a 1448 c 1354 g 1163 t 1 others
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Alignment Scores:
Pred. No.: 6,55e-271 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 6 Gaps: 0
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DB 1431 CTGAGCCTCTTCTCATCCAGGCGCGCTGTGTAGCAGGCTGTGTGCCCGGATCCC 1490
QY 118 ArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
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QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgProAspHisCys 157
DB 1551 GTGTGCTTCACTCCACTGGAGCCCTGTCTGTGACCTCTTCCGGACCCGACCACTGT 1610
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
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QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
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QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
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DB 2091 GATGAGGT 2099
RESULT 15
LOCUS AX267728 4894 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 702 from Patent WO0173032.
ACCESSION AX267728
VERSION AX267728.1 GI:16516400
KEYWORDS human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 702 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..4894
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 928 a 1448 c 1354 g 1163 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 6,55e-271 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 6 Gaps: 0
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DB 1431 CTGAGCCTCTTCTCATCCAGGCGCGGCTGTGTAGCAGGCTGTGTGCCCGGATCCC 1490
QY 118 ArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
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QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgProAspHisCys 157
DB 1551 GTGTGCTTCACTCCACTGGAGCCCTGTCTGTGACCTCTTCCGGACCCGACCACTGT 1610
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
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Qy 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
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Qy 238 SerProHisCysCysProCysArgAlaAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1851 TCGCCCCACTCTCTCCATGCGGGCCGCTGGCTTCCGGAACCTGGGGCCCTGCTT 1910
Qy 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAla 277
Db 1911 CCCCAGGCTGACACCAAGCTGTGTCGCGCATGCCCGCCACCTGCGCGGCTTCTGCTGGCT 1970
Qy 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1971 GAGCTGTGACGCTGGAGGCACTCATGACCTTCACGCTGTTTTACAGGATTTCTGCGGC 2030
Qy 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 2031 GAGGGCTGTACCAAGGCTGCCAGAGCTGAGCGCGGCACCGAGCGCCGGAGACATAT 2090
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LOCUS AX200996 626 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 626 from Patent WO0151633.
ACCESSION AX200996
VERSION AX200996.1 GI:15390823
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 6976)
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Weagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 626 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1. .6976
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1312 a 1996 c 1961 g 1706 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 9.05e-271 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 6 Gaps: 0

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Db 1382 AGGCCCTGGAGCTGGCACTGCTCATCTGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1441
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Qy 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
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Qy 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
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Qy 318 AspGluGly 320
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RESULT 17
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LOCUS AX267731 6976 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 705 from Patent WO0173032.
ACCESSION AX267731
VERSION AX267731.1 GI:16516403
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer.
JOURNAL Patent: WO 0173032-A 705 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1. .6976
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Alignment Scores:
Pred. No.: 9,05e-271 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
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US-09-593-793A-113 (1-553) x AX267731 (1-6976)
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DB 1322 CTGAGCCTCTTTCTCATCCAGGCGCGCTGTGCTAGCAGGCGTGTGTCCCGGATCCC 1381
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DB 1622 TGCCCTTTGGCGTGTCTACCCCTCATCTTCTCACCTGCTAGCAGCCACACTGTGTGGT 1681
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DB 1862 GAGCTGTGACGTGGATGACCTCATGACCTTCACGCTCTTTTACAGGATTTCTGTGGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyr 317
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DB 1982 GATGAAGGT 1990
RESULT 18
AC096533
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LOCUS AC096533 157988 bp DNA linear HTG 18-SEP-2001
DEFINITION Homo sapiens chromosome 1 clone RP11-6B6, WORKING DRAFT SEQUENCE, 7
unordered pieces.
ACCESSION AC096533 AL365261
VERSION AC096533.1 GI:15638681
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 157988)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 157988)
JOURNAL Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Sep 18, 2001 this sequence/version replaced gi:9931838.

Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwghtgs@u.washington.edu
Drafting Center: SC

Project Information
Center project name: chr-1
Center clone name: RP11-6B6 (sc0601)

Summary Statistics
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET; 57% of reads
Chemistry: Dye-terminator 'Big Dye'; 43% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154688 bases at least Q40
Consensus quality: 156347 bases at least Q30
Consensus quality: 157058 bases at least Q20
Insert size: 157388; sum-of-contigs
Quality coverage: 7.3x in 'Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 6264: contig of 6264 bp in length
* 6265 6364: gap of unknown length
* 6365 15785: contig of 9421 bp in length
* 15786 15885: gap of unknown length
* 15886 27947: contig of 12062 bp in length
* 27948 28047: gap of unknown length
* 28048 51992: contig of 23945 bp in length
* 51993 52092: gap of unknown length
* 52093 81154: contig of 29062 bp in length
* 81155 81254: gap of unknown length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2477)
AUTHORS Ansong, W., Winkler, U., Mewes, H.W., Weil, B. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp666D0110) is available at the R2PD in Berlin.
Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
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Berlin-Charlottenburg, GERMANY; Email: clone@rpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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ACCESSION AX200994
VERSION AX200994.1 GI:15390821
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 624 19-JUL-2001;
CORIXA CORPORATION (US)
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US-09-593-793a-113 (1-553) x AX200994 (1-2904)
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ACCESSION AX267729
VERSION AX267729.1 GI:16516401
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 703 04-OCT-2001;
CORIXA CORPORATION (US)
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Qy	365	aAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuTh	385
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Qy	385	rgIlePheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr	405
Db	1022	TGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTTACACACTGGGCTCCCTCTACACCG	1081
Qy	405	gGluIys-GlnValPheLeuProLysTyrArgGlyAspThr-GlyGlyAla-SerSerG	424

Db	1082	
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Db 72 GTGGTGACAGCTTCACGCCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCGCCC 131

QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416

Db 132 TACACACTGGCTCCCTCTACACACCGGGAGACAGCTGTCTCTGCCCAATACCGAGGG 191

QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436

Db 192 GACACTGGAGGTGCTAGCAGTAGGACAGCTGATCACCAGCTTCTCGCAGGCCCTAAG 251

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456

Db 252 CCGGAGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGTGGCTGTCCACCT 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476

Db 312 CCACCCGCGCTCGCGGGCCCTCGCTGTGATGTCTCGTAGCTGTGGTGGGTGAG 371

QY 477 ProThr 478

Db 372 CCCACC 377

RESULT 27

AX140520

LOCUS AX140520 789 bp DNA linear PAT 31-MAY-2001

DEFINITION Sequence 10 from Patent WO0134802.

ACCESSION AX140520

VERSION AX140520.1 GI:14280638

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 789)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0134802-A 10 17-MAY-2001;

FEATURES

source Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 122 a 250 c 221 g 182 t 14 others

ORIGIN

Alignment Scores:

Pred. No.: 1.64e-120 Length: 789

Score: 122.00 Matches: 122

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 22.06% Indels: 0

DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX140520 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376

Db 12 GCCAGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCC 71

QY 377 ValValThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396

Db 72 GTGGTGACAGCTTCACCGGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCGCCC 131

QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416

Db 132 TACACACTGGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGTGGCTGTCCACCT 191

QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436

Db 192 GACACTGGAGGTGCTAGCAGTAGGACAGCTGTGATGACAGCTTCTCGCCAGGCCCTAAG 251

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456

Db 252 CCGGAGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGTGGCTGTCCACCT 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476

Db 312 CCACCCGCGCTCGCGGGCCCTCGCTGTGATGTCTCGTAGCTGTGGTGGGTGAG 371

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456

Db 252 CCGGAGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGTGGCTGTCCACCT 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476

Db 312 CCACCCGCGCTCGCGGGCCCTCGCTGTGATGTCTCGTAGCTGTGGTGGGTGAG 371

QY 477 ProThr 478

Db 372 CCCACC 377

RESULT 28

AX200380

LOCUS AX200380 789 bp DNA linear PAT 29-AUG-2001

DEFINITION Sequence 10 from Patent WO0151633.

ACCESSION AX200380

VERSION AX200380.1 GI:15390176

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 789)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0151633-A 10 19-JUL-2001;

FEATURES

source Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 122 a 250 c 221 g 182 t 14 others

ORIGIN

Alignment Scores:

Pred. No.: 1.64e-120 Length: 789

Score: 122.00 Matches: 122

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 22.06% Indels: 0

DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX200380 (1-789)

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QY 377 ValValThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396

Db 72 GTGGTGACAGCTTCACCGGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCGCCC 131

QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416

Db 132 TACACACTGGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGTGGCTGTCCACCT 191

QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436

Db 192 GACACTGGAGGTGCTAGCAGTAGGACAGCTGTGATGACAGCTTCTCGCCAGGCCCTAAG 251

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456

Db 252 CCGGAGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGTGGCTGTCCACCT 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476

Db 312 CCACCCGCGCTCGCGGGCCCTCGCTGTGATGTCTCGTAGCTGTGGTGGGTGAG 371

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QY 477 ProThr 478
Db 372 CCCACC 377

RESULT 29
AX267036
LOCUS
DEFINITION Sequence 10 from Patent WO0173032.
ACCESSION AX267036
VERSION AX267036.1 GI:16515821
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 10 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1..789
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 122 a 250 c 221 g 182 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 1.64e-120 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 6 Gaps: 0
US-09-593-793a-113 (1-553) x AX267036 (1-789)
QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
Db 12 GCCAGTGTGGCAGCTTCCTCTGCGGTGGCGGTGGCCACATGCTGTCCACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
Db 72 GTGGTGACAGCTTCAGCCGCCCTCACCAGGTTACCTTCACGCCCTGCAGATCCTGTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCCTCCCTACACCCGGAGAGCAGGTGTTCTTCCGCCAAATACCGAGG 191
QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACATGGAGGTGCTAGCAGTAGGACAGCCTGATCACCAGCTTCCTGCGAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
Db 252 CTTGGAGCTCCCTTCCTTAATGACACAGCTGGGTGCTGGAGGAGGTGCTGCTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCCGCGCTCTGGGGGCCCTCTGCCCTGTATGCTCGTACGCTGCTGGTGGGTGAG 371
QY 477 ProThr 478
Db 372 CCCACC 377

RESULT 30
AR112280
LOCUS
DEFINITION Sequence 1 from patent US 6130043.
ACCESSION AR112280
VERSION AR112280.1 GI:14092183
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 247)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroppe,S.D. and Yu,H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 4 10-OCT-2000;
Location/Qualifiers
1..247
/organism="unknown"
BASE COUNT 27 a 85 c 77 g 58 t
ORIGIN
Alignment Scores:
Pred. No.: 4.24e-78 Length: 247
Score: 82.00 Matches: 82
US-09-593-793a-113 (1-553) x AR112280 (1-258)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGGCTGCCAGAGCTGAGCCGGCCGAGGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCGATGGCAGCCTGGGGCTGTTCTTCGAGTGGCCCATCTCCCTGGCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGACCGCGCTGTCGAGCGATTTCGCGACTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCTCTGTGGCTGCGGTGCCACATGCTTCCACAGTGTGCCCGTGTG 241
QY 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCCGCC 256
RESULT 31
AR112283
LOCUS
DEFINITION Sequence 4 from patent US 6130043.
ACCESSION AR112283
VERSION AR112283.1 GI:14092183
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 247)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroppe,S.D. and Yu,H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 4 10-OCT-2000;
Location/Qualifiers
1..247
/organism="unknown"
BASE COUNT 27 a 85 c 77 g 58 t
ORIGIN
Alignment Scores:
Pred. No.: 4.24e-78 Length: 247
Score: 82.00 Matches: 82
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QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGGCTGCCAGAGCTGAGCCGGCCGAGGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCGATGGCAGCCTGGGGCTGTTCTTCGAGTGGCCCATCTCCCTGGCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGACCGCGCTGTCGAGCGATTTCGCGACTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCTCTGTGGCTGCGGTGCCACATGCTTCCACAGTGTGCCCGTGTG 241
QY 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCCGCC 256
RESULT 31
AR112283
LOCUS
DEFINITION Sequence 4 from patent US 6130043.
ACCESSION AR112283
VERSION AR112283.1 GI:14092183
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 247)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroppe,S.D. and Yu,H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 4 10-OCT-2000;
Location/Qualifiers
1..247
/organism="unknown"
BASE COUNT 27 a 85 c 77 g 58 t
ORIGIN
Alignment Scores:
Pred. No.: 4.24e-78 Length: 247
Score: 82.00 Matches: 82
US-09-593-793a-113 (1-553) x AR112280 (1-258)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGGCTGCCAGAGCTGAGCCGGCCGAGGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCGATGGCAGCCTGGGGCTGTTCTTCGAGTGGCCCATCTCCCTGGCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGACCGCGCTGTCGAGCGATTTCGCGACTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCTCTGTGGCTGCGGTGCCACATGCTTCCACAGTGTGCCCGTGTG 241
QY 379 ThrAlaSerAlaAla 383
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FEATURES
  source      Location/Qualifiers
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/sex="Female"
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BASE COUNT  97 a 128 c 115 g 66 t
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Alignment Scores:
Pred. No.:      5,72e-64      Length:      406
Score:          69.00      Matches:      69
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      12.48%      Indels:      0
DB:              11      Gaps:      0

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QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
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DB 268 GCATTCCTGTGGCTGCGCGGTGCCACATGCTGTGCCACAGTGGCGGTGGTGGACGCT 209
|||||
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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DB 208 TCAGCGCGCCCTCACCGGTTTCAGTTTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 149
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DB 148 TCCCTATACCCACCGGAGAGCAGGTA 122
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RESULT 35
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LOCUS
DEFINITION Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
AC126523
AC126523
VERSION AC126523.1 GI:21700488
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 198037)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loussegh,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Ph,L.L., Quiles,M., Ren,Y.,
Rivers,M., Rojas,A., Rojibokan,I., Roife,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
Tanton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 198037)
Worley,K.C.
Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 198037)
Worley,K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKBO
Center clone name: CH230-65F14
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q30
Consensus quality: 166549 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1063: contig of 1063 bp in length
* 1064 1163: gap of unknown length
* 1164 2325: contig of 1162 bp in length
* 2326 2425: gap of unknown length
* 2426 3556: contig of 1131 bp in length
* 3557 3656: gap of unknown length
* 3657 4752: contig of 1096 bp in length
* 4753 4852: gap of unknown length
* 4853 5972: contig of 1120 bp in length
* 5973 6072: gap of unknown length
* 6073 7818: contig of 1746 bp in length
* 7819 7918: gap of unknown length
* 7919 9266: contig of 1348 bp in length

```


Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 43 Row: p Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Location/Qualifiers

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CDS

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CCRMPTLRFLVAFELCSWMALMTFTLYTDFVGEGLYQGVPAEPGTEARRHYDEGI
RMGSLGLFLOCAISLVFLVMDRLVOKFRTSVYASVMTFPVAAAATCLSHSVVVT
ASAALTGTFESALOTLPYTLASLYHREKQVLPKYRGDAGSGEDSOTTSFLPGPKP
GALPFGNHVSGSGSLIAPPALCGASCNDVSMRVVVGPEPPEARVTVGRGICLDLAIL
DSAFLLSVAFLFMSGLVSIVQSHSVTAYMWSAAGLGLVLIYFATQVVFVDKNDLAKYSV"
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BASE COUNT 519 a 728 c 691 g 673 t

Alignment Scores:
 Pred. No.: 1.63e-52 Length: 2611
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 10.67% Indels: 0
 DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x BC034084 (1-2611)

QY 262 GlnLeuCysArgMetProArgThrLeuArgArgLeuPheValAlaGlnLeuCysSer 281

Db 475 CAGCTGTGTCGGCAGCGCTGCACCTACCCGACTCTTTGTGGTGAGCTGTGCAGC 534

QY 282 TrpMetAlaLeuMetPheThrLeuPheThrArgPheValGlyGlyLeuTyr 301

Db 535 TGGATGGCACTTATGACTTTCACACTGTTCTACACGGACTTCGTGGAGAGGGCTGTAC 594

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

Db 595 CAGGTGTACCCAGAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGCAGCGC 651

RESULT 37

BC031381

LOCUS BC031381 3354 bp mRNA linear ROD 07-AUG-2002

DEFINITION Mus musculus, clone MGC:32471 IMAGE:5050610, mRNA, complete cds.

ACCESSION BC031381

VERSION BC031381.1 GI:21594808

KEYWORDS MGC.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3354)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg, R.

AUTHORS

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 45 Row: 1 Column: 2
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Location/Qualifiers

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/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
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/db_xref="LocusID:212980"
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FSVYAFMISLGGCGLGLLPALDWDTSVLAPYLGTEECFLGLTLFLICMAATLFTV
EEAVLGPPEAGELLVSAVSRRCCPCVHGLAFNLGTLFRLQQLCCRMPTLRFLV
AELCSWMALMTFTLYTDFVGEGLYQGVPAEPGTEARRHYDEGIIRMSGLFLQCAI
SLVFLVMDRLVOKFRTSVYASVMTFPVAAAATCLSHSVVVTASAATLGTFTFSAL
OILPYTLASLYHREKQVLPKYRGDAGSGEDSOTTSFLPGPKGALPFGNHVSGS
SGLIAPPALCGASCDVSMRVVVGPEPPEARVTVGRGICLDLAILSDAFLLSVAFLS
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CDS

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FSVYAFMISLGGCGLGLLPALDWDTSVLAPYLGTEECFLGLTLFLICMAATLFTV
EEAVLGPPEAGELLVSAVSRRCCPCVHGLAFNLGTLFRLQQLCCRMPTLRFLV
AELCSWMALMTFTLYTDFVGEGLYQGVPAEPGTEARRHYDEGIIRMSGLFLQCAI
SLVFLVMDRLVOKFRTSVYASVMTFPVAAAATCLSHSVVVTASAATLGTFTFSAL
OILPYTLASLYHREKQVLPKYRGDAGSGEDSOTTSFLPGPKGALPFGNHVSGS
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BASE COUNT 662 a 922 c 934 g 836 t

ORIGIN

Alignment Scores:

Pred. No.: 2.05e-52 Length: 3354

Score: 59.00 Matches: 59

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 10.67% Indels: 0

DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x BC031381 (1-3354)

OY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 464 AGCGCTGCTAGCGACCGAAAGTCAGCTCCTGCTGTCACCTTGGC 523
OY 28 LeuGluValCysLeuAlaAGlyIleThrTyrValProLeuLeuLeuGluValGly 47
|||||
Db 524 CTGAGGTGCTGCTGCTGCGCATACCTATGTGCCACCCCTCTGCTGGAGTCGGG 583
OY 48 ValcLuGlyLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
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Db 584 GTGAGGAGAAATTCATGACCATGTGTGGGATGGCCCATGCTAGCCCTGGT 640

RESULT 38
AC107837/c
LOCUS
DEFINITION Mus musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
pieces
AC107837
VERSION AC107837.2 GI:20148020
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 178567)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-272H13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178567)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,I., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Neill,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
TITLE Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 178567)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,I.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collimore,A.,
Cooke,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Neill,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
TITLE Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Apr 14, 2002 this sequence version replaced gi:18308540.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20597
Center clone name: 272_H13
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175041 bases at least Q40
Consensus quality: 176485 bases at least Q30
Consensus quality: 177028 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 177367; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 58509: contig of 58509 bp in length
* 58510 58609: gap of 100 bp
* 58610 59459: contig of 850 bp in length
* 59460 59559: gap of 100 bp
* 59560 60623: contig of 1064 bp in length
* 60624 60723: gap of 100 bp
* 60724 62950: contig of 2227 bp in length
* 62951 63050: gap of 100 bp
* 63051 65309: contig of 2259 bp in length
* 65310 65409: gap of 100 bp
* 65410 67839: contig of 2430 bp in length
* 67840 67939: gap of 100 bp
* 67940 69956: contig of 2017 bp in length
* 69957 70056: gap of 100 bp
* 70057 73550: contig of 3494 bp in length
* 73551 73650: gap of 100 bp
* 73651 81298: contig of 7648 bp in length
* 81299 81398: gap of 100 bp
* 81399 91238: contig of 9840 bp in length
* 91239 91338: gap of 100 bp
* 91339 127752: contig of 36414 bp in length
* 127753 127852: gap of 100 bp
* 127853 177486: contig of 49634 bp in length
* 177487 177586: gap of 100 bp
* 177587 178567: contig of 981 bp in length.

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1..58509

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misc_feature		70057..73550	
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misc_feature		81399..91238	
misc_feature		/note="assembly_fragment"	
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misc_feature		177587..178567	
misc_feature		/note="assembly_fragment"	
misc_feature		clone_end:T7	
misc_feature		vector_side:right"	
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ORIGIN			
Alignment Scores:			
Pred. No.:	7.69e-51	Length:	178567
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	10.67%	Indels:	0
DB:	2	Gaps:	0
US-09-593-793A-113 (1-553) x AC107837 (1-178567)			
Qy	262	GlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSer	281
Db	170571	CAGCTGTGCTGCCGATGCTCGCACCTTGTGGCTGAGCTGTGCAGC	170512
Qy	282	TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr	301
Db	170511	TGGATGGCACTATGACTTTACACTGTCTACACGGACTTGTGGGAGAGGGGCTGTAC	170452
Qy	302	GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	170451	CAGGCTGTACCCAGAGCGAGCCAGCAGCCAGGCCCCGAGACACTATGATGAAGGT	170395
RESULT 39			
AR112284			
LOCUS	AR112284	231 bp	DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 5 from patent US 6130043.		
ACCESSION	AR112284		
VERSION	AR112284.1	GI:14092184	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 231)		
AUTHORS	Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.		
TITLE	Reagents and methods useful for detecting diseases of the prostate		
JOURNAL	Patent: US 6130043-A 5 10-OCR-2000;		
FEATURES	Location/Qualifiers		
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BASE COUNT	41 a	68 c	61 g 61 t
ORIGIN			
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Pred. No.:	1.11e-26	Length:	231
Score:	34.00	Matches:	57
Percent Similarity:	98.28%	Conservative:	0
Best Local Similarity:	98.28%	Mismatches:	1
Query Match:	6.15%	Indels:	1
DB:	6	Gaps:	0
US-09-593-793A-113 (1-553) x AR112284 (1-231)			
Qy	496	AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln	515
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Qy	516	LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle	535
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Qy	536	TyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	122	TACTTTGTACACAGGTAGTATTGACAGAGCGGACTTGGCCAAATACTCAGCG	175
RESULT 40			
BC024519			
LOCUS	BC024519	1593 bp	mRNA linear ROD 07-AUG-2002
DEFINITION	Mus musculus, clone IMAGE:4984191, mRNA, partial cds.		
ACCESSION	BC024519		
VERSION	BC024519.1	GI:19353990	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1593)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdpaxil@stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 59 Row: p Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.		
FEATURES	Location/Qualifiers		
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BASE COUNT 358 a 401 c 398 g 436 t

ORIGIN

Alignment Scores:

Pred. No.: 7,64e-25 Length: 1593
Score: 33.00 Matches: 60
Percent Similarity: 96.77% Conservative: 0
Best Local Similarity: 96.77% Mismatches: 1
Query Match: 5.97% Indels: 2
DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x BC024519 (1-1593)

QY 485 GlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnVal 504

Db 131 GGACGGGCAATTGGCTGGACCTCTGGACAGTGCCTTCTGCTGCCAGGTG 190

QY 505 AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524

Db 191 GCTCCGTCCTCTTTCATGGCTGCCATTGTCTCCAGCTGAGCCA-CTCTGTCACTGCCTATAT 249

QY 524 tValSerAlaAlaGlyLeuGlyLeuValAlaIleIleTyrPheAlaThrGlnValValPheAs 544

Db 250 GTATCAGCTGCAGGCTTGGGTCTGGTCCCAATTACTTTGCTACACAGAGTAGTGTGA 309

QY 544 phys 545

Db 310 CAAG 313

RESULT 41

AC126523/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS

***, 65 unordered pieces.

ACCESSION AC126523

VERSION AC126523.1 GI:21700488

KEYWORDS HTG: HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 198037)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,

Bouch,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,

Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,

Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,

Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,

Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,

Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,

Mareshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

2 (bases 1 to 198037)

Worley,K.C.

Direct Submission

Submitted (06-JUL-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 198037)

Worley,K.C.

Direct Submission

Submitted (14-JUL-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine

Genome Center

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRBQ

Center clone name: CH230-65F14

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator, Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 149884 bases at least Q40

Consensus quality: 159599 bases at least Q30

Consensus quality: 166549 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 65 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

* 1063: contig of 1063 bp in length

* 1064: gap of unknown length

* 1164: contig of 1162 bp in length

* 2326: gap of unknown length

* 2426: contig of 1131 bp in length

* 3557: gap of unknown length

* 3657: contig of 1096 bp in length

* 4753: gap of unknown length

* 4853: contig of 1120 bp in length

* 5973: gap of unknown length

* 6073: contig of 1746 bp in length

* 7819: gap of unknown length

* 7919: contig of 1348 bp in length

* 9267: gap of unknown length

* 9367: contig of 1248 bp in length

* 10615: gap of unknown length

* 10715: contig of 1200 bp in length

* 11915 12014: gap of unknown length
* 12015 14075: contig of 2061 bp in length
* 14076 14175: gap of unknown length
* 14176 15601: contig of 1426 bp in length
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* 15702 17277: contig of 1576 bp in length
* 17278 17377: gap of unknown length
* 17378 18657: contig of 1280 bp in length
* 18658 18757: gap of unknown length
* 18758 20392: contig of 1635 bp in length
* 20393 20492: gap of unknown length
* 20493 21641: contig of 1149 bp in length
* 21642 21741: gap of unknown length
* 21742 23412: contig of 1671 bp in length
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* 30817 32509: contig of 1693 bp in length
* 32510 32609: gap of unknown length
* 32610 34220: contig of 1611 bp in length
* 34221 34320: gap of unknown length
* 34321 35560: contig of 1240 bp in length
* 35561 35660: gap of unknown length
* 35661 37768: contig of 2108 bp in length
* 37769 37868: gap of unknown length
* 37869 39562: contig of 1694 bp in length
* 39563 39662: gap of unknown length
* 39663 41676: contig of 2014 bp in length
* 41677 41776: gap of unknown length
* 41777 43658: contig of 1882 bp in length
* 43659 43758: gap of unknown length
* 43759 45624: contig of 1866 bp in length
* 45625 45724: gap of unknown length
* 45725 48100: contig of 2376 bp in length
* 48101 48200: gap of unknown length
* 48201 50489: contig of 2289 bp in length
* 50490 50589: gap of unknown length
* 50590 52329: contig of 1740 bp in length
* 52330 52429: gap of unknown length
* 52430 54544: contig of 2115 bp in length
* 54545 54644: gap of unknown length
* 54645 56752: contig of 2108 bp in length
* 56753 56852: gap of unknown length
* 56853 58639: contig of 1787 bp in length
* 58640 58739: gap of unknown length
* 58740 60931: contig of 2192 bp in length
* 60932 61031: gap of unknown length
* 61032 63481: contig of 2450 bp in length
* 63482 63581: gap of unknown length
* 63582 66000: contig of 2419 bp in length
* 66001 66100: gap of unknown length
* 66101 68760: contig of 2660 bp in length
* 68761 68860: gap of unknown length
* 68861 71024: contig of 2164 bp in length
* 71025 71124: gap of unknown length
* 71125 73169: contig of 2045 bp in length
* 73170 73269: gap of unknown length
* 73270 76108: contig of 2839 bp in length
* 76109 76208: gap of unknown length
* 76209 79687: contig of 3479 bp in length
* 79688 79787: gap of unknown length
* 79788 82504: contig of 2717 bp in length
* 82505 82604: gap of unknown length
* 82605 86873: contig of 4269 bp in length
* 86874 86973: gap of unknown length
* 86974 91613: contig of 4640 bp in length
* 91614 91713: gap of unknown length

* 91714 94992: contig of 3279 bp in length
* 94993 95092: gap of unknown length
* 95093 97134: contig of 2042 bp in length
* 97135 97234: gap of unknown length
* 97235 100423: contig of 3189 bp in length
* 100424 100523: gap of unknown length
* 100524 104682: contig of 4159 bp in length
* 104683 104782: gap of unknown length
* 104783 108313: contig of 3531 bp in length
* 108314 108413: gap of unknown length
* 108414 113868: contig of 5455 bp in length
* 113869 113968: gap of unknown length
* 113969 117789: contig of 3821 bp in length
* 117790 117889: gap of unknown length
* 117890 120979: contig of 3090 bp in length
* 120980 121079: gap of unknown length
* 121080 123743: contig of 2664 bp in length
* 123744 123843: gap of unknown length

Alignment Scores:
Pred. No.: 6.21e-23 Length: 198037
Score: 33.00 Matches: 60
Percent Similarity: 96.77% Conservative: 0
Best Local Similarity: 96.77% Mismatches: 1
Query Match: 5.97% Indels: 2
DB: 2 Gaps: 0

US-09-593-793A-113 (1-553) x AC126523 (1-198037)

QY 485 GlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnVal 504
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Db 59276 GGACGGGGCATTGCTGGACCTTGCATCTCCGACAGTGCCTTCTGCTGCCAGGTG 59217

QY 505 AlaProSerLeuPheMetClySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
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Db 59216 GCTCCGTCCTCTTCATGGGCTCCATTGCTCCAGCTGAGGCCA-CTGTGTACCTGCCTATAT 59158

QY 524 TvalSerAlaAlaGlyLeuGlyLeuValAlaIleIleYrPheAlaThrGlnValValPheAs 544
|||||
Db 59157 GGTATCAGCTGCAGGCTGGGTCTGTCGCCCATTTACTTTGTACACAGGTAGTGTTC 59098

QY 544 pLys 545
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Db 59097 CAAG 59094

RESULT 42
AX201081
LOCUS AX201081
DEFINITION Sequence 711 from Patent WO0151633.
ACCESSION AX201081
VERSION AX201081.1 GI:15390884
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
COMPOSITIONS and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 711 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Score: 20.00 Matches: 20
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.62% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX201081 (1-60)

QY 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472
Db 1 CTGCTCCACCTCCACCCGCGCTCTGCGGGGCTCTGCTGTGTGATCTCCGTACGTGTG 60

RESULT 43
AX267880

LOCUS AX267880 60 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 854 from Patent WO0173032.
ACCESSION AX267880
VERSION AX267880.1 GI:16516516
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: WO 0173032-A 854 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..60
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/db_xref="taxon:9606"

BASE COUNT 4 a 25 c 16 g 15 t
ORIGIN

Alignment Scores:
Pred. No.: 3.29e-12 Length: 60
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.62% Indels: 0
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US-09-593-793A-113 (1-553) x AX267880 (1-60)

QY 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472
Db 1 CTGCTCCACCTCCACCCGCGCTCTGCGGGGCTCTGCTGTGTGATCTCCGTACGTGTG 60

RESULT 44
AX201091

LOCUS AX201091 57 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 721 from Patent WO0151633.
ACCESSION AX201091
VERSION AX201091.1 GI:15390888
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 57)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: WO 0151633-A 721 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers

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/db_xref="taxon:9606"
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Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.17% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX201091 (1-57)

QY 45 GluValGlyValGluGluLysPheMetThrMetVal 56
Db 19 GARGTNGGNGTGARGAARATTYATGACNATGGTN 54

RESULT 45
AX267890

LOCUS AX267890 57 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 864 from Patent WO0173032.
ACCESSION AX267890
VERSION AX267890.1 GI:16516520
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: WO 0173032-A 864 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..57
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 8 a 5 c 11 g 12 t 21 others
ORIGIN

Alignment Scores:
Pred. No.: 0.00118 Length: 57
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.17% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX267890 (1-57)

QY 45 GluValGlyValGluGluLysPheMetThrMetVal 56
Db 19 GARGTNGGNGTGARGAARATTYATGACNATGGTN 54

Search completed: February 19, 2003, 06:11:58
Job time : 3202 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 01:33:08 ; Search time 2887 Seconds
(without alignments)
5574.594 Million cell updates/sec

Title: US-09-593-793a-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLRHRKAQLL.....AIYFATQVDFKSLAKYSA 553

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=GenEmbl -QFWT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09593793.ecgn.1.1724.@runat_13022003_161308_21553 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*

- 1: gb.ba:*
- 2: gb.htg:*
- 3: gb.in:*
- 4: gb.om:*
- 5: gb.ov:*
- 6: gb.pat:*
- 7: gb.ph:*
- 8: gb.pl:*
- 9: gb.pr:*
- 10: gb.ro:*
- 11: gb.sts:*
- 12: gb.sy:*
- 13: gb.un:*
- 14: gb.vi:*
- 15: em.ba:*
- 16: em.fun:*
- 17: em.hum:*
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- 19: em.mu:*
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- 21: em.or:*
- 22: em.ov:*
- 23: em.pat:*
- 24: em.ph:*
- 25: em.pl:*
- 26: em.ro:*
- 27: em.sts:*
- 28: em.un:*

- 29: em.vi:*
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- 32: em.htg.other:*
- 33: em.htg.mus:*
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- 38: em.sy:*
- 39: em.htgo.hum:*
- 40: em.htgo.mus:*
- 41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2861	100.0	3320	6	AX327336	Sequence
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4	2861	100.0	3410	6	AX200480	Sequence
5	2861	100.0	3410	6	AX267136	Sequence
6	2861	100.0	3410	6	AX429961	Sequence
7	2861	100.0	3410	9	AY033593	Homo sapi
8	2798	97.8	3514	9	AB060851	Macaca fa
9	2716.5	94.9	4034	9	AB060895	Sequence
10	2716.5	94.9	4034	6	AX267730	Sequence
11	2602	90.9	3354	10	BC031381	Mus muscu
12	2601	90.9	2133	6	AX343857	Sequence
13	2566	89.7	2917	9	AB062977	Macaca fa
14	2538.5	88.7	4894	6	AX200993	Sequence
15	2538.5	88.7	4894	6	AX267728	Sequence
16	2144	74.9	6976	6	AX200996	Sequence
17	2144	74.9	6976	6	AX267731	Sequence
18	2144	74.9	157988	2	AC096533	Homo sapi
19	2099	73.4	2611	10	BC034084	Mus muscu
20	2051	71.7	178567	2	AC107837	Mus muscu
21	1920.5	67.1	2904	6	AX200994	Sequence
22	1920.5	67.1	2904	6	AX267729	Sequence
23	1742	60.9	198037	2	AC126523	Rattus no
24	1696	59.3	1593	6	AX343860	Sequence
25	1403.5	49.1	1203	6	AX201078	Sequence
26	1403.5	49.1	1203	6	AX267877	Sequence
27	1287	45.0	2152	6	AR112295	Sequence
28	1270	44.4	2143	6	AR112294	Sequence
29	1179.5	41.2	2477	9	HSB804244	Homo sapi
30	919	32.1	789	6	AX106229	Sequence
31	919	32.1	789	6	AX140520	Sequence
32	919	32.1	789	6	AX200380	Sequence
33	919	32.1	789	6	AX267036	Sequence
34	673	23.5	198037	2	AC126523	Rattus no
35	512	17.9	1593	10	BC024519	Mus muscu
36	489.5	17.1	1986	10	AF360357	Mus muscu
37	489.5	17.1	1998	10	AF034377	Mus muscu
38	488.5	17.1	1650	9	AF172849	Homo sapi
39	458.5	16.0	18567	2	AC018319	Drosophil
40	458.5	16.0	165852	3	AC010022	Drosophil
41	458.5	16.0	176929	3	AC091203	Drosophil
42	458.5	16.0	286784	3	AE003552	Drosophil
43	456	15.9	1980	5	AF332510	Oryzias l
44	446	15.6	2256	10	AB075229	Rattus no
45	440	15.4	255	6	AR112282	Sequence
46	428	15.0	406	11	HSP54C06	AL033941 H. sapiens
47	423	14.8	258	6	AR112280	Sequence
48	418	14.6	247	6	AR112283	Sequence
49	357	12.5	217	6	AR112281	Sequence
50	347.5	12.1	1858	8	DCSUT2	Y16768 Daucus carota

51	346.5	12.1	1661	8	AF021808	Vitis vin
52	346.5	12.1	1796	8	AB036758	Daucus ca
53	346.5	12.1	2135	6	AX306541	Sequence
54	346	12.1	2130	8	AF021809	Vitis vin
c	340	11.9	123280	2	AC117076	Dictyoste
56	338	11.8	1872	8	AF167416	Apium gra
57	338	11.8	1907	8	AF167415	Apium gra
58	337.5	11.8	2004	8	VF293774	V.faba mRNa
59	336.5	11.8	1654	8	AF182445	Vitis vin
60	332.5	11.6	1954	8	AF063400	Apium gra
61	332.5	11.6	1782	8	AY065840	Brassica
62	330	11.5	1548	6	AX259895	Sequence
63	330	11.5	1773	6	AX36575	Sequence 2
64	330	11.5	1773	6	AR084457	Sequence 3
65	330	11.5	1773	6	I36755	Sequence 3
66	330	11.5	1988	8	STSUCTR	S.cuberosum
67	329.5	11.5	2034	8	AF109922	Pisum sat
68	328.5	11.5	1785	6	AX259876	Sequence
69	328.5	11.5	1785	8	AJ289165	Arabidops
70	327.5	11.4	1713	8	AB071809	Oryza sat
71	325.5	11.4	2137	8	AF166498	Lycopersi
72	324.5	11.3	1695	8	AF191025	Alonsoa m
73	324.5	11.3	1798	8	AY091774	Arabidops
74	324.5	11.3	1969	6	AX36574	Sequence 1
75	324.5	11.3	1969	6	AR084456	Sequence 1
76	324.5	11.3	1969	6	I36754	Sequence 1
77	324.5	11.3	1969	6	SOS21	S.coleraceae
78	323.5	11.3	1570	8	AY113946	Arabidops
79	323.5	11.3	1787	8	AT5UC25	A.thaliana
80	323.5	11.3	1800	8	AY048256	Arabidops
81	323.5	11.3	1803	8	AY088566	Arabidops
82	323.5	11.3	1857	8	AY050986	Arabidops
83	323	11.3	9319	8	DCA303199	Daucus ca
84	318.5	11.1	1985	8	AF242307	Euphorbia
85	317.5	11.1	1614	8	NTSUT1A	N.tabacum S
86	317.5	11.1	1834	8	AB008464	Zea mays
87	316.5	11.1	1824	8	AF176950	Lycopersi
88	313.5	11.0	1818	6	AX259902	Sequence
89	311	10.9	1956	8	RCSCR1R	R.comunis
90	309.5	10.8	2386	8	AY098894	Citrus si
91	307.5	10.7	1466	8	AF237780	Solanum t
92	307.5	10.7	1503	6	AX259875	Sequence
93	307.5	10.7	1503	6	AX259900	Sequence
94	306.5	10.7	1756	8	AY098891	Citrus si
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VERSION	AX327336.1	GI:18097882			
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REFERENCE	1				
AUTHORS	Lau, T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W., Steinbrecher, R., van Heuit, P.T. and Wu, J.				
TITLE	Dna encoding the prost 03 polypeptide				
JOURNAL	Patent: WO 0181577-A 1 01-NOV-2001;				
FEATURES	SCHERING AKTIENGESSELLSCHAFT (DE)				
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LOCUS
DEFINITION Sequence 110 from Patent WO0125272.
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VERSION AX106329.1 GI:13922014
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3410)
AUTHORS Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 110 12-APR-2001;
CORIXA CORPORATION (US)
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REFERENCE 1 (bases 1 to 3410)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 110 19-JUL-2001;
CORIXA CORPORATION (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Xu, J., Dillion, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL
PATENT: WO 0173032-A 110 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
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US-09-593-793A-113 (1-553) x AX267136 (1-3410)

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ACCESSION AX429961
VERSION AX429961.1 GI:21541123
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Reed,S.G., Xu,J., Dillon,D.C., Rettler,M.W. and Harlocker,S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0198339-A 100 27-DEC-2001;
CORIXA CORPORATION (US)
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Location/Qualifiers
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BASE COUNT 667 a 1014 c 945 g 783 t 1 others
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Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3410)
AUTHORS Xu, J., Kalos, M., Stolk, J. A., Zasloff, E. J., Zhang, X., Houghton, R. L.,
Filho, A. M., Nolasco, M., Badaro, R. and Reed, S. G.
TITLE Identification and characterization of prostein, a novel
prostate-specific protein
JOURNAL Cancer Res. 61 (4), 1563-1568 (2001)
MEDLINE 21139094
PUBMED 11245466
REFERENCE 2 (bases 1 to 3410)
AUTHORS Xu, J., Kalos, M., Stolk, J. A., Zasloff, E. J., Zhang, X., Houghton, R. L.,
Filho, A. M., Nolasco, M., Badaro, R. and Reed, S. G.
TITLE Direct Submission
JOURNAL Submitted (27-Apr-2001) Antigen Discovery, Corixa Corporation, 1124
Columbia Street, Seattle, WA 98104, USA
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REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skelky, J.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 625 19-JUL-2001;
CORIXA CORPORATION (US)
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VERSION AX267730.1 GI:16516402
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1
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 704 04-OCT-2001;
CORIXA CORPORATION (US)
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VERSION BC031381.1 GI:21594808
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SOURCE house mouse.
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Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NTH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stoik, J.A., Skeiky, J.A., Wang, A. and Meagher, M.J.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0151633-A 623 19-JUL-2001;		
FEATURES	CORIXA CORPORATION (US)		
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H.,
Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skelky, Y. A., Hepler, W. T.
and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 702 04-OCT-2001;
CORIXA CORPORATION (US)
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/db_xref="taxon:9606"
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Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservatives: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
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KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 6976)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 626 19-JUL-2001;
CORIXA CORPORATION (US)
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DEFINITION Sequence 705 from Patent WO0173032.
ACCESSION AX267731
VERSION AX267731.1 GI:16516403
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0173032-A 705 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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BASE COUNT 1312 a 1996 c 1961 g 1706 t
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Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
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LOCUS
DEFINITION AC107837 178567 bp DNA linear HTG 14-APR-2002
MUS musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
pieces.
ACCESSION AC107837
VERSION AC107837.2 GI:20148020
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178567)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
MUS musculus, clone RP23-272H13
Unpublished
2 (bases 1 to 178567)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collinmore,A., Cook,A.,
Cook,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Lander,E., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 178567)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepe,Y., Colangelo,M., Collins,S., Collinmore,A.,
Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Hulme,W., I.I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,

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Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 14, 2002 this sequence version replaced gi:18308540.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20597
Center clone name: 272_H13
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175041 bases at least Q40
Consensus quality: 176485 bases at least Q30
Consensus quality: 177028 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 177367; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 58509: contig of 58509 bp in length
* 58510 58609: gap of 100 bp
* 58610 59459: contig of 850 bp in length
* 59460 59559: gap of 100 bp
* 59560 60623: contig of 1064 bp in length
* 60624 60723: gap of 100 bp
* 60724 62950: contig of 2227 bp in length
* 62951 63050: gap of 100 bp
* 63051 65309: contig of 2259 bp in length
* 65310 65409: gap of 100 bp
* 65410 67839: contig of 2430 bp in length
* 67840 67939: gap of 100 bp
* 67940 69956: contig of 2017 bp in length
* 69957 70056: gap of 100 bp
* 70057 73550: contig of 3494 bp in length
* 73551 73650: gap of 100 bp
* 73651 81298: contig of 7648 bp in length
* 81299 81398: gap of 100 bp
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* 91239 91338: gap of 100 bp
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* 127753 127852: gap of 100 bp
* 127853 177486: contig of 49634 bp in length
* 177487 177586: gap of 100 bp

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LOCUS             Sequence 703 from Patent WO0173032.
DEFINITION        AX267729
ACCESSION         AX267729
VERSION           AX267729.1 GI:16516401
KEYWORDS
SOURCE            human.
ORGANISM          Homo sapiens
                  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
                  Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
                  Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
                  and Henderson,R.A.
TITLE             Compositions and methods for the therapy and diagnosis of prostate
                  cancer
JOURNAL           Patent: WO 0173032-A 703 04-OCT-2001;
                  CORIXA CORPORATION (US)
FEATURES           Location/Qualifiers
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Alignment Scores:
Pred. No.:        1.43e-116          Length:          2904
Score:            1920.50            Matches:        390
Percent Similarity: 77.23%           Conservative:    0
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Db	1500	GCCAAATACTACGC 1514	
RESULT	23		
LOCUS	AC126523	198037 bp DNA linear	HTG 14-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS		
ACCESSION	AC126523		

VERSION
KEYWORDS
SOURCE
ORGANISM

AC126523.1 GI:21700488

HTG; HTGS_PHASE1.

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 198037)

REFERENCE

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbuorne, H.C., Amarantunga, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbata, J., Benton, J., Bimadé, K., Blankenburg, K., Bonnin, D.,
Bouch, J., Bowie, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegue, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
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Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 198037)

Worley, K.C.

Direct Submission

Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 198037)

Worley, K.C.

Direct Submission

Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GKBO

Center clone name: CH230-65F14

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator; Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q30
Consensus quality: 166549 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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US-09-593-793A-113 (1-553) x AC126523 (1-198037)

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DEFINITION AX343860
VERSION AX343860.1 GI:18491927
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
1 cabazon Silva,T.E. and Delisse,A.M.
AUTHORS Triple fusion proteins comprising ubiquitin fused between
TITLE thiodoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 6 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
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/db_xref="taxon:32630"
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ACCESSION AX201078
VERSION AX201078.1 GI:15390883
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,F.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 708 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
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Score: 1403.50 Matches: 267
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Best Local Similarity: 97.45% Mismatches: 2
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Gaps: 1
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DEFINITION Sequence 851 from Patent WO0173032.
ACCESSION AX267877
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 851 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..1203
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ORIGIN
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Pred. No.: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 6 Gaps: 1
US-09-593-793a-113 (1-553) x AX267877 (1-1203)
QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCGAGGACCCCGCGCGAATTACATCACCTATGTGCGCGCTCTGCTGCTG 438
QY 45 GluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGAGAGATTTCATGACCATGGTCTGGGCATTGGTCCAGTGTGGGC 498
QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGTCGCCGCTCCTAGGCTCAGCCAGTGCAGCTGGCGTGGACGCTATGGCCGC 558
QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTTCATCTGGGCAGTGTCTTGGGCATCCTGCTGAGCCTCTTTCATATCCCA 618
QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCCGGCTGGCTAGCAGGCTGCTGTCGCCGGATTCGCCAGGCCCTGAGGCTGGCAGT 678
QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheTrpProLeuGlu 144
Db 679 CTCATCTTGGGGCTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAG 738
QY 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCTTCTCTGACCTCTTCCGGGACCGGACCACTGTGCGCAGGCTTACTTGTCTAT 798
QY 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCTCAGTCAGTCTTGGGGCTGCTGCGGTACCTCTGCTGCCATTCAGTGGGAC 858
QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTTGGCCCTTACCTGGCCACCCAGGAGGAGTGCCTCTTGGCCTGCTCACC 918
QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluLeuAlaLeuGly 224
Db 919 CTCATCTTCTCCTACCTTTCAGCAGGCTGCTGGGCTACCTCTGCTGCCATTCACCTCCAG 978
QY 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAGAGGCTGTGGCCCTCTCTTTCGCCCCCTCTCTTGGCCTGCTCACC 1038
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTTCCCGGCTGACGAGCGCTGGC 1098
QY 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGCCGATGCCCCCGCACCCCTGCGCGGCTCTTTCGTGGCTGAGCTGTGACGCTGGATGCA 1158
QY 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGCGAG 1200

RESULT 27
AR112295
LOCUS AR112295 2152 bp DNA linear PAT 16-MAY-2001
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DEFINITION Sequence 16 from patent US 6130043.

ACCESSION AR112295

VERSION AR112295.1 GI:14092195

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2152)

AUTHORS

Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,

Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,

Roberts-Rapp, L., Russell, J.C., Strope, S.D., and Yu, H.

Reagents and methods useful for detecting diseases of the prostate

Patent: US 6130043-A 16 10-OCT-2000;

Location/Qualifiers

1. 2152

/organism="unknown"

BASE COUNT 419 a 622 c 569 g 542 t

ORIGIN

Alignment Scores:

Pred. No.: 2,66e-75 Length: 2152

Score: 1287.00 Matches: 255

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 44.98% Indels: 0

DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AR112295 (1-2152)

Qy 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318

Db 2 GGGCTGTACACGGCGTGCACAGAGCTGAGCGGGACACCGAGCGCGGAGACATATGAT 61

Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338

Db 62 GAAGCGGTTCGGATGGGCGCTGGGCTGTCTCGAGTGGCCATCTCCCTGGTCTTC 121

Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358

Db 122 TCTCTGTGTCATGACCGCGTGTGCAGGATTCGGCACTCGCAGCAGTCTATTGGCCAGT 181

Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378

Db 182 GTGGCAGCTTTCCCTGTGGCTGCGCGTGCACATCCCTGTCCACAGTGTGGCGGTGGT 241

Qy 379 ThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398

Db 242 ACAGCTTCAGCGCGCTCACCGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 301

Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418

Db 302 CTGGCTCCCTCTACACCGGGAGACAGAGTGTCTCTGCCCAATAACCGAGGGGACACT 361

Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438

Db 362 GGAGGTGCTAGCAGTGAGGACAGCTGATGACAGCTTCCTTCGCGAGGCGCTTAAGCCTTGA 421

Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProPro 458

Db 422 GCTCCCTTCCTTAATGACACGTGGGTGCTGGAGGAGTGGCCCTGCTCCCACTCCACCC 481

Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478

Db 482 CGCGCTTCGGGGCGCTCTGCTGTGATGTCTCCGTAGCTGTGGTGGTGGGAGCCACCC 541

Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498

Db 542 GAGGCCAGGGTGGTTCGGGGCGGGGATCTGCGCTGGACCTCGCCATCTCGATAGTCC 601

Qy 499 PheLeuLeuSerGlnValAlaProSerLeuMetGlySerIleValGlnSerGln 518

Db 602 TTCCTGTGTCGCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTTGCCAGCTCAGCCAG 661

Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538

Db 662 TCTGTCACTGCCTATATGCTGTGCGCAGCGCTGGTGTGGTGCCTATTACTTTGCT 721

Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553

Db 722 ACACAGGTAGTATTGTACAGAGCGACTTGGCCAAATACTCAGCG 766

RESULT 28

LOCUS

AR112294

Sequence 15 from patent US 6130043.

ACCESSION

AR112294

VERSION

AR112294.1 GI:14092194

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 2143)

AUTHORS

Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,

Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,

Roberts-Rapp, L., Russell, J.C., Strope, S.D., and Yu, H.

Reagents and methods useful for detecting diseases of the prostate

Patent: US 6130043-A 15 10-OCT-2000;

Location/Qualifiers

1. 2143

/organism="unknown"

BASE COUNT 418 a 621 c 563 g 541 t

ORIGIN

Alignment Scores:

Pred. No.: 3.42e-74 Length: 2143

Score: 1270.00 Matches: 252

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 44.39% Indels: 0

DB: 6 Gaps: 0

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Db 3 CAGGCGCTGCCAGAGCTGAGCGGGACCGAGCGCGGAGACACTATGATGAAGCGCTT 62

Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341

Db 63 CGGATGGCAGCGTGGGCTGTCTCTCGAGTGGCCATCTCCCTGGTCTCTCTCTGGTC 122

Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361

Db 123 ATGGACCGGCTGGTGCAGCGATTCGGCACTCGACAGTCTATTGGCCAGTGTGGCAGCT 182

Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381

Db 183 TTCCTGTGGCTGGCGGTGCCACATGCTGTGCCACAGTGTGGCGTGGTGCAGAGTTCA 242

Qy 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401

Db 243 GCCGCCCTCACCGGTTTACCTTCTCAGCCTGCAGATCTCTGCCCCATACACACTGGCCCTCC 302

Qy 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421

Db 303 CTCCTACACCGGGAGAGCAGCTGTCTCTGCCCAATAACCGAGGGGACACTGGAGTGTCT 362

Qy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441

Db 363 AGCAGTGAGGACAGCTGATGACAGCTTCTTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTC 422

Qy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCys 461

Db 423 CCTAATGGACACGGGTGGTGTGGAGGAGTGGCTGTCCACCTCCACCCGCGCTTCGC 482

Qy 462 GlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481

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Db 483 GGGGCTCTGGCTGTGATGTCCTCCGTAGCTGTGGTGGGTGAGCCACCGAGGCCAGG 542
Qy 482 ValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGGCGGGGATCTGCGCTGACCTCGCCATCTCGGATAGTGCCTCTCTGCTG 602
Qy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCCAAGTGGCCCATCCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGCTACT 662
Qy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGGTGTCTGCGCGAGGCTGGTGTCTGGTGCCTATTACTTTGCTACACAGTA 722
Qy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTTGACAAGAGGACTTGCCCAATACTCAGCG 758

RESULT 29
LSM804244          2477 bp  mRNA  linear  PRI 10-JUL-2002
LOCUS              Homo sapiens mRNA; cDNA DKEZp666D0110 (from clone DKEZp666D0110).
DEFINITION         AL832933
ACCESSION          AL832933.1  GI:21733520
VERSION            human.
KEYWORDS
SOURCE
ORGANISM            Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS            Ansorge,W., Wirkner,U., Mewes,H.W., Weill,B. and Wiemann,S.
TITLE              Direct Submission
JOURNAL            Submitted (09-JUL-2002) 1. D-85764 Neuberberg, GERMANY
COMMENT            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                    Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                    Heidelberg/Germany) within the cDNA sequencing consortium of the
                    German Genome Project.
                    This clone (DKFZp666D0110) is available at the RZPD in Berlin.
                    Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                    Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                    information about the clone and the sequencing project is available
                    at http://mips.gsf.de/proj/cDNA/.
FEATURES
source
1..2477
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp666D0110"
/tissue_type="stomach"
/clone_lib="666 (synonym: hsto2). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
polyA_signal       2425..2430
polyA_site         2447
BASE COUNT         505 a 713 c 634 g 625 t
ORIGIN
Alignment Scores:
Pred. No.:         3.28e-68          Length:          2477
Score:             1179.50          Matches:         258
Percent Similarity: 78.47%          Conservative:    8
Best Local Similarity: 76.11%       Mismatches:     29
Query Match:       41.23%          Indels:         45
DB:                9              Gaps:          5

US-09-593-793A-113 (1-553) x LSM804244 (1-2477)
Qy 228 ProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysProCysArgAlaArg 247
Db 142 CCTGGTTCACGGCGAGTGGCCCTCTCG-TCCCCCAACGACTTTCACAAATATCTCACC 200
Qy 248 LeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMet 267
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Db 201 AGCGCTTTCAG-|||||:-|-----CTCAGCGCT 221
Qy 268 ProArgThrLeuArgArg-LeuPheValaIaGluLeuCysSerTrpMetAlaLeuMetTh 287
Db 222 CCTAGAAGCGTCTTGAAGCCTA-|||:-|-----TGGCCAGCTGTCTTTGT 260
Qy 287 rPheThrLeu-|||:-|-----PheTyrThrAspPh 295
Db 261 GTTCCTCTCACCCCGCTGTCTCTCACAGCTGAGACTCCACGAAACCTTCAGACTACCTT 320
Qy 295 eValGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgAr 315
Db 321 CQTC-|||:-|-----GCCTTGC 347
Qy 315 gHisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSe 335
Db 348 CACATCTCTCTGAGGCGTTCGGATGGGAGCTGGGGCTGTTCCTGCGAGTGGCCATCTC 407
Qy 335 rLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTy 355
Db 408 CCTGTCTCTCTCTGTCATGGACCGCTGTGTGCAGCGATTTCGCGACTCGAGCAGTCTA 467
Qy 355 rLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerVa 375
Db 468 TTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCACATGCCCTGTCCACAGTGT 527
Qy 375 lAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLe 395
Db 528 GGCCGTGTGTACAGGCTTCAGCCGCCCTCAGCGGGTTCACCTTCTCAGCCCTGCGAGATCT 587
Qy 395 uProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrAr 415
Db 588 GCCCTACACACTGGCTCCCTCTACCCCGGAGAGCAGGTGTTCCTGCCCAATACCG 647
Qy 415 gGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPr 435
Db 648 AGGGACACTGGAGGTGTAGCAGTGTAGGACAGCCCTGTATGACCACTTCCTGCCAGGCC 707
Qy 435 oLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPr 455
Db 708 TAAGCTCGAGCTCCCTTCCTTAATGGACAGCTGGGTGCTGGAGGACGTGGCTGCTCC 767
Qy 455 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValG 475
Db 768 ACCTCCACCGCGCTCTGGGGGCTCTGCGCTGTATGTCCTCCGTACGTGTGGTGGTGG 827
Qy 475 yGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLe 495
Db 828 TGAGCCCAACCGAGGCGAGGTGGTTCCGGGGCGGGGCGATCTGCCCTGGACCTCGCCATCT 887
Qy 495 uAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValG 515
Db 888 GGATAGTGCCTTCCTGCTGTCCCAGTGGCCCATCCCTGTTATGGGCTCCATTGTCCA 947
Qy 515 nLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaI 535
Db 948 GCTCAGCCAGTCTGTCACTGCCATATATGGTGTCTGCCGAGGCCCTGGGTCTGTGGTGGCAT 1007
Qy 535 eTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1008 TTACTTTCCTACACAGGTAGTATTGTGACAAGAGCGACTTGGCCAAATACTCAGCG 1062

RESULT 30
AX106229          789 bp  DNA  linear  PAT 30-APR-2001
LOCUS              Sequence 10 from Patent WO0125272.
DEFINITION         AX106229
ACCESSION          AX106229
VERSION            AX106229.1  GI:13921915
KEYWORDS           human.
SOURCE             Homo sapiens
ORGANISM            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 789)
XU, J., SKEIKY, Y. A., REED, S. G. and CHEEVER, M. A.
Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0125272-A 10 12-APR-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..789
Location/Qualifiers
misc_feature
/db_xref="taxon:9606"
BASE COUNT 122 a 250 c 221 g 182 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AX106229 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGATGCTGTCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGCCGTGGTGACAGCTTACAGCCGCTCACCGGGTTACCTTCTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlnValPheLeuProLys 413
Db 123 ATCTGCGCTACACACTGGCGTCCCTTACCCAGGAGAGAGAGAGAGAGAGAG 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACAGCTGATGACAGCTTCTCGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGTGGAGCAGTGGCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCGCGCTCTGGGGGCTCTGCCGTGTATGTCCTCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGAGGTGTCCGGGGCGGGGCACTGCTGGAGCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGATGATGTC-TTCCTGCTGCCANGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuValVal 533
Db 482 GTCCAGCTACGCCAGTGTGCTACCTGCTATATGTTGTTGCTGCCGAGGCTGGGTCTGGTC 541
QY 534 AlaTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTTCATTGCTACACAGGTANTATTGACAAAGAACGANTTGGCCAAATCTACGCG 600
RESULT 31
AX140520
LOCUS AX140520 789 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 10 from Patent WO0134802.
ACCESSION AX140520
VERSION AX140520.1 GI:14280638
KEYWORDS

human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 789)
AUTHORS XU, J., DILLON, D. C., MITCHAM, J. L., HARLOCKER, S. L., JIANG, Y.,
REED, S. G., KALOS, M. D., RETTER, M. W., STOLK, J. A., DAY, C. H.,
SKEIKY, Y. A. and WANG, A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 10 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..789
Location/Qualifiers
misc_feature
/db_xref="taxon:9606"
BASE COUNT 122 a 250 c 221 g 182 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AX140520 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
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Db 482 GTCCAGCTACGCCAGTGTGCTACCTGCTATATGTTGTTGCTGCCGAGGCTGGGTCTGGTC 541
QY 534 AlaTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 32
AX200380
LOCUS AX200380 789 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 10 from Patent WO0151633.

ACCESSION AX200380
VERSION AX200380.1 GI:15390176
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 10 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Source 1..789
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 122 a 250 c 221 g 182 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AX200380 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGGCAGCTTCCCTGTGGGTGGCGGTGCACATGCTGTCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTGACAGCTTCAGCCGCTCAGCGGTTACACCTTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTCCCTACACTGGCTTCCCTTACCCAGGAGAGACAGGTGTCTGTCCGCCAAA 182
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Db 303 CTCCACCTCCACCCGCGCTCTGGCGGCGGTGTGGGTGTGGGTGTGGGTGTGGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGAGGTGTGGCGGCGGCGGTGTGGGTGTGGGTGTGGGTG 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
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RESULT 33

AX267036
LOCUS AX267036 789 bp
DEFINITION Sequence 10 from Patent WO0173032.
ACCESSION AX267036
VERSION AX267036.1 GI:16515821
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 10 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
Source 1..789
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 122 a 250 c 221 g 182 t 14 others
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Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AX267036 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
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Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTGACAGCTTACCGCGCTCAGCGGTTACACCTTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTCCCTACACTGGCTTCCCTTACCCAGGAGAGACAGGTGTCTGTCCGCCAAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGCTAGCAGTGGAGACAGCTGATGACAGCTTCCGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTAAGCCCTGGAGCTTCCCTTCCCTAATGGACAGTGGGTGTGGAGGAGTGGCCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCCGCGCTCTGGCGGCGGTGTGGGTGTGGGTGTGGGTGTGGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGAGGTGTGGCGGCGGCGGTGTGGGTGTGGGTGTGGGTG 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGTGATAGTGC-TTCCCTGTGTCCCGAGTGGCGGCGGTGTGGGTGTGGGTGTGGGTG 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuValVal 533
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Db      542 CC-ATTACTTGTACACAGGTANTATTTCACAGAAGCAGTTCGCCAAATACTACGCG 600
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AC126523/c
LOCUS   AC126523              198037 bp    DNA        linear    HTG 14-JUL-2002
DEFINITION
Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.
ACCESSION
AC126523.1 GI:21700488
VERSION
HTG: HTGS_PHASE1.
KEYWORDS
Norway rat.
SOURCE
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 198037)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Aisbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouack,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
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Homsif,I., Howard,S., Huber,J., Huiy,K.S., Hume,J., Jackson,B.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratochvic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,G., Mawhney,E., Mcleod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
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Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usman,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 198037)
Worley,K.C.
Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 198037)
Worley,K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine

Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKBQ
Center clone name: CH230-65F14
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q30
Consensus quality: 166549 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
consists of 65 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1063: contig of 1063 bp in length
1163: gap of unknown length
1164: contig of 1162 bp in length
2326: gap of unknown length
2425: contig of 1131 bp in length
3557: gap of unknown length
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4753: gap of unknown length
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5972: gap of unknown length
6073: contig of 1746 bp in length
7819: gap of unknown length
9266: contig of 1348 bp in length
9367: gap of unknown length
10614: contig of 1248 bp in length
10715: gap of unknown length
11914: contig of 1200 bp in length
11915: gap of unknown length
12015: contig of 2061 bp in length
14075: gap of unknown length
14176: contig of 1426 bp in length
15601: gap of unknown length
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25187: gap of unknown length
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28698: gap of unknown length
28699: contig of 1918 bp in length
30717: gap of unknown length
30817: contig of 1693 bp in length
32609: gap of unknown length
32610: contig of 1611 bp in length
34320: gap of unknown length
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35561: gap of unknown length
35661: contig of 2108 bp in length
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*	58640	59739:	gap of	unknown	length
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*	61032	63481:	contig of	2450	bp in length
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*	63582	66000:	contig of	2419	bp in length
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LOCUS Mus musculus, clone IMAGE:4984191, mRNA, partial cds.
DEFINITION BC024519
ACCESSION BC024519.1 GI:19353990
VERSION BC024519.1 GI:19353990
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.
Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shoc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 59 Row: p Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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BASE COUNT 358 a 401 c 398 g 436 t
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Db 2 CCCATGACAGCTGGGCTCTGGCAGCAGCGCATCTTGGCCCTCCACCTGCACCTCTGT 61
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Db 302 GTGTTGACAGACGACTTTGGCCAAATACTCA 334

RESULT 36
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LOCUS Mus musculus B/Alm-1-like protein mRNA, complete cds.
DEFINITION AF360357
ACCESSION AF360357
VERSION AF360357.1 GI:15028432
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Fukamachi, S., Shimada, A. and Shima, A.
1 (bases 1 to 1986)
Mutations in the gene encoding B, a novel transporter protein,
reduce melanin content in medaka
JOURNAL Nat. genet. 28 (4), 381-385 (2001)
MEDLINE 21372467
PUBMED 11479596
REFERENCE 2 (bases 1 to 1986)
AUTHORS Fukamachi, S., Shimada, A. and Shima, A.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2001) Integrated Biosciences, University of
Tokyo, Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
FEATURES
Location/Qualifiers
1. 1986
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CDS

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KEYWORDS
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               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE         1 (bases 1 to 1998)
               Newton,J.M., Cohen-Barak,O., Hagiwara,N., Gardner,J.M.,
               Davissou,M.T., King,R.A. and Brilliant,M.H.
               Mutations in the human orthologue of the mouse underwhite gene (uw)
               underlie a new form of oculocutaneous albinism, OCA4
JOURNAL       Am. J. Hum. Genet. 69 (5), 981-988 (2001)
MEDLINE       21473748
PUBMED        11574907
REFERENCE     2 (bases 1 to 1998)
AUTHORS       Newton,J.M., Cohen-Barak,O., Hagiwara,N., Gardner,J.M.,
               Davissou,M.T., King,R.A. and Brilliant,M.H.
TITLE         Direct Submission
JOURNAL       Submitted (11-MAY-2001) Pediatrics, University of Arizona, 1501 N
               Campbell Ave, Tucson, AZ 85724, USA
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VERSION AC018319.1 GI:6552872
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SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
REFERENCE 1. (bases 1 to 18567)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10214336 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
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AC010022
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VERSION
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SOURCE fruit fly.
ORGANISM Drosophila melanogaster
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Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 165852)
AUTHORS Muzny, D., Scherer, S., Adams, M.D., Holt, R.A., Evans, C.A.,
Gocayne, J.D., Tabor, P., Williamson, A., Homs, F.H.,
Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayele, M., Scott, G.S., Worley, K.W., Amaratides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Cencar, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,

Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J., Hostin, D., Howland, T.J., Hume, J., Ibegwam, C., Jalali, M., Kovar, C., Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moly, M., Murphy, B., Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V., Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M., Xiang, J., Zaveri, J.S., Zhou, J., Zorrilla, S., Smith, H.O., Wheeler, D., Weinstein, G., Gibbs, R. and Venter, J.C.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 165852)

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Denny, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisleged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Siason, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

3 (bases 1 to 165852)

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Denny, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,

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Direct Submission

TITLE

JOURNAL

Submitted (01-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS

5 (bases 1 to 165852)

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Denny, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisleged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Siason, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission

TITLE

JOURNAL

Submitted (29-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

6 (bases 1 to 165852)

AUTHORS

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Anaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binaige, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferreguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hensandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, T., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S., Ushani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R.,

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SOURCE		Drosophila melanogaster.	
ORGANISM		Drosophila melanogaster.	
REFERENCE			
AUTHORS			

TITLE	Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.
JOURNAL	The genome sequence of <i>Drosophila melanogaster</i>
MEDLINE	Science 287 (5461), 2185-2195 (2000)
PUBMED	20196006
REFERENCE	10731132
AUTHORS	2 (bases 1 to 286784)
TITLE	Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
JOURNAL	Direct Submission
COMMENT	Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
FEATURES	On Oct 9, 2000 this sequence version replaced gi:7294927.
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QY 518 nSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAl 538
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RESULT 43
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VERSION AF332510.1 GI:15004312
KEYWORDS Oryzias latipes.
SOURCE Oryzias latipes.
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REFERENCE 1 (bases 1 to 1980)
AUTHORS Fukumachi,S., Shimada,A. and Shima,A.
TITLE Mutations in the gene encoding B, a novel transporter protein,
reduce melanin content in medaka
JOURNAL Nat. Genet. 28 (4), 381-385 (2001)
MEDLINE 21372467
PUBMED 11479596
REFERENCE 2 (bases 1 to 1980)
AUTHORS Fukumachi,S., Shimada,A. and Shima,A.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2000) Integrated Biosciences, University of
Tokyo, Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
FEATURES
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polya_signal 1949..1954
BASE COUNT 425 a 519 c 489 g 547 t
ORIGIN
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Alignment Scores:

Pred. No.: 5, 07e-21 Length: 1980

Score: 456.00 Matches: 144

Percent Similarity: 39.77% Conservative: 95

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US-09-593-793a-113 (1-553) x AF332510 (1-1980)
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QY 32 LeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGlyValGluGluLys 51
Db 409 TATGCGGTGAAGCGGCATTTGTCACACGGTCTCTCAGCGTAGGTCTCCCGCCAGT 468
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QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
Db 529 GGCTCAGCAAGTGACTACTGCGGCTTCTCTGGGAAGGAGGAGGCCCTACATC----- 582
QY 92 LeuSerLeuGlyIleLeu-----LeuSerLeuPheLeu-----102
Db 583 CTGTGCTCGGTATCCTCATGCTGTGGGGCTCAGCATGTTTCTCAATGGAGATCAGTG 642
QY 103 -----IleProArgAlaGlyTrpLeuAlaGlyLeuLeuCys 114
Db 643 GTCTCAGAGCTCGTCAGTCAGAGTCATCCAGAGTAGCTGG-----684
QY 115 ProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPhe 134
Db 685 -----GCCATCGTGGTGGTGCATGTTTGGGGTGTGCTGTGTCACATTT 726
QY 135 CysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerSerAspLeu-----PheArg 152
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QY 153 AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGly 172
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QY 193 GlyThrGlnGluCysLeuPhe-----GlyLeuLeuThrLeu 205
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QY 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
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QY 257 LeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheVal 276
Db 1246 -----TTGATGAAAGCTATCTTCAACATCGCAAAACCACTACCGCTTCTCTGTGATC 1296
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Qy	297	GlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHis	316
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Qy	337	ValPheSerLeuValMetAspArgLeuGlnArgPheGlyThrArgAlaValLeu	356
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Qy	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
Db	1537	ATGGGCTACTTGTTCGGCATGGGTACCATCTAATTTGGCTCTTCCACGAAGTCATA	1596
Qy	377	ValValThrAlaSerAlaValLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
Db	1597	GCCACGCTCATCTCTGCAGCTGTGTGGCGTCATGTCTAGCACCTCTACACGATCCG	1656
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Db	1657	TTCACCTTAATTCGTAGTATCAGCGGGAGGAGGAAAGTA---AAGCTGGAGGA	1713
Qy	417	AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
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Db	1882	TTC	1884
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AB075229			
LOCUS			
DEFINITION			
AB075229			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			

Past-A, a new class proton-associated sugar transport facilitator in the central nervous system
Unpublished
2 (bases 1 to 2256)
Shimokawa,N.
Direct Submission
Submitted (03-DEC-2001) Noriaki Shimokawa, Gunma University School of Medicine, Physiology 1st Division; 3-39-22 Showa-machi, Maebashi, Gunma 371-8511, Japan (E-mail:simokawa@med.gunma-u.ac.jp, Tel:81-27-220-7923, Fax:81-27-220-7926)
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BASE COUNT 419 a 728 c 629 g 480 t

ORIGIN

Alignment Scores:
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Percent Similarity: 33.33% Conservative: 79
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DB: 10 Gaps: 15

US-09-593-793A-113 (1-553) x AB075229 (1-2256)

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Qy 37 ThrTyrValProLeuLeuGluValGlyValGluLysPheMetThrMetVal 56
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Qy 57 LeuGlyIleGlyProValLeuValCysValProLeuLeuGlySerAlaSerAsp 76
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Qy 77 HisTrpArgGlyArgTyrArgArgArgPropheIleTrpAlaLeuSerLeuGlyIle 96
Db 436 CGATGTACTCAAGTGTGGAAGGAGAGCGCTTTCATCTTGTCTGCGCATAGGGCG 495
Qy 97 LeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuCysProAsp 116
Db 496 TTGCTGGCCCTCTCGCTCTCTCTCAAT---GGAAGGGACATTTGTTATGGCCCTGGCTGAC 552
Qy 117 Pro-----ArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAsp 133
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Qy	307	AlaGluProGlyThrGluAlaLeuArgHisTyrAspGluGlyValArgMetGlySerLeu	326
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Qy	367	GlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGly	386
Db	1864	GGATGGCCCACTCTCCAGGAACCTGTAGTGGTCTCTCCTCTGCACCCACCTACGCG	1923
Qy	387	PheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlu	406
Db	1924	ATCTGTCTCCAGCTCTGTACCTGCCCTACTCTCTCTCTGGATTACTACCAAGT	1983
Qy	407	LysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSer	426
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Qy	487	GlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuSerGlnValAlaPro	506
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Qy	507	SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSer	526
Db	2083	TCTCTGCTCTCGGGGCC-----CTGACCTCC	2109
Qy	527	AlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPhe	543
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VERSION	ARL11282.1	GI:14092182	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 255)		
AUTHORS	Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.		
TITLE	Reagents and methods useful for detecting diseases of the prostate		
JOURNAL	Patent: US 6130043-A 3 10-OCT-2000;		
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Pred. No.:	440.00	Matches:	83
Score:			

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ORIGIN					
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Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 15.38% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AR112282 (1-255)

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DB	2	ACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA	61
QY	399	LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr	418
DB	62	CTGGCTCCCTCTACCAACCGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACT	121
QY	419	GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly	438
DB	122	GGAGGTGCTAGCAGTGAGACAGCCCTGATGACACAGCTTCCTGCCAGGCCCTAAGCCTGA	181
QY	439	AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro	458
DB	182	GCTCCCTTCCCTAATGGACACGTTGGGTGCTGGANGCAGTGGCTGCTCCACCTCCACCC	241
QY	459	AlaLeuCysGly	462
DB	242	GCGCTCTGCGGG	253

Search completed: February 19, 2003, 04:49:56
Job time : 3498 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 01:25:58 ; Search time 228 Seconds
(without alignments)
54622.084 Million cell updates/sec

Title: US-09-593-793a-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLHRKRAQLL.....AIYFATQVVFEDSLAKYSA 553

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45
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-NO_XLPXY -NO_MAP -LARGOQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2861	100.0	1662	24	ABN81324	Human mast cell re
2	2861	100.0	2582	24	ABK92217	Prostate cancer-as
3	2861	100.0	3320	24	AAS14962	DNA encoding human
4	2861	100.0	3410	19	AAV61201	Full length cDNA s
5	2861	100.0	3410	19	AAV58586	Prostate tumour sp
6	2861	100.0	3410	21	AAW9473	cDNA sequence of h
7	2861	100.0	3410	21	AAA06349	Human immunogenic
8	2861	100.0	3410	22	AAS63557	Human prostate cDN
9	2861	100.0	3410	22	AAS10108	Human prostate tum
10	2861	100.0	3410	22	AAH93465	Human prostate-spe
11	2861	100.0	3410	22	AAH84779	Human prostate-spe
12	2861	100.0	3410	22	AAH02530	Prostate tumour an
13	2861	100.0	3410	24	ABL94929	Human LI-12 cDNA s
14	2861	100.0	3410	24	ABK29017	Human breast tumou
15	2716.5	94.9	4034	22	AAS64040	Human prosate cDNA
16	2716.5	94.9	4034	22	AAH93868	P553S cDNA splice
17	2716.5	94.9	4034	24	ABL95411	Human P553S splice
18	2601	90.9	2133	24	ABA91283	Thioredoxin-ubiqui
19	2538.5	88.7	4894	22	AAS64038	Human prosate cDNA
20	2538.5	88.7	4894	22	AAH93866	P553S cDNA splice
21	2538.5	88.7	4894	24	AAH95409	Human P553S splice
22	2400.5	83.9	3878	22	AAH05230	Human secreted pro
23	2144	74.9	6976	22	AAS64041	Human prosate cDNA
24	2144	74.9	6976	22	AAH93869	P553S cDNA splice
25	2144	74.9	6976	24	ABL95412	Human P553S splice
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28	1920.5	67.1	2904	24	ABL95410	Human P553S splice
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30	1604	56.1	1604	24	ABN81320	Human mast cell re
31	1403.5	49.1	1203	22	AAS64153	Human /M. tubercul
32	1403.5	49.1	1203	22	AAH93917	Ra12-P501S-E2 cons
33	1403.5	49.1	1203	24	AAH95524	Ra12-P501S-E2 cons
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35	1287	45.0	2133	22	AAH07155	Prostate gene PS10
36	1287	45.0	2152	20	AAV71181	Consensus sequence
37	1270	44.4	2124	21	AAH64927	Human prostate-rel
38	1270	44.4	2124	22	AAH07601	Prostate gene PS10
39	1270	44.4	2143	20	AAV71180	Clone 1711346IH t
40	1170.5	40.9	2462	21	AAZ45677	cDNA sequence of a
41	919	32.1	789	19	AAV61144	3' cDNA sequence o
42	919	32.1	789	19	AAV58487	3' fragment of pro
43	919	32.1	789	21	AAA06250	Human immunogenic
44	919	32.1	789	22	AAS63458	Human prostate cDN
45	919	32.1	789	22	AAH93366	Human prostate-spe
46	919	32.1	789	22	AAH93366	Human prostate-spe
47	919	32.1	789	22	AAH02431	Prostate tumour an
48	919	32.1	789	22	AAH02431	Human LI-12 3' cDN
49	829	29.0	742	21	AAZ45675	cDNA sequence of a
50	829	29.0	742	21	AAZ45675	Drosophila melanog
51	520.5	18.2	2052	23	ABL07785	Drosophila melanog
52	458.5	16.0	4437	23	ABL07784	Human polynucleoti
53	457.5	16.0	2476	22	AAI59383	PS108 gene-specifi
54	440	15.4	255	20	AAV71168	Human prostate-rel
55	440	15.4	255	21	AAC63193	Prostate gene PS10
56	440	15.4	255	22	AAH07589	PS108 gene-specifi
57	423	14.8	258	20	AAV71166	Human prostate-rel
58	423	14.8	258	21	AAC63191	Prostate gene PS10
59	423	14.8	258	22	AAH07589	PS108 gene-specifi
60	418	14.6	247	20	AAV71169	Human prostate-rel
61	418	14.6	247	21	AAC63194	Prostate gene PS10
62	418	14.6	247	22	AAH07590	PS108 gene-specifi
63	357	12.5	217	20	AAV71167	Human prostate-rel
64	357	12.5	217	21	AAC63192	Prostate gene PS10
65	357	12.5	217	22	AAH07588	Human prostate-rel
66	357	12.5	1885	20	AAZ23129	Soybean sucrose tr
67	346.5	12.1	2135	24	AAZ47773	Glycine max sucros

68 330 11.5 1548 22 AAI68588 S. tuberosum SUT1
69 328.5 11.5 1785 22 AAI68575 A. thaliana SUT2 e
70 326.5 11.4 2375 20 AAZ23128 Rice sucrose trans
71 325.5 11.4 2030 20 AAZ23135 Wheat sucrose tran
72 323.5 11.3 1803 21 AKA2576 Arabidopsis thalia
73 317.5 11.1 1977 20 AAZ23126 Corn sucrose trans
74 313.5 11.0 1818 22 AAI68593 S. tuberosum SUT2
75 313 10.9 2083 20 AAZ23133 Wheat sucrose tran
76 307.5 10.7 1503 22 AAI68574 L. esculentum SUT4
77 307.5 10.7 1503 22 AAI68592 S. tuberosum SUT4
78 306.5 10.7 2088 20 AAZ23124 Corn sucrose trans
79 306 10.7 1628 21 AAC53258 Arabidopsis thalia
80 300 10.5 1625 21 AAC54585 Arabidopsis thalia
81 300 10.5 2160 20 AAZ23134 Wheat sucrose tran
82 294.5 10.3 1533 22 AAI68573 A. thaliana SUT4 e
83 293.5 10.3 6918 21 AAC74763 Human ORFX ORF318
84 267 9.3 958 22 AAI61169 Human polynucleoti
85 247 8.6 231 20 AAV71170 PS108 gene-specific
86 247 8.6 231 21 AAC63195 Human prostate-rel
87 247 8.6 231 22 AAS07591 Prostate gene PS10
88 235 8.2 1041 20 AAZ23130 Soybean sucrose tr
89 219.5 7.7 510 21 AAZ45681 cDNA sequence of a
90 203 7.1 828 24 ABK93112 Human prostate spe
91 197.5 6.9 1653 20 AAZ23127 Rice sucrose trans
92 197 6.9 432 22 AAD05262 Human secreted pro
93 195.5 6.8 1355 22 AAI68576 L. esculentum SUT2
94 192 6.7 435 20 AAX40506 Human secreted pro
95 191 6.7 349980 22 AAF86431 Pyrococcus abyssi
96 184.5 6.4 1249 21 AAC49139 Arabidopsis thalia
97 169 5.9 271 24 ABK93110 Human prostate spe
98 169 5.9 1251 21 AAC33335 Arabidopsis thalia
99 162 5.7 612 24 ABK93111 Human prostate spe
100 161 5.6 307 22 ABA11517 Human nervous syst

ALIGNMENTS

RESULT 1
ABN81324
ID ABN81324 standard; cDNA; 1662 BP.
XX AC ABN81324;
XX DT 30-AUG-2002 (first entry)
XX DE Human mast cell related splice variant gene MC14 SEQ ID NO 12.
XX KW Human; mast cell; MC; antiallergic; antinflammatory; antiasthmatic;
XX KW vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
XX KW gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS /*tag= a
XX FT /*product= "MC14 alternatively spliced variant"
XX PN WO200246389-A2.
XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US46180.
XX PR 08-DEC-2000; 2000US-251935P.
XX PR 14-MAR-2001; 2001US-275479P.
XX PR 28-MAR-2001; 2001US-279115P.
XX PR 02-APR-2001; 2001US-280143P.
XX PA (UNIO) UCB SA.
XX PI Nocka K, Pirozzi G, Einstein R;
XX

DR WPI; 2002-508560/54.
DR P-PSDB; ABB77575.
XX Novel isolated nucleic acids that are differentially expressed in mast
PT cells in patients with allergic hypersensitivity, encoding proteins
PT associated with mast cell degranulation and allergic hypersensitivity
PT
XX
XX
PS Claim 1; Page 115-117; 119pp; English.
XX
CC The invention relates to isolated nucleic acid (ABN81319-ABN81324),
CC corresponding to genes differentially expressed in mast cells following
CC activation or in patients with allergic hypersensitivity disease, (I)
CC that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of
CC (II) if at least 6 amino acids. (II) is useful for identifying binding
CC partners. (I) or (II) is useful for diagnosing or treating a disease
CC state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,
CC urticaria or atopic dermatitis or mastocytosis) in a subject which
CC involves determining the level of expression of (I) or (II). A computer
CC system, comprising a database containing information identifying the
CC expression level in a tissue or at least one mast cell of (I), is useful
CC for presenting information to identify the relative expression level of
CC (I). (II) is used as a marker to detect, diagnose or identify an allergic
CC response in a patient. The protein can also serve as a target that
CC modulate gene expression or activity and as an antigen to raise
CC polyclonal or monoclonal antibodies. (II) is useful for identifying
CC agents that modulate expression of the protein or agents, such as
CC agonists or antagonists. The agonists or antagonists are useful for
CC modulating biological activity and function of (II) and thus are useful
CC for alleviating disease conditions such as allergic hypersensitivity,
CC seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
XX
SQ Sequence 1662 BP; 229 A; 551 C; 511 G; 371 T; 0 other;

Alignment Scores:

Pred. No.: Length: 1662
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-593-793a-113 (1-553) x ABN81324 (1-1662)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 1 ATGGTCCAGAGGCTGTGGGTGAGCCCTGCTGGCGCAGCGAAGCCAGCTCTGTGCTG 60
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 61 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCGG 120
Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 121 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGAGTTCATGACCATGGTGTGTGGGCATGTGT 180
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 181 CCAGTGTCTGGGCTGTGTCTGCTGGCTCCAGTGTAGGCTAGCCAGTACCATGGCGTGA 240
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 241 CGCTATGGCGCGCGCGGCTTCATCTGGGCACGTGCTCTGGGCATCTCTGTGAGCCCTC 300
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 301 TTTCATCATCCCAAGGCGCGGCTGGCTAGCAGGCTGCTGTCCCGATCCAGGCCCTCG 360
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 361 GAGCTGGCACCTGCTCATCTCTGGCGGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 420
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

Db 421 ACTCCACTGGAGGCGCTCTCTGACCTCTTCCGGGACCCGAGCACTGTGCGCAGGCC 480
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 481 TACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGCTGGGTACCTCTGCTGCTGCC 540
Qy 181 IleAspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 541 ATTGACTGGGACACCACTGCGCTGCGCCCTTACCTGGGCACCCAGAGAGTGCCTTTT 600
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 601 GGCCTGCTCACCTCATCTTCTCACCTGCGTAGCAGCCACACTGCTGCTGGCTGAGGAG 660
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 661 CGAGCGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGCGCCCCCTCTCTTGTGCGCCCCAC 720
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 721 TGCTGTCCATGCGCGGCGCTTGTGCTTCCGGAACCTGGGCGCCCTGCTTCCCGCGCTG 780
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 781 CACCAGCTGTGCTGCGCATGCGCGCACCTGCGCGCGCTTCTGCTGAGCTGTGC 840
Qy 281 SerTyrMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
Db 841 AGCTGATGGCACTCATGACCTTACGCTTACGCTTTTACAGGATTTCTGGGCGAGGGCTG 900
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 901 TACCAGGCGGTGCCAGAGCTGAGCGGCGCACCAGAGCGCCGAGACACTATGATGAGGC 960
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 961 GTTCGGATGGGCGAGCTGGGCGTGTCTCTGCGAGTCGCGCATCTCCCTGCTCTCTCTG 1020
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1021 GTCATGGACCGGCTGGTGAGCGATTCGCGACTCGAGCAGTCTATTTGGCCAGTGTGCA 1080
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1081 GCTTTCCTGTGGTGGCGGTGCCATGCTGTCCTCCACAGTGTGGCGGTGGTACACT 1140
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1141 TCAGCGCGCTCACCGGTTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1200
Qy 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1201 TCCCTCTACCAACCGGGAAGAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGT 1260
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1261 GCTAGCACTGAGGACAGCTGATGACCACTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1320
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1321 TTCCCTAATGACACGTGGGTGCTGGAGCGACTGGCGCTTCTCCACCTCCACCGCGCTC 1380
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1381 TCGGGGGCTCTGCTGTGATGTCCTGATGCTGTGGGTGGGGAGCCACCGAGGCC 1440
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1441 AGGGTGGTTCCGGGCGGGGATCTGCTGGACCTCGCATCTGGATAGTGCCTTCTCTG 1500
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||

Db 1501 CTGTCCCCAGTGGCCCCCATCCCTGTGTTATGGGCTCCATGTGCCAGCTCAGCAGTCTGTC 1560
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1561 ACTGCTATATGCTGTGCGCAGCGCTGGGCTGTGGTCTGGTCCCATTTACTTTGCTACACAG 1620
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1621 GTAGTATTGTACAGAGCGACTTGGCCAAATACTCAGCG 1659
RESULT 2
ABK92217
ID ABK92217 standard; DNA; 2582 BP.
XX
AC ABK92217;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #103.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX
(EOSB-) EOS BIOTECHNOLOGY INC.
XX
Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
WPI; 2002-471335/50.
XX
P-PSDB; ABG61900.
XX
Detecting a prostate cancer-associated transcript in a cell in a
patient, useful for diagnosing prostate cancer (PC) or screening
modulators of PC, by determining if prostate cancer-associated genes
are expressed in a prostate tissue -
XX
Claim 22; Page 386; 436pp; English.
XX
The present invention relates to methods of detecting a prostate
cancer-associated transcript in a cell from a patient. The method
comprises contacting a biological sample from the patient with
prostate cancer-associated polynucleotides (designated PC genes) that
selectively hybridise to a sequence that is at least 80% identical
to them. The prostate cancer-associated polynucleotide sequences
are differentially expressed in prostate tumour tissue or in
prostate cancer and are derived from the tissues of various
organisms such as humans or other mammals (e.g. mice, sheep and dogs).
The methods of the invention are useful for diagnosing and treating
prostate cancer in mammals. The prostate cancer-associated genes are
useful for diagnosing or treating prostate cancer, as well as for
identifying modulators of prostate cancer or agents that inhibit
prostate cancer. The nucleic acid sequences are particularly useful
in gene therapy, as a vaccine or in antisense applications.
XX
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
sequences.

XX Sequence 2582 BP; 407 A; 822 C; 785 G; 566 T; 2 other;

Alignment Scores:
Pred. No.: 1-le-218 Length: 2582
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793a-113 (1-553) x ABK92217 (1-2582)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 310 ATGGTCCAGAGGCTGGGTGAGCGGCTGCTGGGCACCGAAGACCCAGCTCTGTG 369
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db 370 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGCGCAGGCATCACCTATGTGCGG 429
Qy 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 430 CCTCTGCTGCTGAAGTGGGGTAGAGGAAGTTTCATGACCATGCTGGGCATGTGT 489
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlyLysAlaSerAspHisTrpArgGly 80
Db 490 CCAGTCTGGGCTGGTCTGTGTCGGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGA 549
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 550 CGCTATGGCCGCGCGGCGCTTCATCTGGGCACCTGCTCTGGGCATCTGCTGAGCCCTC 609
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 610 TTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCTG 569
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 670 GAGCTGGCACTGCTATCTGCGGCTGGGCTGCTGGACTTCTTGGCCAGGTGTCTTC 729
Qy 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 730 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCGCGGACCGGACCACTGTGCCAGGCC 789
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 790 TACTCTGTCTATGCCCTTCATGATCAAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 849
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 850 ATTGACTGGGACACCACTGCCCTGGCCCTTACCTGGGCACTGCCAGGAGGTGCCTCTTT 909
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 910 GGCCCTGCTCACCTCATCTCTCCTGCTGAGCAGCCACACTGCTGGTGGCTGAGGAG 969
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 970 GCAGCGCTGGGCCCCACCGAGCGCAGAGGGGCTGTGGGCCCTCTCTGTGCGCCAC 1029
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1030 TGCTGTCCATGCGCGCGCTTGGCTTTCGGAACCTTGGGCGCCCTGCTCCCGCGCTG 1089
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1090 CACCAGCTGTGTCGCGATGCCCGCACCCCTGCGCGGCTCTGCTGGCTGAGCTGTGC 1149
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1150 AGCTGGATGGCACTCATGACCTTCAGGCTGTGTTTACAGGATTTCTGGGCGAGGGGCTG 1209

Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1210 TACCAGGGCGTCCAGAGCTGAGCGGCGCAGCGGCGGAGACACTATGATGAAGGC 1269
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1270 GTTCGGATGGGAGCGCTGGGCTGTCTTCGAGTGGCCATCTCCCTGGTCTTCTCTCG 1329
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1330 GTCATGGACCGGCTGGTCAGCGATTCGCACTCGAGCAGTCTATTTGGCCAGTGTGGA 1389
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1390 GCTTTCCCTGTGCTGCCGTGCCACATGCCGTGCCACAGTGTGCCGTGTGTGACAGCT 1449
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1450 TCAGCGCGCCTCAGCGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTTACACACTGG 1509
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1510 TCCTCTTACCACCGGAGAGGAGGAGGTTCCTGCCAAATACCGAGGGACACTGGAGT 1569
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1570 GCTAGCAGTGAAGACAGCCTGATGACCACTTCTCCTGCCAGGCCCTAAGCCTGGAGTCC 1629
Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1630 TTCCCTTAATGGACAGTGGGTGCTGGAGCAGTGGGCTCTCCACCTCCACCCGCGCTC 1689
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1690 TCGGGGCTCTGCCCTGTGATGCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGG 1749
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1750 AGGGTGGTTCGCGGCGGGGCATCTGCTGGACCTGCGCCATCTCGCATAGTGCCTTCTG 1809
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1810 CTGTCCCAAGTGGCCCACTCCCTGTTTATGGGCTCCATGTCCAGTCCAGCCAGTCTGT 1869
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1870 ACTGCTATATGTTGCTGCCCGAGCGCTGGTCTGGTGGCCATTTACTTTGCTACACAG 1929
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1930 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1968

RESULT 3
AAS14962
ID AAS14962 standard; cDNA; 3320 BP.
XX
AC AAS14962;
XX
DT 14-FEB-2002 (first entry)
XX
DE DNA encoding human PROST 03.
XX
KW Human; PROST 03; metastasis; prostate cancer; tumour; immune response;
XX
KW cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
XX CDS 282..1943
FT /*tag= a
FT /product= "PROST 03"
XX
PN W0200181577-A2.

XX 01-NOV-2001.
XX 26-APR-2001; 2001WO-US13323.
XX 27-APR-2000; 2000US-200065P.
XX 20-APR-2001; 2001US-0200065.
XX (SCHD) SCHERING AG.
XX
PI Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Steinbrecher R;
PI Van Heuit PT, Wu J;
XX WPI; 2002-041404/05.
DR P-PSDB; AAU10324.
XX
PT Novel PROST 03 polypeptides and polynucleotides useful in research,
PT diagnosis and therapeutic applications, particularly for use in cancer
PT therapeutics -
XX
PS Claim 6; Fig 1; 77pp; English.
XX
CC The invention relates to an isolated PROST 03 polypeptide (I) and to
CC the polynucleotide (II) encoding PROST 03. Fragments of (I) were used
CC to generate antibodies (III) to PROST 03. (III) is useful for selectively
CC destroying a cell expressing (I), and for treating a disease-state
CC associated with expression of PROST 03 in a human patient. (III) is
CC useful for diagnosing metastasis associated with (I), in a subject.
CC (I) is also useful for diagnosing and treating diseases of cell
CC proliferation such as prostate cancers. (I) is also useful for generating
CC antibodies to PROST 03. (III) is useful in detecting the levels of PROST
CC 03 polypeptides in cells and tissues, and in targeting drugs to primary
CC and metastatic tumours. (I) is also useful for stimulating immune
CC response to PROST 03 containing cells. (II) is useful in diagnostic
CC assays for detecting the levels of polynucleotides encoding PROST 03 in
CC cells and tissues. (II) is useful as DNA probes, as targets for antisense
CC and ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents
CC the coding sequence of human PROST 03.
XX
SQ Sequence 3320 BP; 585 A; 1013 C; 944 G; 778 T; 0 other;

Alignment Scores:
Pred. No.: 1.53e-218 Length: 3320
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x AAS14962 (1-3320)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db ATGGTCCAGAGGCTGGGTGAGCCGCTGCTGCGCACCGAAAGCCAGCTCTTGCTG 341
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db GTCAACCTGCTAACTTTGGCTGGAGGTGTGTTGGCCGCGCAGGCATCACCTATGTGCG 401
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db CCTCTGCTGCTGGAAGTGGGGTAGAGGAAGTTATGACCATCGTGGGCAATGTGT 461
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db CCAGTGTGGGCTGTGCTGTCTCCGCTCTCTAGCTCAGCCAGTGACCACTGGCGTGA 521
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db CGCTATGGCCGCCGCCCTTTCATCTGGGCACTGTCTTGGGCACTCTCTTGGGCACTCT 581

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGCGCGGATCCAGGCCCTG 641
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db GAGCTGGCACTGCTCATCTGGGCGTGGGGCTGCTGGACTTCTGTGGCAGGTGCTTC 701
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGACCACTGTGCCAGGCC 761
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db TACTCTGTATGCTTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 821
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db ATTGACTGGACACAGTGCCTGGCCCTTACCTGGGCACCCAGGAGGTGCTCTTT 881
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db GGCTCTGCTACCTCATCTCTCACTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 941
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db GCAGGCTGGGCCCCACCGAGCCAGAGAGGCTGTGGCCCCCTCTCTTGTGCGCCAC 1001
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db TGTCTGCTCATCGCGCGCTGGCTTTCCCGAACCTGGCGCCCTGCTCCCGGCTG 1061
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db CACCAGCTGTGTGCGCATGCCCGCACCTGCGCGGCTCTTCTGGCTGAGCTGTGC 1121
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db ACCTGGATGGCACTCATGACCTTCAGCTGTGTTTACAGGATTTCTGCGCGGAGGCTG 1181
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db TACCAGGCGGTGCCAGAGCTGAGCGGCGCACCGAGGCGCGGACACTATGATGAAGGC 1241
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db GTTCGATGGGCGAGCTGGGGCTGTTCCTGCGAGTGGCCATCTCCCTGCTCTCTCTG 1301
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db GTCATGGACCGGCTGGTGCAGCGATTGGCACTCCGAGCAGTCTATTGGCCAGTGGCA 1361
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db GCTTTCCCTGTGGCTGCGCGGTGCCACATGCTGCCACAGTGTGCCGCTGGTGCAGCT 1421
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db TCAGCGCGCTTCACCGGTTTCACTTTCAGCCCTGCGAGATCTCCCTTACACACTGGCC 1481
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db TCCCTCTACCACCGGAGAGCAGGCTGTTCCTGCCCAATACCCGAGGGGACACTGGAGT 1541
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db GCTAGCAGTGAAGACAGCTGATGACCACTTCTTCCGCCAGGCCCTTAAGCCTGGAGCTCC 1601
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db TTCCCTAATGGAACAGTGGGTGCTGGAGCACTGGCGCTGCCACCTCCACCCGCGCTC 1661
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480

Db 1662 TCGGGGCTCTCCCTGTGATGTCCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1721
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1722 AGGGTGTTCGGGGCGGGGCATCTGCTGGACCTGCCATCTGGATAGTGGCTTCCG 1781
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1782 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1841
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1842 ACTGCCATATGTGCTGCCGAGGCTGGGTCGTGGTCCCATTTACTTGTGTACACAG 1901
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1902 GTAGTATTTGCAAGAGGACACTTGGCCAAATACTACGCG 1940
RESULT 4
AAV61201
ID AAV61201 standard; cDNA; 3410 BP.
AC AAV61201;
XX
DT 06-JAN-1999 (first entry)
XX Full length cDNA sequence of prostate tumour clone L1-12.
DE Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
KW Homo sapiens.
OS
PN WO9837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-0503492.
XX
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
XX WPI; 1998-609886/51.
DR P-PSDB; AAW71869.
XX
XX Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
PT
PS Claim 3; Page 79-80; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00 Conservative: 0
Best Local Similarity: 100.00 Mismatches: 0
Query Match: 100.00 Indels: 0
DB: 19 Gaps: 0

US-09-593-793A-113 (1-553) x AAV61201 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGCACCGGAAAGCCAGCTCTTGGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGACGATCATCTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACCATGCTGTGGCATTTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisThrArgGly 80
Db 464 CCAGTCTGGGCTGTGCTGTGTCGCTAGGCTCAGCCAGTACCCACTTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTTCATCTGGGCATCTCCTTGGGCATCTCTGTAGACCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGCTGTGTGCCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGTGGCATGCTCATCTGGCGTGGGCTGTGTGACTTCTGTGCCAGGTGCTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCTGCTCTGACCTCTTCCGAGGACCGGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATGCTTATGCTATGATCATGCTTGGGGGCTGTGTGGGCTTACCTCTGCCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCTGCTGGCGCTTACCTGGGCGCACCCAGGAGGTGCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGCTCACCTCATCTTCTCCTACCTGCTAGCAGCACACTGCTGTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCGCGCCACCGAGCGCAGAGAGGCTGTGGCGGCTTGTGTGGCGGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACCTGGGCGGCTGTCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuLeuArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTGCGCATGCCCGCACCTGCGCGGCTTCTGTGGCTGAGTGTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTACCGCTTTCACCGATTTCTGTGGCGGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGCGGTGCCAGAGCTGAGCGGGCACCGAGGCGCGGAGACACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCGTGGGCTGTTCCTGCGAGTGGCGCTCTCTCTCTCTCTCTCTCT 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCAGCGATTTCGGCACTTCGAGCAGTCTATTGTGCCAGGTG 1363

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Oy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCTTTCCCTGTGGTGCCTGCCACATGCTGTGCCACAGTGTGGCGTGACAGCT 1423
Oy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCCTCCCTACACACTGGCC 1483
Oy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCCAGGAGGAGAGCAGTGTTCCTGCCAATACCGAGGGGACACTGGAGT 1543
Oy 421 AlaSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGGAGCAGCCTGATGACCACTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
Oy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACAGTGGGTGCTGGAGGCAAGTGGCTCTCCACCTCCACCCGCGCTC 1663
Oy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGGAGCCACACAGGCC 1723
Oy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCGGGGCGGGCATCTGCTGGACCTCGCCATCTCGATAGTGCCTTCCTG 1783
Oy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTGTCAGCTCAGCCAGTCTGTC 1843
Oy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGCTGTCTGCCAGCCCTGGGCTGGTCTGGTCCCATTTACTTTGCTACACAG 1903
Oy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTGACAGAGGACTTGGCCAAATACTCAGCG 1942
RESULT 5
AAV58586
ID AAV58586 standard; cDNA; 3410 BP.
XX
AC AAV58586;
XX
DT 08-DEC-1998 (first entry)
XX
DE Prostate tumour specific gene clone L1-12.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 284..1945
FT /*tag= a
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03690.
XX
PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-0806596.
PR 01-AUG-1997; 97US-0904809.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
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DR WPI; 1998-480805/41.
DR P-PSDB; AAW69385.
XX
PT Novel human prostate specific tumour protein and fragments - useful
XX for detecting and treating prostate cancers
PS Claim 1; Page 84-85; 141pp; English.
XX
CC This sequence represents a human prostate tumour specific gene, and can
CC be used in the method of the invention. The method is for detecting
CC prostate cancer comprises contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as
CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may
CC also be conjugated to a therapeutic agent for use in therapy of prostate
CC cancers.
XX
SQ Sequence 3410 BP; 657 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-593-793A-113 (1-553) x AAV58586 (1-3410)
Oy 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGTGTAGCGCTGTGTGGCGCACCGAAAGCCAGCTTGTCTG 343
Oy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 403
Oy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTGTGTGTGGAGTGGGGTAGAGGAGAGTTCATGACCATGCTGCTGGGCATCTGCTG 463
Oy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGTGGCTGTGTGTCTCCCGCTCTAGGCTCAGCCAGTGACCACTGGCGTGA 523
Oy 81 ArgTyrGlyArgArgProPheIleThrPalaLeuSerLeuGlyIleLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCTTTCATCTGGGCATCTGCTGGGCATCTGCTGAGCCTC 583
Oy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGGCCGGATCCAGGCCCTTG 643
Oy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGTGTGGACTTCTGTGGCCAGGTGTGCTTC 703
Oy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTCTCTCTGACCTCTCCGGGACCCGACCACTGTGCCAGGCC 763
Oy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGGTACTCTCTGCTGCC 823
Oy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACAGTGCCTTGCCCTTACCTGGGCACTCCAGGAGGAGTGCCTCTTT 883
Oy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 884 GGCTGTCTCACCTCATCTTCTCCTACCTGCGGTAGCAGCACACTGCTGTGTGCTGAGGAG 943
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||
Db 944 GCAGCGCTGGCCGCCACCAGCAGCAGAGGGCTGTGCGCCCTCTCTGTGCGCCAC 1003
|||
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||
Db 1004 TGCTGTCCATGCGGGCGCGCTGGCTTTCCGGAACCTGGGCGCCTGTCTCCCGGGCTG 1063
|||
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||
Db 1064 CACCAGCTGTGTGCGCATGCCCGCACCCCTGCGCGGCTCTCTGTGGCTGAGCTGTGC 1123
|||
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
|||
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGTGGCGAGGGCTG 1183
|||
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
|||
Db 1184 TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCGAGGGCCGGAGACACTATGATGAAGGC 1243
|||
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||
Db 1244 GTTCGGATGGCAGCTGGGGCTGTCTTCAGTGGCGCATCTCCCTGGCTCTCTCTCTG 1303
|||
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||
Db 1304 GTCTGGACCGGCTGGTGCGAGCTCGGCACTCGAGCAGTCTATTGGCCAGTGGCA 1363
|||
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
|||
Db 1364 GCTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCGGTGACAGCT 1423
|||
QY 381 SerAlaAlaLeuThrClyPheThrPheSerAlaLeuGlnIleLeuProTyrThrIleuAla 400
|||
Db 1424 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
|||
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||
Db 1484 TCCTCTACACACCGGAGAGCAGGTGTCTTGCCCAATACCGAGGGGACACTGGAGT 1543
|||
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||
Db 1544 GCTAGCAGTGGAGACAGCTGTATGCCAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
|||
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
|||
Db 1604 TTCCCTAATGGACAGCTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCCCGGCTC 1663
|||
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
|||
Db 1664 TCGGGGCGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGTGAGCCCGAGGCC 1723
|||
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleAspSerAlaPheLeu 500
|||
Db 1724 AGGTGGTGTCCGGGCGGGGCACTGCTGGACCTCGCCATCGCCATCTGGATAGTCCCTC 1783
|||
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||
Db 1784 CTGTCCAGGTGGCCCATTCCTGTATGGGCTCATTTGTCCAGCTCAGCCAGTCTGTC 1843
|||
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||
Db 1844 ACTGCTATATGTTGTCGCCCGAGGCGCTGGGTCTGGTCCCATTTACTTTCTCTACACAG 1903
|||
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||
Db 1904 GTAGATTATTGACAAGCGCACTTGGCCAAATACTCAGCG 1942
|||
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RESULT 6

AAC79473

ID AAC79473 standard; cDNA; 3410 BP.

XX

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AC AAC79473;
XX
DT 07-FEB-2001 (first entry)
XX
DE cDNA sequence of human breast tumour clone P501S.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy;
breast cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200061756-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09688.
XX
PR 09-APR-1999; 99US-0288950.
PR 02-JUL-1999; 99US-0346327.
XX
PA (CORI-) CORIXA CORP.
PI Reed SG, Xu J, Dillon DC;
XX
DR WPI; 2000-638568/61.
DR P-PSDB; AAB28527.
XX
PT A novel isolated polypeptide comprising an immunogenic portion of a
breast cancer protein useful in the detection and treatment of breast
cancer -
XX
PS Claim 26; Page 91-92; 95pp; English.
XX
CC The present sequence was isolated from a breast tumour cDNA library. It
is provided in a specification relating to compounds for immunotherapy
and diagnosis of breast cancer. Breast tumour antigens and the
polynucleotides that encode them may be used in the production of a
pharmaceutical composition to be used in the treatment of breast cancer.
Pharmaceutical T cells and incubated antigen presenting cells are also
required. The polypeptides and polynucleotides may also be used to
produce a vaccine.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 1,58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-593-793a-113 (1-553) x AAC79473 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCGCTGTGCGGCACCGGAAAGCCAGCTCTGTCTG 343
|||
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
|||
Db 344 CTCACCTGCTAACCTTTGGCGTGGAGGTGTGTTGGCGCGCAGCATCACCTATGTGCGG 403
|||
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
|||
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGTGGGCATGGT 463
|||
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||
Db 464 CCAGTGTCTGGGCGCTGTGTGTCTCCCGCTCTTGTAGGCTCAGCCAGTGCACCTGGCGTGA 523
|||
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||
Db 524 CGCTATGCGCGCGCGCGCTTCATCTGCGGCACGTGTCTTGGGCATCTCTGTGAGCCTC 583
|||
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XX SQ Sequence 3410 BP; 667 A; 1015 C; 945 G; 782 T; 1 other;

Alignment Scores:

Pred. No.: 1 58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-593-793a-113 (1-553) x AAA06349 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCACAGAGGTGTGGGTGAGCCGCTGCTGCGGCACCGAAAGCCAGCTCTTGTGCT 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
DB 344 GTCACCTGCTAACCTTTGGCCCTGGAGGTGTGTTTGGCCGACGATCACCATTGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CTTCTGCTGCTGAAGTGGGGGTAGAGGAGAGTTTATGACCATGGTGTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGCCCTGCTCTGTCCTCCGCTCCTAGGCTAGCCAGTACCCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCTCTGTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCAGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGCCCTGCTCTCTGACCTTCCCGGGACCCGAGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCCCTCATGATCAGTCTTGGGGGTGCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGTGCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCTCTCTCACCTCATCTCTCTACCTCGTAGCAGCCACACTGTGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCCCTGGGCCCCACCGAGCCAGAGAGGCTGTGGCCCCCTTGTGTGGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTGTCCATGGCGGCCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCACCTGTGTGCGGCGATGCCCGCACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGATTTCTGTGGGCGAGGGGCTG 1183
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QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGCGTGCCTCCAGAGCTGAGCGCGGCACCGAGGCCGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGCAGCCTGGGCTGTTCCTGCACTGGCCATCTCCCTGGTCTTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTATGACCGGCTGTGTGAGCGATTTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGTGCCACATGCTCTCCACAGTGTGGCCGTGGTACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCCCTCACCGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCCTCTACACCGGAGAGCAGGTTCCTGCCCAATACCGAGGGCACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGACAGCCTGATGACCACTTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuLeuProProProAlaLeu 460
DB 1604 TTTCCCTAATGGACACTGGGTGCTGGAGCAGTGGGCTGCTCCCACTCCACCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGGGGCTCTGCCCTGTGATGCTCCGTACGTGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGTTCGCGGCGGGGCATCTGCCTGGACCTGCCATCCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCCTATATGTTGTCTGCCGAGCCCTGGTCTGTGTGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 8
AAS63557
ID AAS63557 standard; cDNA; 3410 BP.
XX
AC AAS63557;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #109.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
XX WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
```


QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGGTTCCGGCGCGGCATCTGCTGGACCTCGCCATCTGGATAGTGCCTTCCTG 1783

QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCAGGTGGCCCAATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843

QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuAlaGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCCATATGGTGTCTGCCGAGCCCTGGTCTGGTGGCCATTACTTCTCTACACAG 1903

QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 9

AAS10108

ID AAS10108 standard; cDNA; 3410 BP.

XX AAS10108;

XX 24-OCT-2001 (first entry)

XX Human prostate tumour cDNA L1-12.

DE Human; prostate tumour protein; prostate cancer; ss.

KW Homo sapiens.

XX US6262245-B1.

PN 17-JUL-2001.

XX 25-FEB-1998; 98US-0030607.

XX 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

PR 09-FEB-1998; 98US-0020956.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC;

DR WPI; 2001-440862/47.

DR P-PSDB; AAU04961.

XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient

XX Claim 3; Column 118-121; 105pp; English.

CC The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.

SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:

Pred. No.:	1.58e-218	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-593-793A-113 (1-553) x AAS10108 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||

Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGGACCGGAAAGCCAGCTCTTGTCTG 343

QY 21 ValAsnLeuLeuThrPheClyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGCTTTTGGCCGAGGATCACCTATGTGCGG 403

QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAGTGGGGTAGAGAGATTATGACCATGCTGTGGCAATGTTGT 463

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
|||||
Db 464 CCAAGTGGGGCTGGTGTGCTCCGCTCTAGGCTCAGCCAGTACACCTGGCGTGA 523

QY 81 ArgTyrGlyArgArgProPheIleTyrPheLeuLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCCGCGCGGCTTCACTGGGCACCTGCTTGGGCATCTGCTGAGCCCTC 583

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCCCAGGCCCTG 643

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 644 GAGCTGGACCTGCTCATCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTCTTC 703

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGGCTGCTCTGACCTCTTCCGGGAGCCCGGACCTGTGCCAGGCG 763

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCTGCC 823

QY 181 IleAspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
|||||
Db 824 ATTGACTGGACACCTGCTGCTGGCCCTACCTGGGACCCAGGAGAGTGCCTCTTT 883

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
|||||
Db 884 GGCCTGCTCACCTCATCTTCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGGCTGGGCCCCACCGAGCCAGAGAGGCTGCGGCCCTCTCTCTGTGCCCCAC 1003

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGCGCGCGCTTGGCTTCCGSAACCTGGGCGCCCTGCTTCCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGCTGCGCATGCCCGCACCCGCGGCTCTTGGTGGCTGAGCTGTGC 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyLeu 300
|||||
Db 1124 AGCTGGATGGCACTCATGACCTTACGCTGTTTACAGGATTTCTGGCGGAGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGCGGTCAGAGCTGAGCGGGACCCGAGGCGGAGACACTATGATGAGGC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGATGGGAGCGCTGGGGCTGTTCTGTCAGTGGGCATCTCCCTGCTCTCTCTG 1303

QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGCTGTCAGCGATTGCGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363

QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCTTTCCTGTGGCTGCCGCTGCCACATGCTTCCACAGTGTGGCGGTGGTACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400


```
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTCTCCATGCGCGCCGCTTGCTTTCGGAACCTGGCGCCCTCTCCCGGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGlnLeuCys 280
DB 1064 CACCAGCTGTGCTGCGCATGCCCGCACCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlnGlyLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGlnProGlyThrGluAlaArgArgHisTyrAspGlnGly 320
DB 1184 TACCAGGGCGTCCCGACAGCTGAGCGCGCACCGAGCGCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGACGCTGGGGCTGTCTCGCAGTCGCGCATCTCCCTGGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGCTGGTCAGCGATTCCGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCTCTGGCTGCCGGTGCCACATGCTGCTCCACAGTGTGGCGTGGTACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCGCTTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCCTCTACCAACCGGAGGAGGAGGTGTCTTGCCCAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGGACAGCTGATGACACAGCTTCTGCGCCAGGCGCTTAAGCCTGGAGTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
DB 1604 TTTCCCTAATGGACAGCTGGGTGCTGGAGGCACTGGCCCTGCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
DB 1664 TCGGGGGCTCTGCTGTGTGTCTCCGTACGTGTGGTGGTGGGACCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGGTTCCGGCGCGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCCAAGTGGCCCACTCCGCTGTTTATGGCTCATTTGTCCAGCTCAGCAGCTGTCTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCTATATGGTGTCTGCGCGAGCGCTGGGTCTGGTGGCCATTTACTTGTGTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 11
AAH84779
ID AAH84779 standard; cDNA; 3410 BP.
XX AC AAH84779;
XX AC AAH84779;
XX DT 25-SEP-2001 (first entry)
```

```
DE Human prostate-specific cDNA sequence LI-12/P501S.
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX Homo sapiens.
OS WO200134802-A2.
PN 17-MAY-2001.
PD
PF 09-NOV-2000; 2000WO-US30904.
XX 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
DR
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX Claim 5; Page 164-165; 325pp; English.
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-593-793a-113 (1-553) x AAH84779 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
DB 284 ATGTGTCAGAGGCTGTGGTGCAGCGCTGCTGGCGCACCGGAAAGCCAGCTCTGTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaIleGlyIleThrTyrValPro 40
DB 344 GTCAACCTGCTAACTTTGGCTGTGGAGGTGTGTTGGCCGCGAGGCATCACCTATGTGCG 403
QY 41 ProLeuLeuGluValGlyValGlyGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CCTCTGCTGGAGTGGGGGTAGAGGAGAGTTTCATGACCATGGTCTGGGCATTTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGCGCTGGTGTGTGTCCTCCGCTCCTAGGCTCAGCAGTGACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgPropheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
```

D	B	524	CGCTATGGCCGCCGCGCCTTTCATCTGGGCACACTGTCTTGCGGCATCTCTGCTGAGCCCTC	583
Q	Y	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
D	B	584	TTTCTCATCCCAAGGCCGCGTGGCTAGCAGGGCTGCTGTGCCGGATCCACAGGCCCTG	643
Q	Y	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
D	B	644	GAGCTGGCACATGCTCATCTCGGGCGTGGGCTGTGGACTTCTGTGGCAGGTGTCTTC	703
Q	Y	141	ThrProLeuGluAlaLeuSerAspLeuPheArqAspProAspHisCysArgGlnAla	160
D	B	704	ACTCCACTGGAGGCCCTGCTCTCTGACCTCTCCGGGACCAGGACACTGTGCCAGGCC	763
Q	Y	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
D	B	764	TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGCTGCCCTGCTGCTGCTGCC	823
Q	Y	181	IleAspTTPAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
D	B	824	ATTGACTGGGACACCAAGTGGCCCTGGCCCCCTACCTTGGGCACCCAGAGGAGTGCCTTT	883
Q	Y	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
D	B	884	GGCTGCTCACCTCATCTTCTCCTACCTGCTGAGCAGCACCACTGCTGGTGGCTGAGGAG	943
Q	Y	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
D	B	944	GCAGGCTGGGCCCCCACCCAGCAGCAGAAAGGCTGTGGCCCCCTCTGTGCGCCCCAC	1003
Q	Y	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
D	B	1004	TGCTGTCCATCCGGCGCCGCTTGCTTTCGGAACCTTGGCGGCCCTGCTTCCCGCGGTG	1063
Q	Y	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
D	B	1064	CACCAGCTGTGCTGCCGATGCCCGCACCTTCCCGCCGCTCTTCTGCTGGCTGAGCTGTGC	1123
Q	Y	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
D	B	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACAGGATTTGCTGGCGAGGGCTG	1183
Q	Y	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
D	B	1184	TACCAGGCGCTGCCAGAGCTGAGCGGGCACCGAGGCCCGAGACACTATGATGAAGGC	1243
Q	Y	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
D	B	1244	GTTCCGATGGCAGCCTGGGGCTGTCTCTGAGTGGCCATCTCCCTGGTCTTCTCTCTG	1303
Q	Y	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
D	B	1304	GTCATGGACCGCTGGTGCAGGATTCGGCACTTCGAGCAGTCTATTTGGCCAGTGTGCA	1363
Q	Y	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380
D	B	1364	GCTTTCCTGCTGGCTGGCGGTGCCAATGCTGCTGCCAATACCCAGGGGACACTGGAGGT	1423
Q	Y	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
D	B	1424	TCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTCGAGATCCCTGCCCTACACATGGCC	1483
Q	Y	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
D	B	1484	TCCCTCTACCAACCGGAGACAGGTGTCTGCTGCCAATAACCCAGGGGACACTGGAGGT	1543
Q	Y	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
D	B	1544	GCTAGCAGTAGGACAGCCTGATCACCAGCTTCTCTGCCAGGCCCTTAAGCCCTGGAGCTCCC	1603
Q	Y	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuLeuProProProAlaLeu	460
D	B	1604	TTCCCTTAATGGACAGTGGGTGCTGGAGGCAAGTGGCTTCCCACTCCACCCGCGCTC	1663

Pred. No.:	1.58e-218	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0
US-09-593-793a-113 (1-553) x AAH02530 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
Db	284	ATGGTCCAGAGCGTGTGGGTGAGCCGCTGCTGCCGACCGGAAAGCCAGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCACCTCTCAACCTTTGGCCCTGAGGAGTGCTTTGGCCGACAGGATCACCTATGTGCG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATTGGTGTGGGCATTGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTCTGGGCTGCTGTGTCGCCGCTCCTAGGCTCAGCCAGTAGCACCTGGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCCTGCTGAGCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCACAGGCCCTG	643
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTATCTGGCGGTGGGGCTGCTGGAGCTTCTGGCCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGAGGCGCTGCTCTGACCTCTCCGGGACCGGACCACTGTGCCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGTATGCTTTCATGATCATGCTCTTGGGGCTGCTGGGTACCTCTGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTGCTGCCCCCTACCTGGGCACCGAGGAGTGCCCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GCCCTGCTCACCCCTCATCTTCCTCACCCTGCGTAGCAGCCACACTGCTGGTGGCTGAGG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTGCGGCCCTCTCTTGTGCGCCCC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TCCTGTCCATGCGGGCGCGCTTGGCTTTCGGGAACCTTGGGGCGCCCTGCTTCCCCCGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGTCGCGCATGCCCGCACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACAGGATTTCTGTGGCGGAGGGGTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGGCGTCCCCAGAGCTAGCGCGGCCACCGAGGCCCGGAGACACTATGATGAAGC	1243

Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGGACCGGCTGGTCAGCGATTGGCACTCGGACAGTCTATTGGCCAGTGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCTTTCCCTGTGGCTGCCGTCACATGCCGTGCCAGTGTGCCGTGGTGACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGGCCCTCACCGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCAACCGGAGAGGAGGTTCCTGCCCAATACCGAGGGACACTGGAGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTACAGTAGGACAGCGCTGATGACAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACGTGGTCTGGAGGACGTGGCTGCCACCTCCACCCCGGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCTCTGCTGCTGTGATGCTCCGTAAGTGTGGTGGTGAGCCACCCAGGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTTGGTTCCGGCGCGGGCATCTGCCGTGACCTGCCATCCTGGATAGTCCCTTCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCCAAGTGGCCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCTATATGTTGCTGCCGAGCGCTGGTCTGGTGGCATTTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTGTGACAGAGGACTTGGCCAAAFACCTCAGCG	1942
RESULT 13			
ABL94929			
ID	ABL94929	standard; cDNA; 3410 BP.	
XX	ABL94929;		
AC	ABL94929;		
DT	19-JUL-2002	(first entry)	
XX	Human L1-12	cDNA sequence SEQ ID NO 110.	
DE	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;		
KW	gene therapy; gene; ss.		
XX	Homo sapiens.		
OS	US200202248-A1.		
PN	21-FEB-2002.		
PD	12-JAN-2001; 2001US-0759143.		
XX	25-FEB-1997; 97US-0806099.		
PR	01-AUG-1997; 97US-0904804.		
PR	09-FEB-1998; 98US-0020956.		
PR	25-FEB-1998; 98US-0030607.		


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PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
WPI; 2002-255649/30.
DR
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
PS Claim 1; SEQ ID NO 110; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793a-113 (1-553) x ABL94929 (1-3410)
QY 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGGTGAGCCCTGCTGCGGACCCGGAAGCCAGCCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCGG 403
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QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGCATGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGGTCTGTGTCGCCGTCTTAGGCTCAGCCAGTACACACTGGCGTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCGCGGCCCTTCATCTGGGCACATGTCCTTGGGCATCCTGCTGAGCCFC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGTGTGCCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTTTC 703
QY 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTGCTCTGTGACCTCTTCCGGGACCCGACACTGTGCGCCAGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCGCTGGCCCTACCTGGGCAACCAGGAGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGCTCACCTCATCTTCTCCTGCTAGCAGCCACACTGCTGCTGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCCACCAGGCGCAGAGAGGCTGTGCGCCCCCTCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACCTGGGCGCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCCGATGCCCGCACCTGCGCCGCTCTTCTGCTGAGTGTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCAGGCTGTTCACAGATTCGTGGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGCGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCGAGCTGGGGCTGTCTCTGCACTGCGGCTGCTGCTGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGGCAGGATTCGGCACTCGAGGAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGCTGCCACATGCTTCCACAGTGTGCCGCTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCCTGCTGCTTACACACTGGCC 1483
```

QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACGGGAGAGCAGGTGTTCTCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCCTGATGACACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACACTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGGCGGGCCCTCGCTGTGATGCTCCGTACGTGTGGTGGTGGCTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCCGGGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCTTCTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCAATCCCTGTTTATGGGTCCATTTGTCAGCTCAGCCACTGTCTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGTGCTGCGCAGGCTGGGTCTGGTGGCAATTTACTTTGGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 1942
RESULT 14
ABK29017
ID ABK29017 standard; cDNA; 3410 BP.
XX
AC ABK29017;
DT 23-APR-2002 (first entry)
XX
DE Human breast tumour polypeptide full length cDNA clone #3..
XX
KW Human: breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
KW Immunostimulant.
XX
OS Homo sapiens.
XX
PN WO200198339-A2.
XX
PD 27-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-US19032.
XX
PR 22-JUN-2000; 2000US-0602877.
PR 12-OCT-2000; 2000US-0687507.
PR 06-FEB-2001; 2001US-0778381.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX
DR WPI; 2002-147792/19.
XX
PT Polynucleotides encoding breast tumour polypeptides, useful for treating
PT breast cancer or stimulating an immune response -
XX
PS Claim 1; Page 143-144; 150pp; English.
XX
CC The invention relates to polynucleotides encoding breast tumour
CC polypeptides. The sequences are useful for treating cancer, preferably
CC breast cancer, in a patient or for stimulating an immune response. The
CC polynucleotides and polypeptides are also useful in the diagnosis and
CC monitoring of breast cancer. A method for detecting the presence of a

CC cancer in a patient, comprises obtaining a biological sample from the
CC patient, contacting the biological sample with a binding agent that binds
CC to a breast tumour polypeptide, detecting in the sample an amount of
CC polypeptide that binds to the binding agent, and comparing the amount of
CC polypeptide to a predetermined cut-off value, therefore determining the
CC presence of a cancer in the patient. Sequences ABK28920-ABK29025
CC represent cDNA clones encoding human breast tumour polypeptides of the
CC invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-593-793A-113 (1-553) x ABK29017 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGGGTGAGCCGCCCTGCTGCGGACCCGGAAAGCCAGCTCTTGGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGGCATCACCATTGTCGCG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGAGAGTTCATGACCATGCTGTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTCTGGGCTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGCTCTTGGGCATCTGCTGAGSCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTTCTCATCCCAAGCGCGGCTGGCTAGCAGGGGCTGCTGTGCCCGGATCCAGGCCCTCG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGCGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTTCTCCGGGACCCGCGACCATGTCGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCATGCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 824 ATTGACTGGGACACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCCTCATCTCTCCTACCTGCTAGCAGCCACACTGCTGCTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGGCCCCACCGAGCCAGCAGAGGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTTCATGCTGGGCGCGCTTGGCTTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCCGATGCGCCACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrLeuPheValGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCGTGGCGAGGGGTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGCGCCAGGAGCCGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGCGAGCTGGGGCTGTCTCTGAGTGCAGTCATCCTGCTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTCGCGATTCGCGACTCGAGCAGTCTATTGGCCAGTGTGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTGTGGCTGCGGGTCCACATGCTCCAGAGTGTGGCGTGGTGACACT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGTTCACTTCTCAGCCCTGCAGATCTCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGGAAGCAGGTGTCTGTCCTGTCCTGTCCTGTCCTGTCCTG 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCACTGAGGACGCTGATGCCAGCTTCTGTCAGGCGCTTACGCTGAGACTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACAGCTGGGTGCTGGAGGACGTGGCTTCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCTCTGCTGTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1723
QY 481 ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCGCGCGCGGGGATCTGCTGACCTTCGCTGCTGCTGCTGCTGCTGCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCGCCATCCTGTTTATGGCTCCATTGCTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTGCGCGAGGCTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGCACTTGGCCAAATACTCAGCG 1942
RESULT 15
AAS64040
ID AAS64040 standard; cDNA; 4034 BP.
XX AC AAS64040;
XX AC AAS64040;
XX AC AAS64040;
DT 29-JAN-2002 (first entry)
DE Human prostate cDNA P553s splice variant #3.
XX Human; prostate cancer; ss: cytostatic; immunostimulant; tumour.
XX Homo sapiens.

XX WO200173032-A2.
PN XX
PD 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US099919.
PF XX
XX 27-MAR-2001; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
PT Claim 1; Page 483-484; 579pp; English.
PS The invention relates to isolated prostate-specific
XX polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes,
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
Alignment Scores:
Pred. No.: 6,72e-207 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservat: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 22 Gaps: 1
US-09-593-793A-113 (1-553) x AAS64040 (1-4034)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGTCCAGAGGCTGTGGGTGAGCGGCTGCTGCGGACCGGAAAGCCAGCTCTTGTCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGGCTGGAGGTGTGTTGGCCGAGCATCACCTATGTGCGC 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGTGAAGTGGGGGTAGAGGAGAAAGTTCATGACCATGCTGGCATTTGGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCACTGTGTGGGCTGGTGTGTGTCTCCGCTCTAGGCTCAGCCAGTGCACCTGGCGTGA 520

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuSerLeu 100
Db 521 CGTATGGCGCGCGCGCTTCATCTGGGACATCTCTGGGCATCTCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGAGGCTGCTGTGCCGATCCAGGCGCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGCGCTGCTCTGTACCTCTTCGSGGACCCGACACCTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 761 TACTCTGTCTATGCCCTTCATGATCATGTGGGGCTGGCTGGGCTACCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCACTGCTGCGCCCTACCTGGGACCCAGGAGAGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCCCTGCTCACCTCATCTCTCACCTGCTAGCAGCCACACTGCTGTGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCGCCACCAGGACGACAGAGGGCTGTGCGCGCCCTCTCTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATGCGCGCGCTGTGGCTTCGGAACCTGGGCGCCCTGCTCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTCGCGCATGCCCGCACCTCGCGCGGCTCTCTGTGGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCAGCTGTGTTTACACGGATTTCTGTGGCGAGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGlu--- 319
Db 1181 TACCAGGGGCTGCCAGAGCTGAGCGGGCACCGAGGCGCGAGACACTATGATGAAGT 1240
QY 319 ----- 319
Db 1241 AAGGCGCTTGGCAGCCAGCAGAGGCTGGTGTGGAGCGCGCCACCAGACGACACTCGGG 1300
QY 319 ----- 319
Db 1301 GCTGTGCTGGGCTGTGGCTCTCCATCCTGCGCCCGACTTCTCTGTCCAGAAAGTGGGG 1360
QY 319 ----- 319
Db 1361 ATGGAGCCCATCTGCATACAGGCTTCTCATGGGTGTGGAACATCTCTGCTTGGGTTTC 1420
QY 319 ----- 319
Db 1421 AGGAAGGCTCTGGTGTCTTAGGAGTCTGATCAGAGTGTGTTGCCCCAGTTTGTACAGAAG 1480
QY 319 ----- 319
Db 1481 GAAAGCGGAGCTTATTCAAAGCTTAGAGGGAGTGGAGGTTAAGGCTGGATTTCAGAT 1540
QY 319 ----- 319
Db 1541 CTGGCTGGTTCCAGCGCAGTGTGCCCTGTCTCCCCACGACCTTCCAAATAATCTCA 1600
QY 319 ----- 319

Db 1601 CCAGCGCTTCCAGCTCAGGCGTCTTAGAAGGCTCTTGAAGCCTATGGCCAGCTGTCTTT 1660
QY 319 ----- 319
Db 1661 GTGTTCCTCTCACC CGCTGTCTCAGAGCTGCCAGGAAACCTTCAGACTACC 1720
QY 319 ----- 319
Db 1721 TTCCTCTGCCCTTCAGCAAGGGGCTTGCCACATTTCTTGAGGCTCAGTGGAGAACCTA 1780
QY 319 ----- 319
Db 1781 GACTCCCATTTGCTAGAGGTAGAAAGGAGGTGTGGGAGCAGGCGTGTCCACAGC 1840
QY 319 ----- 319
Db 1841 AGGTCTGTCGTCAGCAGGTACCTGTGGTTCGCGCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
QY 320 ----- GlyValArgMetGlySe 325
Db 1901 CCTTCCCTCCAGGCTCTGTCTGTATGGGCCCTCTCCCTCTGCAGGCGTTCGGATGGCAG 1960
QY 325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
Db 1961 CCTGGGGCTGTTCCTGCAGTGGCGCATCTCCCTGTCTCTCTGTCTGTCTGTCTGTCTGT 2020
QY 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaLeuSerValAlaAlaPheProValAl 365
Db 2021 GGTGAGCGATTCGGGACTTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGGC 2080
QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385
Db 2081 TGCCGCTGCCACATGCTGTCCACAGTGTGCGCTGGTGACAGCTTCAGCCGCCCTCAC 2140
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Db 2141 CGGGTTACCTTCTCAGCGCTGCAGATCTGCCCTACACACTGGGCTCCCTCTACACCG 2200
QY 405 gGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAGCAGGTTCTCTGCCCAATACCGAGGGGACACTGGAGGTGCTTAGCAGTGAGGA 2260
QY 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCACTTCTCTCCAGGCGCTAAGCCTGAGCTCCCTTCCCTTAATGGACA 2320
QY 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGCTGGAGCAGTGGGCTGCTCCCACTCCAGCGCGCTCTGCGGGCGCTCTGC 2380
QY 465 aCysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCAGCCAGGCGAGGTTGGTCCCGG 2440
QY 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CGGGGCACTGCTGCGGACCTGCGCATCTGGATAGTGCCTTCTCTGCTCCAGGTGGC 2500
QY 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGT 2560
QY 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCTCCCGCAGGCGCTGGGTGCTGGTCGCATTTACTTTGCTACACAGGTAGTATTTGACAA 2620
QY 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACTTGGCCAATACTACGCG 2645
RESULT 16
AAH93868

QY 319 ----- 319
Db 1541 CTGCTGTTCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTCCAAAATAATCTCA 1600
QY 319 ----- 319
Db 1601 CCAGCGCTTCCAGCTCAGCGCTCCTAGAGCGTCTTGAAGCCTATGGCCAGCTGCTCTTT 1660
QY 319 ----- 319
Db 1661 GTGTTCCCTCTCACCGCCTGTCTCACAGCTGAGACTCCCCAGGAAACCTTCAGACTACC 1720
QY 319 ----- 319
Db 1721 TTCTCTTGCTTTCAGCAAGGGCGTGTGCCACATTTCTCTGAGGTCAGTGGGAAGAACCTA 1780
QY 319 ----- 319
Db 1781 GACTCCCATTTAGAGGTAGAAAGGGAGAGGGTGTGGGGAGCAGGGCTGTCTCCACAGC 1840
QY 319 ----- 319
Db 1841 AGGTCTCGTGACAGGTACCTGTGGTTCGGCCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
QY 320 -----GlyValArgMetGlyse 325
Db 1901 CCTTCCCTCCAGGCTCTGTCTGATGGCCCTCTCCCTCTGCAGGCGTTGGGATGGCAG 1960
QY 325 rleuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
Db 1961 CTTGGGGCTGTTCCTGTCAGTGGCGCATCTCCCTGTCTCTCTCTGTCATGTGACCGCT 2020
QY 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaPheProValAla 365
Db 2021 GTGTGAGCATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTCCCTGTGGC 2080
QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaLeuTh 385
Db 2081 TGCCGGTGCACATGCTGTCCACAGTGTGGCCGTGTGGCAGCTTCAGCGCGCTCAC 2140
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Db 2141 CGGGTTCACCTTCTCAGCCCTGCATGCTGCCCAATACCGAGGGACACTGGAGTGTAGCAGTGA 2200
QY 405 gGlyLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAGCAGGTGTTCTTCCGCCCAATACCGAGGGACACTGGAGTGTAGCAGTGA 2260
QY 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCACTTCTCCAGGCCCTAAGCCTGGAGTGTCCCTTCCCTAATGGACA 2320
QY 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGTGTGGAGCAGTGGCTCTCCCACTCCACCGCGCTCTCGGGGCTCTGC 2380
QY 465 aCysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGTCTCCGTACGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 2440
QY 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CCGGGGCATCTGCCCTGGACCTCGCCATCTGGATAGTGCCTTCTCTGTCTCCAGGTGGC 2500
QY 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCCATCCCTGTTATGGGCTCATGTCTCCAGCTTCAGCAGTGTGTCTGCTATATGGT 2560
QY 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCCTCCGCGAGGCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 2620
QY 545 sSerAspLeuAlaLysTyrSerAla 553

Db 2621 GAGCGACTTGGCCAAATACTCAGCG 2645
RESULT 17
ABL95411
ID ABL95411 standard; cDNA; 4034 BP.
AC ABL95411;
XX
XX 19-JUL-2002 (first entry)
XX Human P553S splice variant SEQ ID NO 704.
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
XX
PN US2002022248-A1.
XX
XX 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-01159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler,WT, Henderson RA;
XX
XX WPI; 2002-2556649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the

PT progression of cancer -
 PS Claim 1; SEQ ID NO 704; 87pp; English.
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 XX
 SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
 Alignment Scores:
 Pred. No.: 6.72e-207 Length: 4034
 Score: 2716.50 Matches: 553
 Percent Similarity: 70.09% Conservative: 0
 Best Local Similarity: 70.09% Mismatches: 0
 Query Match: 94.95% Indels: 236
 Dbs: 24 Gaps: 1
 US-09-593-793A-113 (1-553) x ABL95411 (1-4034)
 Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
 Db 281 ATGGTCCAGAGGCTGGGGTGGCGCTGCTGGGGCACCAGAAAGCCAGCTCTTGCTG 340
 Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
 Db 341 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCGCGAGCATCACCTATGTGCGG 400
 Qy 41 ProLeuLeuLeuGluValGlyValGluGlyPheMetThrMetValLeuGlyIleGly 60
 Db 401 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACATGCTGGTGGCATTTGGT 460
 Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
 Db 461 CCAGTGTGGGCGCTGGTCTGCTCCCGCTCTAGGCTCAGGCAGTGACCACTGGCGTGA 520
 Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
 Db 521 CGCTATGGCCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCTCTGCTGAGCCTC 580
 Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
 Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTCGGGATCCAGGCGCCCTG 640
 Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
 Db 641 GAGCTGGCACATGCTATGCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 700
 Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
 Db 701 ACTCCACTGGAGGCCCTGCTCTGACCTCTCCGGGACCCGGACCACTGTGCCAGGCC 760
 Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
 Db 761 TACTCTGTATGCTTTCATGATCAGTCTGGGGGCTGCCCTGGGCTACCTCTGCTGCC 820
 Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
 Db 821 ATTGACTGGGACACAGTGGCCCTGGCCCCCTTACCTGGGACCCAGGAGAGTGGCTCTTT 880
 Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
 Db 881 GGCCTGCTCACCTTCATCTTCCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
 Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
 Db 941 GCAGCGTGGGCCCCACCGAGCCAGCAGAGGGTGTGGGCCCTCTCTGCTGCCGCCAC 1000
 Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
 Db 1001 TGCTGTCCATCCGGGCGCGCTTGGCTTTCGGAAACCTGGGCGGCTGCTTCCCGCGGCTG 1060

Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
 Db 1061 CACCAGCTGTGCTGCCGATGCCCGCACCTGCCGCGCTCTTCGTGGCTGAGCTGTC 1120
 Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
 Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTCGTGGCGAGGGCTG 1180
 Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu--- 319
 Db 1181 TACCAGGGCGTGGCCAGAGCTGAGCCGGGCACCGAGGCCCCGAGACACATATGATGAAGT 1240
 Qy 319 ----- 319
 Db 1241 AAGGCTTGGCAGCCAGCAGAGGCTGGTGGAGCGCCCCACCAGACGACACCTCGGG 1300
 Qy 319 ----- 319
 Db 1301 GCTGTGCTGGGCTGGTGCCTCTCCATCTGCCCGCACTTCTCTGTCAAGAAAGTGGG 1360
 Qy 319 ----- 319
 Db 1361 ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCTTGGGTTTC 1420
 Qy 319 ----- 319
 Db 1421 AGGAAGGCTCTGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAG 1480
 Qy 319 ----- 319
 Db 1481 GAAAGCGGAGCTTATTCAAAGTCTAGAGGAGTGGAGAGTTAAGGCTGGATTTCAGAT 1540
 Qy 319 ----- 319
 Db 1541 CTGCTGGTTCCAGCGCAGTGTGCCCTCTCTCCCCAACGACTTCCAAATATATCTCA 1600
 Qy 319 ----- 319
 Db 1601 CCAGCGCTCCAGCTCAGGCGTCTTAGAAGCGTCTTGAAGCCTATGSCCAGCTGCTTT 1660
 Qy 319 ----- 319
 Db 1661 GTGTTCCCTCTACCCCGCTGTCTCACAGCTGAGACTCCAGGAAACCTTCAGACTACC 1720
 Qy 319 ----- 319
 Db 1721 TTCCTGCTTACAGAGGGGCGTTGCCACATCTCTGAGGGTCACTGGAAGAACCTA 1780
 Qy 319 ----- 319
 Db 1781 GACTCCCATTCGTAGAGTAGAAGGGAAGGGTCTGGGAGCAGGCGTGGTCCACAGC 1840
 Qy 319 ----- 319
 Db 1841 AGGTCTCGTGCAGCAGTACCTGTGTTCCGCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
 Qy 320 -----GlyValArgMetGlySe 325
 Db 1901 CCTTCCCTCCAGGCTCTGCTGTGATGGCCCTCTCCCTCTCGAGCGGTTCCGATGGGCGAG 1960
 Qy 325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
 Db 1961 CCTGGGCTGTTCCTGCAGTGCAGTCCCACTCTCCCTGCTCTCTCTGTTGTCATGGACCGGCT 2020
 Qy 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 365
 Db 2021 GGTGCAGCATTCGCATCTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGGC 2080
 Qy 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385
 Db 2081 TGCCGGTGGCCACATGCTCTCCACAGTGTGGCGCTGTCAGAGCTTCAGCGCCCTCAC 2140
 Qy 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405

Db 2141 CCGGTTACCTTCTCAGCCCTCAGATCCTGCCCTATACACTGGGCTCCCTTACACCG 2200
Qy 405 gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAGACAGGTGTTCTGCCCAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGA 2260
Qy 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCACTTCTCTCCAGGCCCTAAGCCTGGAGCTCCTTCCCTAATGGACA 2320
Qy 445 sValGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGCGTGTGAGGACAGTGGCTGCTCCACCTCCACCGCGCTCTCGGGGCTCTGC 2380
Qy 465 acYasPValSerValArgValValValGlyCluProThrGluAlaArgValValProGl 485
Db 2381 CNGTGATGTCCTCCGACGTGCTGGTGGTGGAGGCCACCGAGGCGAGGTGGTTCGGG 2440
Qy 485 yArgGlyIleCysLeuAsPLeuAlaIleLeuAsPLeuSerAlaPheLeuLeuSerGlnVal 505
Db 2441 CCGGGGCATCTGCCTGGACCTCGCCATCTCGATAGTGCCTTCTGCTGCCAGGTGGC 2500
Qy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGTCACTGCCCTATATGT 2560
Qy 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCGCCGACGCGCTGGGTGCTGGTCCCATTTACTTTGCTACACAGGTAGTATTTGACA 2620
Qy 545 sSerAsPLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACITGGCCAAATACTCAGCG 2645
RESULT 18
ABA91283
ID ABA91283 standard; DNA; 2133 BP.
XX ABA91283;
XX
XX
DT 08-APR-2002 (first entry)
XX
DE ThioRedoxin-ubiquitin-P501S(aa55-553)His triple gene fusion.
KW ThioRedoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
KW cancer; vaccine; therapy; human; gene; ds.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Escherichia coli.
PN WO200200892-A1.
XX
PD 03-JAN-2002.
XX
PF 19-JUN-2001; 2001WO-EP06952.
XX
PR 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva TEV, Delisse AEF;
XX
DR WPI; 2002-147888/19.
DR P-PSDB; AAM50661.
XX
PT Novel DNA sequence encoding triple fusion protein comprising ubiquitin
PT fused between thioRedoxin and polypeptide of interest, useful for
PT producing recombinant polypeptide of interest suitable for medicinal
PT use -
XX
PS Example 5; Fig 9a; 87pp; English.

XX The present sequence is that of a triple gene fusion comprising,
CC from the 5' end, the trxA thioRedoxin gene from Escherichia coli,
CC the human ubiquitin coding sequence, the prostate antigen P501S
CC (amino acids 55-553) coding sequence, and DNA encoding a histidine
CC tail. The triple fusion was constructed in plasmid pRIT15063,
CC which included the Saccharomyces cerevisiae CUP1 promoter and
CC yeast alpha prepo signal sequence. The triple fusion protein
CC (see AAM50661) was produced in E. coli G1724 transformants. This
CC is an example of the production of triple fusion proteins of the
CC invention comprising ubiquitin fused between thioRedoxin and a
CC protein of interest, in this case P501S(aa55-553). A claimed method
CC of producing a recombinant protein of interest involves: culturing
CC a host cell (preferably E. coli) under conditions which allow
CC for co-expression of the triple fusion and a ubiquitin-specific
CC endoprotease (especially UBPl from Saccharomyces cerevisiae);
CC and recovering the recombinant protein directly from the bacterial
CC cells after it has been subjected to the action of the
CC ubiquitin-specific endoprotease in vivo. In the present case,
CC a p501-like protein of 509 amino acids is generated. The
CC recombinant protein can used as a vaccine for cancer therapy.
XX
SQ Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;

.. Alignment Scores:
Pred. No.: 4.89e-198 Length: 2133
Score: 2601.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.91% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553); x ABA91283 (1-2133)
Qy 53 MetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGly 72
Db 604 ATGACCATGGTGTGGGCAATTGGTCCAGTGTGGGCGCTGGTGTGCCGCTCCTAGGC 663
Qy 73 SerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeu 92
Db 664 TCAGCCAGTGACCACTGGCGTGGAGGCTATGGCCGCCCGCGGCCCTTCTATCTGGGCACTG 723
Qy 93 SerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeu 112
Db 724 TCCTTGGGCATCCTGCTGAGCCTCTTCTCATCCCAAGGCGGCGGTGGCTAGCAGGCTG 783
Qy 113 LeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeu 132
Db 784 CTGTGCCCGGATCCACGAGGCGGCTGGAGCTGGCAGCTGCATCTCTGGGCGTGGGCTGCTG 843
Qy 133 AspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArg 152
Db 844 GACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCGCTGCTCTCTGACCTCTCTCGG 903
Qy 153 AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGly 172
Db 904 GACCGGACCACTGTGCCAGGCGCTACTCTGTCTATGCTTTCATGATCAGTCTTGGGCGC 963
Qy 173 CysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeu 192
Db 964 TGCCCTGGGCTACCTCTGCTGCCATTGACGGGACACAGTGGCGCTGGCGGCTTACCTG 1023
Qy 193 GlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAla 212
Db 1024 GGCACCCAGGAGGAGTGCCTCTTTGGCCCTGGCTCACCTCATCTTCTCACCTGCCTAGCA 1083
Qy 213 AlaThrLeuLeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeu 232
Db 1084 GCCACACTGCTGCTGAGGAGGAGCGCTGGGCGGCCACCGAGCCAGCAGAGGCGCTG 1143
Qy 233 SerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsn 252
Db 1144 TCGGCGGCGGCTCTCTTGTGCGCCACAGTGTCCATCGCGGCGGCGGCTTGGCTTTCGGAAC 1203

QY 253 LeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArg 272
|||||
Db 1204 CTGGGGCCCTGCTCCCGGGTGCACACAGTGTGCTGCCGATGCCCGACCTGGCC 1263

QY 273 ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyr 292
|||||
Db 1264 CGGCTCTTCGTGGCTGAGCTGTGACGTGGATGGCAGCTCATGACCTTCACGCTGTTTAC 1323

QY 293 ThrAspPheValGlyGluLeuTyrGlnGlyValProArgAlaGluProGlyThrGlu 312
|||||
Db 1324 ACGGATTCGTGGCGAGGGGTGTACACAGGGCGTGCACAGAGCTGAGCGGGCACCGAG 1383

QY 313 AlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCys 332
|||||
Db 1384 GCCCGGAGACACTATGATGAGCGCTGCGATGGCGACCTGGTCTTCAGTGC 1443

QY 333 AlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArg 352
|||||
Db 1444 GCATCTCCCTGGTCTTCTCTGTGTCATGGACCGGCTGGTGCAGGATTCGGCAGCTGA 1503

QY 353 AlaValTyrLeuAlaSerValAlaPheProValAlaAlaGlyAlaThrCysLeuSer 372
|||||
Db 1504 GCAGTCTATTTGGCCAGTGTGCAGCTTTCCTGTGGCTGGCGGTGCCACATGCCGTGCC 1563

QY 373 HisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeu 392
|||||
Db 1564 CACAGTGTGGCGTGTGCAGCTTCAGCGGCCCTCACCGGGTTCACCTTCACGCCCTG 1623

QY 393 GlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuPro 412
|||||
Db 1624 CAGATCCTGCCCTACACACTGGCCCTCCCTCTACCACCGGAGACAGGTGTTCCTGCC 1683

QY 413 LysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeu 432
|||||
Db 1684 AAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATCACCAGCTTCCTG 1743

QY 433 ProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGly 452
|||||
Db 1744 CCAGGCCCTAAGCTGGAGTCCCTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGC 1803

QY 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472
|||||
Db 1804 CTGCTCCACCTCCACCCCGGCTGTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTG 1863

QY 473 ValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeu 492
|||||
Db 1864 GTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCGGGGCCGGGGCATCTGCTGGACCTC 1923

QY 493 AlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySer 512
|||||
Db 1924 GCCATCCTGGATAGTCCCTTCTGCTGTCCAGGTGGCCCATCCCTCTTTATGGGCTCC 1983

QY 513 IleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeu 532
|||||
Db 1984 ATTGTCCAGCTCAGCCAGTGTGTACTGCTATATGTGTGTCTGCCGAGGCCGTGGGTCTG 2043

QY 533 ValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSer 552
|||||
Db 2044 GTCCGCAATTTACTTTGCTACACAGGTAGTATTTGACAGAGCGAGCTTGGCCAAATACTCA 2103

QY 553 Ala 553
|||
Db 2104 GCG 2106

RESULT 19
AAS64038
ID AAS64038 standard; cDNA; 4894 BP.
XX
AC AAS64038;
XX
DT 29-JAN-2002 (first entry)
XX

DE Human prosate cDNA p53s splice variant #1.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US099919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
XU Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR N-PSDB; AAU69874, AAU69875.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 480-482; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
polynucleotides, polypeptides, fusion proteins of the polypeptides,
antibodies raised against the polypeptides (or antigenic epitopes
derived from them) and antigen-presenting cells expressing the
polypeptides. The antibodies are useful for detecting the presence of
cancer, especially prostate cancer. The polypeptides, polynucleotides and
the antigen-presenting cells are useful for stimulating and/or expanding
T cells specific for a tumour protein, and for inhibiting the development
of cancer especially prostate cancer. Compositions comprising the
polynucleotide and/or polypeptide are useful for stimulating an immune
response, and for treating cancer. The oligonucleotide is useful for
detecting cancer. The present sequence is a prostate specific
polynucleotide of the invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;

Alignment Scores:
Pred. No.: 1.39e-192 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 22 Gaps: 2

US-09-593-793A-113 (1-553) x AAS64038 (1-4894)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||
Db 274 ATGGTCCAGAGGCTGTGGGTGAGCGCCTGCTGCGGACACGGAAGCCAGCTCTTGGCTG 333

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 334 GTCAACCTGCTAACTTTGGCTTGGAGGTGTGTTGGCCGAGGATCATCATGTGCGC 393

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
|||||

Db 394 CCTCTGCTCTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGGTGCT-GGGTGAGTTC 452
QY 57 ----- 57
Db 453 ACTACATCCTCCTTCTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
QY 57 ----- 57
Db 513 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 572
QY 57 ----- 57
Db 573 GGAGGGTGACCTGGGCTGAGGGGGCACCAAGAGAAAGAAATACCAAGGACATA 632
QY 57 ----- 57
Db 633 CCCAGTCACCTCTGGATCCCTGGTCCCTCCACAGAGCCTGGCTCATAGGAGACATGGAG 692
QY 57 ----- 57
Db 693 AAATGCTCTAACTTTGGCTAGCCCTTTTATAAATTTATAGCGATTATCTCATTTAATGC 752
QY 57 ----- 57
Db 753 TTACAAACCACCATTTGAGGTGATCCATTTACAGAGAAAGAGCAGAGCGCTTTTAAGAGG 812
QY 57 ----- 57
Db 813 TTAGGTAAGTCYTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCA 872
QY 57 ----- 57
Db 873 GGTCTCCAGCGGAGCTTGTCTCTACCCCTAGACAAAGGGTGGACTCCTGACTGCA 932
QY 57 ----- 57
Db 933 GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACAAACCCTCACC 992
QY 57 ----- 57
Db 993 CCCAGGAAGGGGCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTGTAAC 1052
QY 57 ----- 57
Db 1053 GCTGCTCTTTACCCCTCCTAGGTCTCGCCTTTTGAATAAGTATCACCTTCTTAGTGTCTCC 1112
QY 57 ----- 57
Db 1113 ATGCTCAGTTTGTCCATCTGAAATGGGGGCATCTGTAATGCCTGTGTATGAGGAGTA 1172
QY 57 ----- 57
Db 1173 AATTACAGATCCCTGTGAAGACGTAGCACAGTCGAGTAGCGAATGTTATTTCATCC 1232
QY 57 ----- 57
Db 1233 TTCTCAGGAGCTTGGTTCCTCCCTTGGCCCTTTACTTGTCCAGCATTGACTCAT 1292
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1293 ACTACTTCCCTTTTGCAGGCATTGGTCCAGTCTGGGCGCTGGTGTGTCCTCCCTCTTA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrglyArgArgProPheIleTrpAla 91
Db 1353 GCCTCAGCAGTGACCACTGGGCTGGAGCCTATGCCCGCCGCGCCCTTCATCTGGGCA 1412
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTGGGCATCTGCTGAGCCTCTTCTCATCCCAAGGCGCGCTGCTAGCAGG 1472
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGCTGTGCCCCGGATCCCAAGGCCCTTGGAGCTGGCAGCTGCTCATCTGGGCGTGGGGCTG 1532

QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCCAGGTGGCTTCACTCCACTGGAGGCCCTGCTCTCTACCTCTTC 1592
QY 152 ArgAspProAspHisCysArgGlnAlaTyrsValTyrsAlaPheMetIleSerLeuGly 171
Db 1593 CGGGACCCGGACCACTGTGCCAGGCCCTACTGCTGTATGCTTCATGATCAGTCTTGGG 1652
QY 172 GlyCysLeuGlyTyrsLeuLeuProAlaIleAspTTPAspThrSerAlaLeuAlaProTyrs 191
Db 1653 GGCTCCCTGGGCTACTCTGCTGCCATTGACTGGGACACAGTGGCTGGCCCCCTTAC 1712
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1713 CTGGGACCCAGGAGGTGGCTCTTGGCCTGCTCACCTCATCTCTCCTACCTCGCTA 1772
QY 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGCCACACTGCTGGTGGCTGAGGAGGCGGCTGGGCCCCACGAGCGACGAGAAGG 1832
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTCGGGCCCTCTCTGTGCCCCCACTGCTGCTCATGCCGGGCCGCTTGGCTTTCCGG 1892
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGGCCCTGCTTCCCGGCTGCACCAAGCTGTGCTGCCATGCCCGCACCTG 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CGCCGGCTCTTCTGGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTTCACGCTGTT 2012
QY 292 TyrsThrAspPheValGlyGluGlyLeuTyrsGlnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACACGGATTCTGCTGGCGAGGGGCTGTACAGGGCGTGCACAGAGCTGAGCGGGGCACC 2072
QY 312 GluAlaArgArgHisTyrsAspGlu----- 319
Db 2073 GAGGCCCGAGACACTATGATGAAGCTTAAGGCTTGGCAGCCAGCAGAGCTGGTGTGGG 2132
QY 319 ----- 319
Db 2133 AGCCGCCCCACAGACAGACACACTCGGGCTGTGTCTGGGCTGGTGCTCTCCATCCTGGC 2192
QY 319 ----- 319
Db 2193 CCCGACTTCTCTGTTCAGGAAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
QY 319 ----- 319
Db 2253 GTGTGGAACATCTCTGCTTGGGTTTTCAGGAAGGCCCTCTGGCTGCTTAGGAGTCTGATC 2312
QY 319 ----- 319
Db 2313 AGAGTCGTTGCCCCAGTTTTCAGAGAAGAAAGGCGGAGCTTATTCAAAAGTCTAGAGGGAG 2372
QY 319 ----- 319
Db 2373 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCGAGTGTGCCCTCTGCT 2432
QY 319 ----- 319
Db 2433 CCCCCAACGACTTTCCAAATATCTCACAGCGCCTTCCAGCTCAGCGCTCCTAGAAAGG 2492
QY 319 ----- 319
Db 2493 TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCTCTCACCCGCTGTCTCTCACAGCTG 2552
QY 319 ----- 319
Db 2553 AGACTCCAGGAAACCTTCAGACTACCTTCTCTGCTTCCAGCAAGGGCGGTGGCCACA 2612

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QY 319 ----- 319
Db 2613 TTCTCTGAGGTCAGTGAAGAACCAGACTCCCATTCCTAGAGGTAGAGGGAAGGG 2672
QY 319 ----- 319
Db 2673 TGCTGGGAGCAGGCTGGTCCACAGCAGGTCCTGTCAGCAGGTACCTGTGTTCGCC 2732
QY 319 ----- 319
Db 2733 TTCTCATCTCCTGAGACTGCTCGACCCCTCCCTCCAGGCTCTGTCTGATGGCCCCCTC 2792
QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCCTCTCAGGCGCTTCGATGGGCGAGCTGGGCTGTCTCTGAGTCGCCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2853 GGTCTTCTCTGTGTCATGGACCGGCTGGTGCAGCGATTCGGCAGTCGAGCAGTCTATT 2912
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyValAlaThrCysLeuSerHisSerValAl 376
Db 2913 GGCCAGTGTGCAGCTTTCCTCTGGCTGGCTGGCTGGCGGTCCACATGCCCTGCCACAGTGTGC 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGTGACAGCTTCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCC 3032
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGl 416
Db 3033 CTACACACTGGCCCTCCCTTACCACCGGAGAGCAGGTGTCCTGCCCAATACCGAGG 3092
QY 416 yAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACACAGCTTCTGCCAGGCCCTTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGTGGAGGCAGTGGCCTGCTCCACC 3212
QY 456 oProProAlaLeuGlyAlaSerAlaCysAspValSerValArgValValGlyGl 476
Db 3213 TCCACCCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGGTGGTGA 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCCAGCAGGCCAGGTTGGTTCCGGCCGGGGCATCTGCCCTGGACCTCGCCCATCTGA 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
Db 3333 TAGTGCCTTCTGCTGCTCCAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCT 3392
QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536
Db 3393 CAGCCAGTCTGCTACCTGCATATATGGTGTCTCGCCGCGAGGCTGGGTCTGTGGCGCAITTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 3453 CTTTGTACACAGGTAGTATTGTGACAGAGCGCACTTGGCCCAATACACAGCG 3504
RESULT 20
AAH93866
ID AAH93866 standard; cDNA; 4894 BP.
XX AC AAH93866;
XX AC
XX 04-OCT-2001 (first entry)
XX DE
XX DE P553S cDNA splice variant P553S-14.
XX KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX KW cytosstatic; gene therapy; metastasis; ss.
XX
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OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
DR
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines.
XX
PS Claim 1; Page 457-459; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;

Alignment Scores:
Pred. No.: 1.39e-192 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 22 Gaps: 2

US-09-593-793A-113 (1-553) x AAH93866 (1-4894)

QY 1 MetValGlnArgLeuTyrPValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 274 ATGTCACAGAGCTGTGGGTGAGCGCTGCTGCGGCACCGAAAGCCAGCTTGTGCTG 333
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGCAGGCATCACCATTGTGCGG 393
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 394 CCTCTGCTGTGGAAGTGGGGGTAGAGAGAAGTTCATGACCATGGTGCT-GGGTGAGTC 452
QY 57 ----- 57
Db 453 ACTACATCCTCCTTCTTCTTCTTCTTCCAGATACATGCCACCTGGCATGTGGACAGAGTA 512
QY 57 ----- 57
Db 513 CCTCTGCCCTGGGAGCTGCTTGGAGGAGAGAGTGCTGCTGGGAAGGCATTGCTGGGCA 572
QY 57 ----- 57
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Db 573 GGAGGTTGACCCCTGGCTGAGGGGCGACACCAAGAGAAAGAGAAATACCAAGGACATA 632
Qy 57 ----- 57
Db 633 CCCCACTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 692
Qy 57 ----- 57
Db 693 AAATGCTCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTACTCATTTAATGC 752
Qy 57 ----- 57
Db 753 TTACAACCACCATTGAGGTGATCCATTTTACAGAGAAAGAGAGAGGCTTTTAAAGAG 812
Qy 57 ----- 57
Db 813 TTAGTAGTCTTAGCCAAAGCCAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
Qy 57 ----- 57
Db 873 GGTCTCCAGCGGAGCTTGCTTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 932
Qy 57 ----- 57
Db 933 GATAAATTTACAAAAGCCACAGAAGGCAAGTAGTAACCATTTGTGACAAACCCCTCAC 992
Qy 57 ----- 57
Db 993 CCCAGGAAGAGGGCCCTGTGAGGATTCAGGCTCTGGAGTCACACTGCTTGTGTAAC 1052
Qy 57 ----- 57
Db 1053 GCTGCTCTTTACCCCTCCCTAGGTCTCGCGCTTTGAATATCACTTCTTAGTTGCTCC 1112
Qy 57 ----- 57
Db 1113 ATGCCTCAGTTTGTCCATCTGAAATAGGGGCATCTGTAATGCCCTGTGTATGAGAGTA 1172
Qy 57 ----- 57
Db 1173 AATTACAGCATCCCTGTGAGAGCTAGCACAGTGTGAGTAGCGGAATGTTATTTCCATCC 1232
Qy 57 ----- 57
Db 1233 TTCTCAGGAGCTTGTTCCCTCCCTTCCCTTGCCCTTTACTTGTCCAGCATTGACTCAT 1292
Qy 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1293 ACTACTTCCCTTTTGCAGGCATTGGTCCAGTGTGGGCGCTGGTCTGTGTCCTCCCTA 1352
Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
Db 1353 GGCTCAGCCAGTGACCACTGGGCTGGAGCTATGGCGCGCGCCCTTCATCTGGGCA 1412
Qy 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTGGGCATCTGCTGAGCCTTCTCTCATCCCAAGGGCGGCTGGCTAGCAGG 1472
Qy 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGTGTGCCCGGATCCAGGCGCTGGAGCTGGACATGCTCATCTGGGCGTGGGGCTG 1532
Qy 132 LeuAspPheCysGlyInValCysPheTrpProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCAGGTGTCTCACTCCACTGGAGGCGCTGCTCTCTGACCTCTTC 1592
Qy 152 ArgAspProAspHisCysArgGlnAlaTrpSerValTyrAlaPheMetIleSerLeuGly 171
Db 1593 CGGACCCGACCACTGTCCGACGCTTACTCTGTCTATGCTTATGATCATGATCAGTCTTGG 1652
Qy 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspTrpSerAlaLeuAlaProTyr 191
Db 1653 GGCTGCCCTGGGCTACTCTGCTGCCATTTGACTGGGACACCAAGTGGCCCTGGCCCTTAC 1712

Qy 192 LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1713 CTGGCACCAGGAGGAGTGCCTTTTGGCTGTGCACCTCATCTTCTCCTACCTCGGTA 1772
Qy 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGCACACTGCTGGTGGCTGAGGAGCAGCGCTGGGCCCCACAGCCAGCAGCAAGGG 1832
Qy 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTGGGCCCCCTCCTTGTGCCCCACCTGCTGTCCATCGGGGCGCGCTTGGCTTTCCGG 1892
Qy 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGCGGCTGCTTCCCGGCTGCACAGCTGTGTCGCGCATGCCCGCACCTG 1952
Qy 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CGCCGGCTCTTCTGGCTGAGCTGTGACGTGTGATGGCACTCATGACCTTACCGTGT 2012
Qy 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACACGGATTTCTGTGGCGAGGGCTGTACCAGGGCTGCCAGAGCTGAGCCGGGCA 2072
Qy 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 2073 GAGGCCCGAGACACTATGATGAAGGTAAAGGCTTGGCAGCAGCAGAGGCTGTGTGG 2132
Qy 319 ----- 319
Db 2133 AGCCGCCACCAGACAGACACACTCGGGCTGTGTCTGGGCTGGTGCCTTCCATCCTGG 2192
Qy 319 ----- 319
Db 2193 CCCGACTTCTGTCTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
Qy 319 ----- 319
Db 2253 GTGTGAACATCTCTGCTTGGGTTTCAGGAAGGCTCTGGCTGTCTAGGAGTCTGATC 2312
Qy 319 ----- 319
Db 2313 AGAGTCGTTGCCCCAGTTTGTACAGAAAGGCGGAGCTTATTCAAAGTCTAGAGGAG 2372
Qy 319 ----- 319
Db 2373 TGGAGGATTAAGGCTGGATTTCAGATCTGCTGGTTCCAGCCGAGTGTGCCCTCTGCT 2432
Qy 319 ----- 319
Db 2433 CCCCCAACGACTTTCCTCAATATCTCACCAGCGCTTCCAGCTAGGCGTCTTAGAAGCG 2492
Qy 319 ----- 319
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Qy 319 ----- 319
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Db 2613 TTCTCTGAGGTCAGTGGAGAAACCTAGACTCCCATTTGCTAGAGGTAGAAAGGGAAGG 2672
Qy 319 ----- 319
Db 2673 TGCTGGGAGCAGGCTGGTCCACAGAGGTCTCTGTGAGCAGAGTACCTGTGTTCGCC 2732
Qy 319 ----- 319
Db 2733 TTCTCATCTCCTGTAGACTGTCTCCAGCCCTTCCCTCCAGGCTGTGTCTGATGGCCCTC 2792

QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCCTCTCGAGCGTTCGGATGGCAGCGCTGGGGCTGTTCTTGCAGTGGCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2853 GGTCTTCTCTCTGGTCTGAGCGGCTGGTGCAGCGATTGGCAGCTCGAGCAGTCTATT 2912
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GCCCAGTGGGAGGCTTTCCCTGTGGCTGCCGGTGCCACATGCCGTCCACAGTGTGGC 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGTGACAGCTTCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 3032
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGl 416
Db 3033 CTACACACTGGCTCCCTCTACACCGGGAGAGAGGTGTTCCTGCCCAATACCGAGG 3092
QY 416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGTGTAGCAGGTGAGGACAGCCTGATGACCACTTCCCTGCCAGGCCCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGGAGCTCCCTTCCCTAATGACACGTGGTGTGGAGCAGTGGCTGCTCCACCC 3212
QY 456 oProProLaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGl 476
Db 3213 TCCACCCGCGTCTCGGGGCGCTCGCCTGTGATGCTCCGTACGTGTGGTGGTGA 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCCACCGAGGCGGGGTGTTCCGGCGGGGCAATCTGCCGTGGACCTCGCCATCCTGGA 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnIle 516
Db 3333 TAGTGCCTTCTCTGCTGCCAGGTGCCCATCCCTGTTATGGGCTCCATTTGCCAGCT 3392
QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyr 536
Db 3393 CAGCCAGCTGTGCTACTGCTATATGGTGTCTGCCGAGGCCCTGGGTCTGGTGCATTTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 3453 CTTTCTACACAGGTAGTATTGACAGAGGACTTGGCCAAATACTCAGCG 3504
RESULT 21
ABL95409
ID ABL95409 standard; cDNA; 4894 BP.
XX
AC ABL95409;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P553S splice variant SEQ ID NO 702.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.

PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SREI/) SREIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
PS Claim 1; SEQ ID NO 702; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
Alignment Scores:
Pred. No.: 1.39e-192 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 24 Gaps: 2
US-09-593-793A-113 (1-553) x ABL95409 (1-4894)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 274 ATGGTCCAGAGGCTGTGGGTGAGCGCTGCTGGCGCACCGAAGCCACCTCTTGTG 333
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCAACCTGCTAACTTTGGCCTTGGAGGTGTGTTTGGCGCGGCGCATCACCTATGTGCG 393

Qy	41	ProLeuLeuGluValGlyValGlyGluGlyPheMetThrMetValLeu-	57
Db	394	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTCT -GGGTGAGTC	452
Qy	57	-----	57
Db	453	ACTACATCCCTTCCTTCCTGTCGCAGATACATGCCACCTGGCATGTGGGACAGGAGTA	512
Qy	57	-----	57
Db	513	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGTGTCTGCTGGGAAGCATTTGCTGGGCA	572
Qy	57	-----	57
Db	573	GGAGGGTGACCTTGGGCTGAGGGGGCACACCAAGAGAAAGAGAATACCAAGGACATA	632
Qy	57	-----	57
Db	633	CCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG	692
Qy	57	-----	57
Db	693	AAATGCTCCTAACTTTGGCTAGCCCTTTTATAATTATAGCGATTATCTCATTTAATGC	752
Qy	57	-----	57
Db	753	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAAGCAGAGGCTTTTAAAGAGG	812
Qy	57	-----	57
Db	813	TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA	872
Qy	57	-----	57
Db	873	GGTCTCCACGCGAGCTTGTCTTACCCTTAGGACAAAGGGTGGACTCTGACTCTGCA	932
Qy	57	-----	57
Db	933	GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGACAAACCCTCACC	992
Qy	57	-----	57
Db	993	CCCAGGAAGAGGGCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTGTAAC	1052
Qy	57	-----	57
Db	1053	GCTGCCCTTTACCTCCCTAGTCTGCGCTTTGAATAAGTATCACCTTCTTAGTGTCTCC	1112
Qy	57	-----	57
Db	1113	ATGCTCAGTTTCTCCATCTGAANAATGGGGGATCTGTAATGCCCTGTGTATGAGGAGTA	1172
Qy	57	-----	57
Db	1173	AATTACAGCATCCCTGTGAAGAGCTAGCACAGTCTGAGTACGGAATGTTATTTCCATCC	1232
Qy	57	-----	57
Db	1233	TTCTCAGGAGCTTGTTCCTCCCTTGCCTTTTACTTGTCCCAGCCATTGACTCAT	1292
Qy	58	-----GlylleGlyProValLeuGlyLeuValCysValProLeuLeu	71
Db	1293	ACTACTTCCCTTCTTCGAGGCATTTGTCAGTGTGGGCTGGTCTGTGTGCCGCTCCTA	1352
Qy	72	GlySerAlaSerAspHisTrpArgGlyArgTyrglyArgArgArgProPheIleTrpAla	91
Db	1353	GGCTACGCCAGTCACCACTGGCGTGGACGCTATGSCGCCGCCGCCCTTCATCTGGGCA	1412
Qy	92	LeuSerLeuGlylleLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly	111
Db	1413	CTGTCTTGGGCATCTGTGTGAGCCTCTTCTCATCCCAAGGGCGGTGGCTAGCAGGG	1472

QY	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuLeuGlyValGlyLeu	131
DB	1473	CTGCTGTGCGCGATCCAGGCGCCCTGGAGCTGGCACTGCTCATCTCGGCGCTGGGCGCTG	1532
QY	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151
DB	1533	CTGGACTCTGTGGCCAGGTGCTTCACTCCACTGGAGCCCTGCTCTGTGACCTCTTC	1592
QY	152	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly	171
DB	1593	CGGAGCCCGACCACTGTGCCAGCCCTACTCTGTCTATGCTTCATGATCAGTCTTGGG	1652
QY	172	GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr	191
DB	1653	GGCTGCTGGGTACCTCCTGCTGCTGCAITGACTGGGACACCAAGTGCCTTGGCCCCCTAC	1712
QY	192	LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal	211
DB	1713	CTGGGCACCCAGAGAGTGCCTTCTTGGCGCTGCTCACCTCATCTTCCTCACTCGGTA	1772
QY	212	AlaAlaThrLeuLeuValAlaGluGluAlaLeuLeuGlyProThrGluProAlaGluGly	231
DB	1773	GCAGCCACACTGCTGGTGCTGAGGAGGAGCGCTGGGCCCCACCCAGCCAGCAGAGGG	1832
QY	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg	251
DB	1833	CTGTGGGCCCCCTCCTTGTGCCCCCACTGCTGCCATGCGGGCCCGCTTGGCTTTCCGG	1892
QY	252	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu	271
DB	1893	AACCTGGGCGCCTGCTTCCCGGCTGCACCACTGCTGTGCCATGCGCGCATGCCGCCACCCCTG	1952
QY	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe	291
DB	1953	CGCCGGCTCTCTGGTGGCTGAGCTGTGCAGTGGATGGCACTCATGACCTTCACGCTGTTT	2012
QY	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr	311
DB	2013	TACACGGATTCTGTGGCGAGGGCTGTACCAAGGGCTGCCACAGAGCTGAGCGGGCACC	2072
QY	312	GluAlaArgArgHisTyrAspGlu	319
DB	2073	GAGGCCCGGAGACATATGATGAAGGTAAGGCGCTTGGCAGCCAGCAGAGGCTGGTGTGGG	2132
QY	319	-----	319
DB	2133	AGCGGCCCAACAGACAGACACTGGGGGCTGTGTCTGGGCTGGTGGCTTCTCCATCTGGC	2192
QY	319	-----	319
DB	2193	CCCGACTTCTGTCTAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2252
QY	319	-----	319
DB	2253	GTGTGGAACATCTCTGTTGCGGTTTCAGGAAGGCGCTCTGGCTGCTTAGAGTCTGATC	2312
QY	319	-----	319
DB	2313	AGAGTCGTTGCCCACTTTGACAGAGAAAGCGCGAGCTTTTCAAAGTCTTAGAGGGAG	2372
QY	319	-----	319
DB	2373	TGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCGCGAGTGTGCCCTTGCT	2432
QY	319	-----	319
DB	2433	CCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGGCGCTCTTAGAAGCG	2492
QY	319	-----	319
DB	2493	TCCTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCTCTCACCGCGCTGTCTTCACAGCTG	2552
QY	319	-----	319

KW	Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW	foetal abnormality; developmental abnormality; haematopoietic disorder;
KW	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW	Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW	psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW	inflammation; neurological disorder; Alzheimer's disease; food additive;
KW	angiogenic disorder; kidney disease; gastrointestinal disorder; allergy;
KW	pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW	cell culture; chemotaxis; vulnery; binding partner identification;
XX	gene therapy; ss.
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	152..1267
FT	/*tag= a
FT	/product= "Human secreted protein"
FT	/transl_except= (pos:209..211, aa:xaa)
FT	/note= "Xaa corresponds to any of the naturally occurring
FT	L-amino acids"
FT	152..295
FT	/*tag= b
FT	296...1264
FT	/*tag= c
FT	/product= "Mature human secreted protein"
XX	
PN	WO200134629-A1.
XX	
PD	17-MAY-2001.
XX	
PF	08-NOV-2000; 2000WO-US30654.
XX	
PR	12-NOV-1999; 99US-0164835.
PR	27-JUL-2000; 2000US-0221142.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;
DR	WPI; 2001-308779/32.
DR	P-PSDB; AAE01362.
XX	
PT	New nucleic acid encoding one of 21 human secreted proteins for
PT	diagnosing, preventing, treating or ameliorating medical conditions,
PT	such as autoimmune disease and cancer, and used as a food additive or
PT	preservative -
XX	
PS	Claim 1; Page 388-389; 490pp; English.
XX	
CC	AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted
CC	protein genes, and AAE01352-AAE01413 represent the proteins they encode.
CC	AAE01415-AAE01433 represent human secreted protein fragments or variants.
CC	The secreted proteins and their genes are useful for preventing, treating
CC	or ameliorating medical conditions, e.g., by protein or gene therapy.
CC	Pathological conditions can be diagnosed by determining the amount of the
CC	new protein in a sample or by determining the presence of mutations in
CC	the new genes. Specific uses are described for each of the 21 genes,
CC	based on the tissues in which they are most highly expressed, and include
CC	developing products for the diagnosis or treatment of proliferative
CC	disorders, cancer, tumours, foetal and developmental abnormalities,
CC	haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC	diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC	neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC	cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC	psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC	angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC	pregnancy-related disorders, endocrine disorders, and infections. The
CC	proteins can also be used to aid wound healing and epithelial cell
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs
CC	before transplantation, for supporting cell culture of primary tissues,
CC	to regenerate tissues, to identify their cognate ligands or binding
CC	partners, and in chemotaxis, and can be used as a food additive or
CC	preservative to modify storage properties. Antibodies specific for a

CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention.

XX
SQ Sequence 3878 BP; 709 A; 1164 C; 1044 G; 951 T; 10 other;

Alignment Scores:
Pred. No.: 1 07e-181 Length: 3878
Score: 2400.50 Matches: 493
Percent Similarity: 67.39% Conservative: 3
Best Local Similarity: 66.98% Mismatches: 4
Query Match: 83.90% Indels: 237
DB: 22 Gaps: 1

US-09-593-793A-113 (1-553) x AAD05230 (1-3878)

QY 54 ThrMetValLeuGlyTleGlyProValLeuGlyValLeuValCysValProLeuLeuGlySer 73
DB 233 TCCCTTCTTGCAGGCATTGGTCCAGTGTGGGCTGGTNTGTCTCCCGCTCCTAGGCTCA 292
QY 74 AlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSer 93
DB 293 GCCAGTGACCACTGGCGWGGAGCGCTATGGCCGCCGCCCTTTCATCTGGGCACTGTCC 352
QY 94 LeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeu 113
DB 353 TTGGGCATCTGCTGAGCCTCTTCTCATCCCNAGGGCCGGCTGGCTAGCAGGGCTGCTG 412
QY 114 CysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAsp 133
DB 413 TGCCCGGATCCCAAGGCCCTGGAGCTGGCACTGTCTCATCTGGCGCTGGGCTGTGGAC 472
QY 134 PheCysGlyClnValCysPheTrpProLeuGluAlaLeuLeuSerAspLeuPheArgAsp 153
DB 473 TTTGTGGCCAGGTGTCTTCACTCCACCTGGAGGCCCTCTCTGTGACCTTTCGGGAC 532
QY 154 ProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCys 173
DB 533 CCGGACCACTGTCCGAGGCCCTACTCTGTCTATGCTTTCATGATCATGCTTGGGGGCTGC 592
QY 174 LeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGly 193
DB 593 CTGGGCTACTCTCTGCTGCCATTGACTGGACACCACTGGCCCTGGCCCTACCTGGGC 652
QY 194 ThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAla 213
DB 653 ACCAGGAGGTGCTCTTTGGCCCTGCTCAGCCCTCATCTCTCCTCAGCTGCTGAGAGCC 712
QY 214 ThrLeuLeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSer 233
DB 713 ACACCTGCTGGTCTGAGGAGGCGGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGCG 772
QY 234 AlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeu 253
DB 773 GCCCCCTCTGTGCGCCCACTGCTCTCCATGCGGGCCCGCTTGGCTTTCGGGAACCTG 832
QY 254 GlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArg 273
DB 833 GGGCCCTCTCTCCCGGGCTGCACCAAGCTGTGTGCTGCCGATGCCCGCACCTTGGCCGG 892
QY 274 LeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThr 293
DB 893 CTCTCTGCTGGCTGAGCTGTGACGTGGATGGCACTCATGACCTTCACGCTGTTTACAGC 952
QY 294 AspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAla 313
DB 953 GATTTCGTGGGCGAGGGGCTGTACCAAGGCGTGCCAGAGCTGAGCGGGCCACCGAGGCC 1012
QY 314 ArgArgHisTyrAspGlu----- 319
DB 1013 CGGAGACACTATGATGAAGGTAAAGGCCCTTGGGAGCCAGCAGAGGCTGGTGGGAGCCGC 1072

QY 319 ----- 319
DB 1073 CCACCAGACGACACTCGGGCTGTGTCTGGGCTGGTCCCTCTCCATCTGCCCCGAC 1132
QY 319 ----- 319
DB 1133 TTCTCTGTCTCAGAAAGTGGGATGGACCCCATCTGCATACAGGGCTTCTCATGGGTGTG 1192
QY 319 ----- 319
DB 1193 AACATCTCTGCTTGGGTTTCAGGAAGGCTCTGGGCTGTCTAGGAGTCTGTATCAGAGTC 1252
QY 319 ----- 319
DB 1253 GTTGCCCCAGTTTGACAGAAGGAAGCGGAGCTTATTCAAAGCTCTAGAGGAGTGGAGG 1312
QY 319 ----- 319
DB 1313 AGTTAAGGCTGGATTTCAGATCTGCTGTCTCAGCGCGAGTGTGCCCTCTGCTCCCCCA 1372
QY 319 ----- 319
DB 1373 ACGACTTTCAAATAATCTCACAGGCGCTTCCAGCTCAGGCGTCTTAGAAGCGCTTGA 1432
QY 319 ----- 319
DB 1433 AGCCTATGGCCAGCTGTCTTTGTGTTCCTCTCACCCGCTGTCTCTCACAGCTGAGACTC 1492
QY 319 ----- 319
DB 1493 CCAGGAACCTTTCAGACTACCTTCTCTCTCCCTTTCAGCAAGGGCGTTGCCACATCTCT 1552
QY 319 ----- 319
DB 1553 GAGGTCAGTGGAGAACCTAGACTCCCATATGCTAGAGTAGAAAGGGAAGGGTCTCG 1612
QY 319 ----- 319
DB 1613 GGAGCAGGCTGGTCCACAGCAGGTCTCGTGACAGAGGTACCTGTGTTCGCCCTCTCA 1672
QY 319 ----- 319
DB 1673 TCTCCTGAGACTGTCTCCGACCTTCCCTCCAGGCTCTGTCTGATGGCCCTCTCCCTC 1732
QY 320 ---- GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPh 338
DB 1733 TCGAGCGTTCGGATGGGCGAGCTGGGCTGTCTCTGCAAGTGGCCATCTCCTGTCTT 1792
QY 338 eSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSe 358
DB 1793 CTCTCTGGTTCATGGACCGGCTGGTGCAGCGATTTCGSCACTCGAGCAGTCTATTTGGCCAG 1852
QY 358 rValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVa 378
DB 1853 TGTGGCAGCTTTCCCTGTGGCTGCCGGTCCACATGCTCTCCACAGTGTGGCCGTGT 1912
QY 378 lThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrTh 398
DB 1913 GACAGCTTCAGCGCCCTCACCAGGTTACCTTTCAGCCCTGCAGATCCTGCCCTTACAC 1972
QY 398 rLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspTh 418
DB 1973 ACTGGCTCCCTCTACCACCGGAGAGAGGAGTGTCTCTGCCCAATACCGAGGGGACAC 2032
QY 418 rGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGl 438
DB 2033 TGGAGTGTAGCAGTGGAGCAGCGCTGATGACCAAGCTTCTCTGCCAGGCCCTTAAGCCTGG 2092
QY 438 yAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPr 458
DB 2093 AGCTCCCTTCCCTTAATGGACAGTGGGTGCTGGAGCAGTGGCTTCCCTCCCACTCCACC 2152

QY 57 ----- 57
Db 1004 ATGCTCAGTTTGTCCATCTGAAATGGGGGCATCTGTAATGCTGTGTTATCAGGAGTA 1063
QY 57 ----- 57
Db 1064 AATTACAGCATCCCTGTGTGAAGACGTAGCACAGTGTGAGTACGGAATGTTATTTCATCC 1123
QY 57 ----- 57
Db 1124 TTCTCAGGAGCTTGGTTCCCTTCCCTTCCCTTACTTGTGCCAGCCATTGACTCAT 1183
QY 58 ----- GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1184 ACTACTTCCCTTCTTGCAGGCATTGGTCCAGTGTGGCCCTGTGTGTGCCCTCCTTA 1243
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
Db 1244 GGCTCAGCCAGTGACCACTGGCGTGGACGTATGGCGCGCGGCCCTTCATCTGGCA 1303
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuLeuProArgAlaGlyTrpLeuAlaGly 111
Db 1304 CTGTCTTGGCATCTTGTGTGAGCCCTTCTTCTATCCCAAGGGCCGCTGGCTAGCAGGG 1363
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1364 CTGCTGTGCCCGGATCCACAGGCCCTGGAGCTGGCACTGCTCATCTGGCGTGGGGCTG 1423
QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1424 CTGGACTTCTGTGGCCAGGTGTGCTTACATCCACTGGAGGCCCTGTCTCTGACCTTTC 1483
QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1484 CGGGACCCGAGCACCTGTGCCAGGCTACTGTCTATGCCCTTCATGATCAGCTGTGGG 1543
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Db 1544 GGCTGCTGGCTACCTTCCTGCCCTGACCTGGGACACCACTGCGCTGGCCCTTCCCTAC 1603
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1604 CTGGGACCCAGAGAGTGCCTTGTGGCTGTCTCACCTCATCTTCTCCTACCTGCGTA 1663
QY 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1664 GCAGCCACACTGTGTGGTGTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAAGGG 1723
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1724 CTGTGGGCCCTTCTTGTGCCCCACTGTGTCCATGCGGGCCCGCTTGGCTTCCCG 1783
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1784 AACCTGGGCGCCCTGTCTCCCGGCTGCACAGCTGTGTGGCGCATGCGCCGACCCCTG 1843
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1844 CGCGGCTCTTCTGTGTGAGCTGTGCAGTGTGATGGCATCATGACCTTCAGCTGTGTT 1903
QY 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 1904 TACACGGATTTCTGGCGAGGGGCTGTACCAAGGCGTGGCCAGAGCTGAGCGGGCACCC 1963
QY 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 1964 GAGGCGGGAGACACTATGATGAAGGTAAAGGCTTGGCAGCCAGCAGAGGCTGGTGTGGG 2023
QY 319 ----- 319
Db 2024 AGCGGCCACACAGAGACACTCGGGGCTGTCTGTGGGCTGTGTCTCTCCATCTCTGGC 2083

QY 319 ----- 319
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QY 319 ----- 319
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QY 319 ----- 319
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QY 319 ----- 319
Db 2624 TTCTCATCTCCCTGAGACTGCTCCGACCCCTTCCCTCCAGGCTCTGTCTGATGGCCCTC 2683
QY 320 ----- GlyValArgMetClySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2684 TCCTCTGAGGGGTTCCGATGGGAGCCTGGGGCTGTTCCTGCACTGGCCATCTCCCT 2743
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2744 GGTCTTCTCTGTGTCATGGACCGGCTGGTGCAGCGATTTCGGCACTCGAGCAGTCTATT 2803
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2804 GGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGC 2863
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2864 CGTGGTGACAGCTTCAGCGCCCTTCACCGGTTTCACCTTCTCAGCCCTCAGATCTGCC 2923
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal----- 409
Db 2924 CTACACACTGGCTCCCTCTACACCCGGAGAGACAGGT- ACTCATTTGCCAGTGGGTGG 2982
QY 409 ----- 409
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QY 409 ----- 409
Db 3043 CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGCTTATCTCTAGCCCCA 3102
QY 409 ----- 409
Db 3103 GGGCCNAGAGGCTTGGCTGCAGAACAGTATAGATTCTGCGGAATGACTTCTCTGGGG 3162
QY 409 ----- 409

Db	3163	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGAA	3222
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Qy	409	-----	409
Db	3283	CAGGCGCTGAATCAGATGACCCCTGGGCCATTACAGCCTCAGCAGCGGAGTGGGAATG	3342
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Qy	409	-----	409
Db	3403	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCTACCCCTTTCTTCTGGCTTAATTTTCT	3462
Qy	409	-----	409
Db	3463	TTTCTGTCTAATTCCTTTTCTTTCCTGCAATCCCTTTTGCCCTCCTTCCCTTTCTCCT	3522
Qy	409	-----	409
Db	3523	TCCCTTCCCTTCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACTTGGG	3582
Qy	409	-----	409
Db	3583	CACGTGTAACTTGTGGGACCTCCTTCTTGGTTGGCCCTACACTAACCCGCCCTCCAG	3642
Qy	409	-----	409
Db	3643	GGGCCCCCTTCTTGGGAAGCCACTAACCCAGGTAGTGGTCATCTCTTCCCTCCA	3702
Qy	409	-----	409
Db	3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCTTGAGGGGCATGAAGTGG	3762
Qy	409	-----	409
Db	3763	GGTGTCCCAAGGGAGGAGAGATGACGAGCTGCTCTCATAGAGCTCTCAGACTAGGGA	3822
Qy	409	-----	409
Db	3823	AGACCTGCCCTGCGTCTCGTAGCATTGAGGAGGAGTAGTAAAGTTCTAGCTGAGA	3882
Qy	409	-----	409
Db	3883	GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGTATGAGGGAGGGGCTAAAGT	3942
Qy	409	-----	409
Db	3943	TTTGGTTGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC	4002
Qy	409	-----	409
Db	4003	CTTCACTCTTCTGCTTGCCTGGGCTGGGGCAGGGGCTGCAATCAGGGCCAGGCCTGA	4062
Qy	409	-----	409
Db	4063	GTATGTGCTGTCGTGCCAGGAAGTTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC	4122
Qy	409	-----	409
Db	4123	ATGCTGTCTCGGACCACTCCAGACTCCAACTCAGCGGACATTCCTGGGGTGGCAGGC	4182
Qy	409	-----	409
Db	4183	AGGAGGAGAAGTCTCTGGGAGCCCCCTTCTTAACAGCAGCTGATGGCAGACTTGGCACTG	4242
Qy	409	-----	409

Db	4243	CACGCTGTCTCCCTGTTCCTTTTGTCCCACTTGTGTGAGCTGCATGTGTAGCCCTGGGCTTCC	4302
Qy	409	-----	409
Db	4303	CTGGTGTCAAGTTTGTAGCTCTGCCATGGCTCCCACCTCGCAAATGCAGCCAACTCAACTC	4362
Qy	409	-----	409
Db	4363	TTCTGGCATGGGACAAATGTTGGATAAGACCTGGCCTTGTCTTAAATAGGAGGCTCTGG	4422
Qy	409	-----	409
Db	4423	GCCATCAAGGCAGGGGTTGGGGGATGGTGTGCACAGTCACTCTGATCTAAGTCAAGA	4482
Qy	409	-----	409
Db	4483	CAGCAGGAAGAAGTGAGAACCTTCAACATTAGCACAGCTGGGGCTGGGGGAGGTGGGA	4542
Qy	409	-----	409
Db	4543	AGGGGACATTCTCTCTGCTTGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGGACA	4602
Qy	409	-----	409
Db	4603	AGGAGCTCATGGCAGGSCAGCTACCCTAGTGGCATCTGGGACCCACAGAGCAGAGCT	4662
Qy	409	-----	409
Db	4663	TCTCTGCACCGGCAANTGAGGATTTCCAGATGTCGGAGTGGAGGCAGGAGGAAGAAG	4722
Qy	409	-----	409
Db	4723	GTTAGGAGAGCCTCGTGGGTTTGGGCCATCAGGGGCCCTGCCCTTGGCTTTTCTCTCTC	4782
Qy	409	-----	409
Db	4783	TGTTCTGTGCATCTCTTACCACCGCTTCTCATTCGCCCTGTCTCTTTCTTACCTTGGAG	4842
Qy	409	-----	409
Db	4843	CTCTGTCTCTCTCATCTGTGATATTTGAGTTTGTCTGCTTACCTTGTCTTAAGAGGCT	4902
Qy	409	-----	409
Db	4903	AGAGGAGACCTAGACTTCTGGGTTACATTTGTCCCCGCCCTACCCGCTTACCCCTTCTCC	4962
Qy	409	-----	409
Db	4963	CACCTCTGAGGAAGGTCCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCTCT	5022
Qy	409	-----	409
Db	5023	GCTCCTGATTCATGAAGTCCCATTTGCCCTGGGATGGAGGCAAGGTCGTCTCTCACA	5082
Qy	409	-----	409
Db	5083	GCTGGGTGTGCCAGTGTGGGTACACACTGTCTCTTCCCTCTTCTTTCACCCCTCT	5142
Qy	410	-----PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe	426
Db	5143	GCCTTAGGTGTCTCTGCCCAAAATACCGAGGGGACACTGGAGGTCTAGCAGTAGGACAG	5202
Qy	426	rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa	446
Db	5203	CCTATGACCAGCTTCTTCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTCTTATGACACGT	5262
Qy	446	lGlyAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCy	466
Db	5263	GGGTCTGGAGCAGTGGCCTGTCTCCACCTCCACCCGGGCTCTGCCGGGCTCTGCTG	5322
Qy	466	sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr	486
Db	5323	TGATGTCTCGTACGTGTGTGTGGTGTAGCCCCACCGAGGCCAGGCTGTTCGGGCGC	5382

QY 486 gGlytLeCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaApr 506
|||||
Db 5383 GGCATCTCGCTGGACCTCGCCATCTGGATAGTCCCTTCCTGCTGCCAGGTGGCCCC 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
|||||
Db 5443 ATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGTCACTGCTATATGGTGT 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspIysSe 546
|||||
Db 5503 TGCCGAGCCCTGGGTCTGGTGGCCATTACTTTGCTACAGGTAGTATTTGCAAGAG 5562
QY 546 rAspLeuAlaLysTyrSerAla 553
|||||
Db 5563 CGACTGTGGCCAAATACTCAGCG 5584
RESULT 24
AAH93869
ID AAH93869 standard; cDNA; 6976 BP.
XX
AC AAH93869;
XX
DT 04-OCT-2001 (first entry)
XX
DE P553S cDNA splice variant P553s-6.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 461-463; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I). (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Alignment Scores:

Pred. No.: 6.81e-161 Length: 6976

Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 22 Gaps: 3
US-09-593-793A-113 (1-553) x AAH93869 (1-6976)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 165 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGCACCCGAAAGCCAGCTCTGTGTG 224
QY 21 ValAsnLeuLeuThrPheClyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
|||||
Db 225 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCG 284
QY 41 ProLeuLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeu----- 57
|||||
Db 285 CCTCTGCTGTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGGTGCT-GGGTGAGTC 343
QY 57 ----- 57
Db 344 ACTACATCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGAGTA 403
QY 57 ----- 57
Db 404 CCTCTGCCCTGGGAGCTGCTTGGAGGAGAGGTGCTGCTGGGAAGGCATTGCTGGGCA 463
QY 57 ----- 57
Db 464 GGAGGTTGACCCCTGGGCTGAGGGGGGCACACCAAGAAAGAAAGAAATACCAAGGACATA 523
QY 57 ----- 57
Db 524 CCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGACCTGGCTCATAGGAGACACTGGAG 583
QY 57 ----- 57
Db 584 AAATGCTCTAACCTTTGGCTAGCCCTTTTATAAATTTATAGCGATTATCTCATTTAATGC 643
QY 57 ----- 57
Db 644 TTACAACCAACCATTTGAGGTGATCCATTTACAGAGAAGGAAGACAGAGGCTTTTAAGAG 703
QY 57 ----- 57
Db 704 TTAGSTAAGTCTTAGCCAAAGCCAAATAGCAGCTCAACAGTAGAGCTGGGACTCCATCAA 763
QY 57 ----- 57
Db 764 GGTCTCCAGCGGAGCTTGTCTCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 823
QY 57 ----- 57
Db 824 GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACAACCCCTCACC 883
QY 57 ----- 57
Db 884 CCCAGGAAGAGGGGCCCCCTGTGAGGATTGTCAGGCTCTGGAGTCAACACTGCTTTGTTGAAC 943
QY 57 ----- 57
Db 944 GCTGCTCTTACCCCTCCCTAGTGTCTGCGCCCTTTGAATAAGTATACACTTMTTAGTTGCTCC 1003
QY 57 ----- 57
Db 1004 ATGCCTCAGTTTGTCCATCTGAAATGGGGCATCTGTAATGCCCTGTGTTATGAGGAGTA 1063
QY 57 ----- 57
Db 1064 AATTACGCATCCCTGTGAAGACGCTAGCACAGTGTGAGTAGCGGAATGTTATTTCATCC 1123
QY 57 ----- 57

Db 1124 TTCTCAGGAGCTTGTTCCCTTCCCTTGCCCTTTACTTGTCCAGCAATTGACTCAT 1183
Qy 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1184 ACTACTTCCCTTCTTGCAGGCAATTGGTCAGTGTGGGCCCTGGTCTGTGTCCCGCTCTTA 1243
Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
Db 1244 GGCCTACGACAGTACCACTGGCGTGGACGCTATGCCCGCGCGCCCTTCATCTGGGCA 1303
Qy 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1304 CTGTCTTGGGCATCTCTGCTGAGCCTCTTCTCATCCCAAGGGCGGCTGGCTAGCAGG 1363
Qy 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeu 131
Db 1364 CTGCTGTGCCGGATGCCAGGCCCTGGAGCTGGACATGCTCATCTGGGGGTGGGGCTG 1423
Qy 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1424 CTGGACTTCTGTGGCCAGGTGTCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTC 1483
Qy 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1484 CGGGACCGGACCACTGTGGCAGGCCCTACTGTGCTTATGCTTTCATCATCATGCTTTGGG 1543
Qy 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Db 1544 GGCCTGCCCTGGGCTACTCTGCTGCCATTGACTGGGACACAGTGGCCCTGGCCCTTAC 1603
Qy 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1604 CTGGCACCCAGGAGGAGTGCCTTTTGGCTGTCTACCCCTCACTTCTCTCACCTGCGTA 1663
Qy 212 AlaAlaThrLeuLeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1664 GCAGCCACACTGCTGGTGGCTGAGAGGACGCGTGGGGCCCAACCGAGCCAGCAGAGG 1723
Qy 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1724 CTGTGGCCCCCTCTCTGTGCCCCACCTGCTGTCCATGCCGGGCCCTGTGGCTTCCGG 1783
Qy 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1784 AACCTGGSCGCCCTGTCTCCCGGCTGCACCACTGTGCTGCCGATSCCCCGCACCTG 1843
Qy 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1844 CGCCGGCTCTTCTGCTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT 1903
Qy 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 1904 TACAGGATTTCTGTGGCGAGGGGTGTACCAGGGCGTGTACCAGGGCGTGGCCAGAGCTGAGCCGGGCACC 1963
Qy 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 1964 GAGGCCCGGAGACACTATGATGAAGGTAAGGCTTGGCCAGCCAGCAGAGGCTGTGTGGG 2023
Qy 319 ----- 319
Db 2024 AGCCGCCACCAAGACGACACTCGGGGCTGTGTCTGGGCTGGTGGCTCTCCATCCTGGC 2083
Qy 319 ----- 319
Db 2084 CCCGACTTCTGTCTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2143
Qy 319 ----- 319
Db 2144 GTGTGGAACATCTGTGTTGCGGTTTCAGGAAGGCTCTGGCTGCTCTAGGAGTCTGATC 2203
Qy 319 ----- 319

Db 2204 AGAGTCTGTGCCCCAGTTTGTACAGAAGGAAAGCGGAGCTTATTCAAAGTCTAGAGGAG 2263
Qy 319 ----- 319
Db 2264 TGGAGGAGTTAAGGCTGGATTTTCAGATCTGCCTGTGTTCCAGCCGCACTGTGCCCTCTGCT 2323
Qy 319 ----- 319
Db 2324 CCCCCAAGCACTTTCAAAATAATCTCACAGCGCCTTCCAGCTCAGGCGTCTTAGAAGCG 2383
Qy 319 ----- 319
Db 2384 TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTCCCTCTCACCCGCTGTCTCTACAGAGTG 2443
Qy 319 ----- 319
Db 2444 AGACTCCCAAGNAACCTTTCAGACTACCTTCTCTGCCCTTCAGCAAGGGGCGTTGCCACA 2503
Qy 319 ----- 319
Db 2504 TTTCTCTGAGGTCAGTGGGAAGAACCTAGACTTCCCATTTCTAGAGGTAGAAAGGGGAAGG 2563
Qy 319 ----- 319
Db 2564 TGCTGGGAGCAGGCTGTGTCACAGCAGGTCTCGTGCAGCAGGTACCTGTGTTCCGCC 2623
Qy 319 ----- 319
Db 2624 TTCTCATCTCCCTGAGACTGTCTCCGACCCCTTCCCTCCAGGCTCTGTCTGATGGGCCCTTC 2683
Qy 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerIle 336
Db 2684 TCCCTCTCAGGCGCTTCGATGGGCAGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCT 2743
Qy 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrIle 356
Db 2744 GGTCTTCTCTCTGGTTCATGGACCGGCTGTGCAGCGATTCGGCACTCGAGCAGTCTATTT 2803
Qy 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2804 GGCCAGTGTGGCAGCTTTCCTGTGGCTGCCGGTGCACATGCCCTGTCCACAGTGTGGC 2863
Qy 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2864 CGTGTGACAGCTTCAGCGGCCCTCACCGGTTACCTTCTCAGCCCTGCAGATCTCTGCC 2923
Qy 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal----- 409
Db 2924 CTACACACTGGCTCCCTCTACCCAGGAGAGCAGGT- ACTCATTTGGCCAGTGGGTGG 2982
Qy 409 ----- 409
Db 2983 AGTCAGGTGGGAGGGTGTCTGGGTTTGTGGAGGCCAACTAGCTCAGAACCTGGTAT 3042
Qy 409 ----- 409
Db 3043 CTGGCAAGCAACTTTGGAGAAATGCTTCTTGAATCAGAGAAGAGCTTATCTTAGCCCA 3102
Qy 409 ----- 409
Db 3103 GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGATTCTTGGGAATGACTTCTCTGGG 3162
Qy 409 ----- 409
Db 3163 TCAGGACTGTGTAGCACTTGAATGGATGATTCAGGAAATGCAAAATACGATAGTGGAA 3222
Qy 409 ----- 409
Db 3223 TCCGGAAGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTGTGTTGTTCTATGAGAGG 3282
Qy 409 ----- 409
Db 3283 CAGGCGCTGAATCAGATGACCCCTTGGGCCATTCAGCCTCAGCAGACGGGAGTGGGAATG 3342

QY 409 ----- 409
Db 3343 GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402
QY 409 ----- 409
Db 3403 TCTGGTCTCTGAGATGGGCGAGGCTCCTTCTTACCCCTTTCTTCTGGCTTATTTTCT 3462
QY 409 ----- 409
Db 3463 TTTCTGTCTAATTCCCTTTTCTTCTGCATCCCTCCTTTGGCTCCTTTCTCTCT 3522
QY 409 ----- 409
Db 3523 TCCCCTTCCCTTCCCTCTGGCAGATATCTGAGCTTGACACCTGACCCACCTCACCTGGG 3582
QY 409 ----- 409
Db 3583 CACTGTGTAAGTTGTGGGACCTCCTTCTTGTGTTGGCCCTACACTAACGAGCCCTCCAG 3642
QY 409 ----- 409
Db 3643 GGGCCCTTTCTTGGGAAGCCACCTAACCCAGGTAGTGTGTCATCTTGTCCCTCCA 3702
QY 409 ----- 409
Db 3703 CTGACCTCACTGAGCTACAAACCTGGGTCTGACTCTGCCCTTGAGGGGCATGAAGTTGG 3762
QY 409 ----- 409
Db 3763 GGTGTCCCAAGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGA 3822
QY 409 ----- 409
Db 3823 AGACCTGCCCTCGTCTCGTAGCACTTGAGGAGAGGAGTAGTAACTTCGTAGCTGAGA 3882
QY 409 ----- 409
Db 3883 GGCTGGTTAACTGAGTAGTACTGCAGGGGTGAGAGGTATGGAGGGGAGGGCTAAGGT 3942
QY 409 ----- 409
Db 3943 TTTGGTTGGGAGGCTGTCTCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC 4002
QY 409 ----- 409
Db 4003 CTTCACTCTTCTGTGCTGGCTGGGGCAGGGGGCTGGCATCAGCGGCCAGGCCTGA 4062
QY 409 ----- 409
Db 4063 GTATGTGCTGCTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAC 4122
QY 409 ----- 409
Db 4123 ATGCTGTCTCTGGACCACTCCAGACTCCAACCTCAGCGACATCTCCTGGGTGGCAGGC 4182
QY 409 ----- 409
Db 4183 AGGGAGGAAGTCTCTGGGAGGCCCTTCCCTAACAGCAGCTGATGGCAGACTTGGCCTG 4242
QY 409 ----- 409
Db 4243 CACGCTGTCTGCTGTCTCTTTGCCCACTTTGTAGCTGCATGCTGACCGTGGGCTTCC 4302
QY 409 ----- 409
Db 4303 CTGGTCTCAGTTTGAGTCTGCCATGGCTCCCACTCGAAATGCAGCAACTCAACTC 4362
QY 409 ----- 409
Db 4363 TTCTGGCATGGGACAAATGTTGGATAAGACCTGGGCTTGTCTTAAATAGGAGGCTCTGG 4422

QY 409 ----- 409
Db 4423 GCCATCAAGGCGAGGGTTGGGGATGTGTGTCGACCAGTCACTCTGATCAAGTCAGA 4482
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QY 409 ----- 409
Db 4543 AGAGGGACATTCTCTCTGCTTGGGTCTACTGATTTCTCCCTGCCCAAGGCTGGGGACA 4602
QY 409 ----- 409
Db 4603 AGGAGCTCATGGCAGGCGACTACCCCTAGTGCATCTGGGACCTCCAGAGAGCAGAGCT 4662
QY 409 ----- 409
Db 4663 TCCTGCAACCGGCAATGAGGATTTCCAGATGTGGAGTGGAGGCGAGCAGGAAGAAG 4722
QY 409 ----- 409
Db 4723 GTTAGGAGACCTGCGTGGGCTTGGGCCATCAGGGCCCTGCCTTGGCTTTTGTTCCTC 4782
QY 409 ----- 409
Db 4783 TGTCTGTGCATCTCTTACCACCGTCTTCATTCCCCCTGTCTTTTCTTACCTTGGAG 4842
QY 409 ----- 409
Db 4843 CTCTGTCTCTGTGATCTGTGATATTGAGTTTGTCTGCCCTTTACCTGTCTTAAGAGGT 4902
QY 409 ----- 409
Db 4903 AGAGGAGACCTAGACTTCTGGGTTTCACTTTGTCCCGGCCCTACCCCGTTACCTTCTCC 4962
QY 409 ----- 409
Db 4963 CACTCTGAGGAAGGTCCTCGTTAGACTTTGGACCAAGTAGGCTCTCCATCTTCTCTCCT 5022
QY 409 ----- 409
Db 5023 GCTCTGATTTCTCATGAGTCCCATTTGCCCTTGGATGGAGGCAAGGCTGTGTCTACA 5082
QY 409 ----- 409
Db 5083 GCTGGGTGCTCCAGTCTGGGTACACACTGTCTCTTCCCTTTTCTTCCACCTCT 5142
QY 410 ----- PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
|||||
5143 GCCTTAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACAG 5202
QY 426 rleuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
|||||
5203 CCTGATGACCACTTCTCTCCAGGCCCTAAGCTTGAGCTTCCCTTCCCTTAATGGACACT 5262
QY 446 lglAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCy 466
|||||
5263 GGTGCTGGAGCAGTGGCTCTCCACCTCCACCGGCTCTGGGGGCTCTGGCTG 5322
QY 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
|||||
5323 TCATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCGCAGGCTGTTCCGGGCGG 5382
QY 486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
5383 GGGCATCTGCTTGGACCTGCCATCTTGGATAGCTTCTCTCTCTCCAGGTGGCCCC 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
|||||
5443 ATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGT 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleIleThrPheAlaThrGlnValValPheAspLysSe 546

|||||
Db 5503 TGCCGAGCGCTGGGCTGGTCCCATTTACTTTGCTACACAGGTAGTATTGACAAGAG 5562
QY 546 rAspLeuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCAAATACTACGCG 5584
RESULT 25
ABL95412
ID ABL95412 standard; cDNA; 6976 BP.
XX AC ABL95412;
XX DT 19-JUL-2002 (first entry)
XX DE Human P553S splice variant SEQ ID NO 705.
XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX KW gene therapy; gene; ss.
OS Homo sapiens.
XX US2002022248-A1.
PN 21-FEB-2002.
PD 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 98US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Harlocker JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX

DR WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX Claim 1; SEQ ID NO 705; 87pp; English.
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
SQ
Alignment Scores:
Pred. No.: 6,81e-161 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 24 Gaps: 3
US-09-593-793A-113 (1-553) x ABL95412 (1-6976)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 165 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCCGACCGGAAAGCCAGCTCTTGCTG 224
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 225 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGAGGCATCACCTATGTGCG 284
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 285 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGTGCT-GGGTGAATC 343
QY 57 ----- 57
Db 344 ACTACATCCTCCTCTCCTGTTCCAGATACATGCCACCTGGCATGTGGACAGGAGTA 403
QY 57 ----- 57
Db 404 CCTCTGCCCTGGAGCTGCTTGGAGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463
QY 57 ----- 57
Db 464 GGAGGTGACCTGGGCTGAGGGGCGACACCAAGAGAAAGAGAATAACCAAGGACATA 523
QY 57 ----- 57
Db 524 CCCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCCTGGCTCATAGAGACACTGGAG 583
QY 57 ----- 57
Db 584 AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 643
QY 57 ----- 57
Db 644 TTACAACCAACCATTTGAGGTGATCCATTTTACAGAGAAGGAAGCAGAGCGCTTTAAGAGG 703
QY 57 ----- 57
Db 704 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGNACAGTAGAGCTGGGACTCCATCAA 763
QY 57 ----- 57
Db 764 GGCTCCCAGCGAGCTTGGCTTCTTACCCTTAGGACAAAGGGGTGGACTCCTGACTCTGCA 823
QY 57 ----- 57
Db 824 GATAAATTTCTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACAACCCCTCAC 883

Qy	57	-----57
Db	884	CCAGGAAGAGGGCCCTGTCAGGATTGCAGGCTCTGGAGTCACACTGCTTGTGAAC943
Qy	57	-----57
Db	944	GCTGCCCTTACCCTCCCTAGGTCTCGGCTTTGAATAAGTATCATCTTMTAGTTGCTCC1003
Qy	57	-----57
Db	1004	ATGCCTCAGTTTGTCCCATCTGAAAAATGGGGGATCTGTAAATGCCCTGTGTTATGAGGAGTA1063
Qy	57	-----57
Db	1064	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTGCGAGTACGGAATCTTATTTCCATCC1123
Qy	57	-----57
Db	1124	TTCTACGGAGCTTGGTTCCCTTCCCTTGTGCCCTTTACTTTGCCAGCCATTGACTCAT1183
Qy	58	-----GlylleGlyProValLeuGlyLeuValCysValProLeuLeu71
Db	1184	ACTACTTCCCTTCTTCAGAGCATTTGTCCAGTCTGGGCTGGTCTGTGTCCCGCTCCTA1243
Qy	72	GlySerAlaSerAspHisTrpArgGlyArgTyrglyArgArgArgPropheIleTrpAla91
Db	1244	GGCTCAGCCAGTGACCACCTGGCGTGGACGCTATGGCCGCGCGCCCTTCATCTGGGCA1303
Qy	92	LeuSerLeuGlylleLeuLeuLeuSerLeuPheLeulleProArgAlaGlyTrpLeuAlaGly111
Db	1304	CTGTCTTGGGCATCTCTGTGACCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGGG1363
Qy	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeulleLeuGlyValGlyLeu131
Db	1364	CTGTGTGCCCGGATCCAGGCCCTTGGAGCTGGCAGTCTCATCTGGGCGTGGGGCTG1423
Qy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe151
Db	1424	CTGGACTTCTGTGCCAGGTGCTTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTC1483
Qy	152	ArgAspProAspHisCysArgGlnAlaTySerValTyraPheMetIleSerLeuGly171
Db	1484	CGGACCCGGACCACTGTCGCCAGGCTACTCTGTCTATGCTTCATGCTTCATGAGTCTTGG1543
Qy	172	GlyCysLeuGlyTyrlleuLeuProAlalleAspTrpAspThrSerAlaLeuAlaProTyr191
Db	1544	GGCTGCTGGGCTACCTTCTGCGCCACTGCTGTCCATGGGACACGAGTGCCCTGGCCCCCTAC1603
Qy	192	LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeullePheLeuThrCysVal211
Db	1604	CTGGGACCCAGGAGTGCCTCTTTGGCTTGCTCACCCCTCATCTTCTCACCTGGGTA1663
Qy	212	AlaAlaThrLeuLeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGly231
Db	1664	GCAGCCACACTGTGTGGTGGCTGAGGAGGAGCGCTGGGGCCGCCAGCAGCAGAGAAGG1723
Qy	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg251
Db	1724	CTGTGCGCCCCCTTCTGTGCGCCCACTGCTGTCCATGCCGGGCCGCTGGCTTTCGG1783
Qy	252	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu271
Db	1784	AACCTGGGCGCCCTGCTTCCCGGCTGCACAGCTGTGCTGCCGATGCCCCCGCACCCCTG1843
Qy	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe291
Db	1844	CGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCAGTCATGACCTTCACGCTGTT1903
Qy	292	TyrThrAspPheValGlyGluGlyLeuTyrglnGlyValProArgAlaGluProGlyThr311
Db	1904	TACACGATTTCTGTGGCGAGGGGCTGTACACAGGCGTGTGCCAGAGCTGTAGCCGGGACCC1963
Qy	312	GluAlaArgArgHisTrpAspGlu-----319

Db	1964	 GAGCCCGGAGACACTATGATGAAGGCTTGGCAGCCAGCAGAGGCTGGTGTGGG	2023
Qy	319	----- -----	319
Db	2024	AGCCGCCACCAAGACGACACTCGGGGCTGTCTGGCGTGGTCCCTCCATCCTGGC	2083
Qy	319	----- -----	319
Db	2084	CCCGACTTCTGTGTGTCAGAAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2143
Qy	319	----- -----	319
Db	2144	GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCTCTGGCTGCTTAGGAGTGTGATC	2203
Qy	319	----- -----	319
Db	2204	AGAGTCGTTGCCCGAGTTTCACAGAAGGAAGGCGGAGCTTAATCAAAGTCTAGAGGGAG	2263
Qy	319	----- -----	319
Db	2264	TGGAGGAGTTAAGGCTGGATTTTCAGATCTGCCTGGTTCCAGCCGAGTGTGCCCTCTGCT	2323
Qy	319	----- -----	319
Db	2324	CCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCAGCTCAGGCGTCTAGAAGCG	2383
Qy	319	----- -----	319
Db	2384	TCTTGAAGCCTATGGCCAGCTGTCTTGTGTGCCCTCTCACCCGCCCTCTCCTCACAGCTG	2443
Qy	319	----- -----	319
Db	2444	AGACTCCAGGAAACCTTCAGACTACCTTCTCTGCCTTCAGCAAGGGCGCTGCCACACA	2503
Qy	319	----- -----	319
Db	2504	TTCTCTGAGGTCAGTGGGAAGACCTAGACTCCCATCCATGCTAGAGTAGAAGGGGAAGGG	2563
Qy	319	----- -----	319
Db	2564	TGCTGGGAGCAGGCTGGTCCACACAGCTCTCGTGCAGCAGGTACCTGTGGTTCGCC	2623
Qy	319	----- -----	319
Db	2624	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAAGCTCTGTGTAGTGGCCCTC	2683
Qy	320	----- -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe	336
Db	2684	TCCTCTGCGAGGCTTCGGATGGCAGCCTGGGCTGTTTCTGCAAGTGGCCATCTCCCT	2743
Qy	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
Db	2744	GGTCTTCTCTGTGTATGACCGCGCTGTCAGCGAGTTTCGCACTCGAGCAGCTATT	2803
Qy	356	uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl	376
Db	2804	GGCCAGTGTGGCAGCTTCCCTGTGCTGCCGTGCCACATGCCCTGCCACAGTGGC	2863
Qy	376	aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396
Db	2864	CGTGTGACAGCTTCAGCCGCCCTACCGGGTTCACTTCTCAGCCCTGCAGATCCTGCC	2923
Qy	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal	409
Db	2924	CTACACACTGGCTCCCTCTTACCACCGGAGAAGCAGGT- ACTCATTTGGCCAGTGGGTGG	2982
Qy	409	----- -----	409
Db	2983	AGTCAGGCTGGGAGGGTGGTCTGGGTTTTTTGGGAGGCCAAGCTAGCTCAGAACCTGGTAT	3042
Qy	409	----- -----	409

Db 3043 CTGGCAAGCAACTTTGGAGAAATGCTTCTTTGAATCAGAGAAGACTTATCCTAGCCCCA 3102
QY 409 ----- 409
Db 3103 GGGCCAGAGGCTTGGCTGCAGACAGTGTAGATTCTGGGAATGACTTCTCTGGGG 3162
QY 409 ----- 409
Db 3163 TCAGGACTGTAGCACTTGAATGGATATTGCAGGAAATGCAAAATACGATAGTGGAA 3222
QY 409 ----- 409
Db 3223 TCCCGAAGGTCAGGCCACGAGAGCCCTAGGCTTCTAGGCTGGTGTCTATGGAGAGG 3282
QY 409 ----- 409
Db 3283 CAGGGGCTGAATCAGATGACCCCTGGGCCATTACGCTTCAGCAGACGGAGTGGGAATG 3342
QY 409 ----- 409
Db 3343 GTCCAGCCTTAGCAACACCTTTCTTCAGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402
QY 409 ----- 409
Db 3403 TCTGGTCTGAGATGGGCGAGGCTCCTTCCTACCCCCCTTCTTCTGGCTTATTTTCT 3462
QY 409 ----- 409
Db 3463 TTCTGTCTAATTCCTTTTCTTCTCGATCCCTCTTTGGCCCTTCCCTTCTCCT 3522
QY 409 ----- 409
Db 3523 TCCCCCTTCCCTTCCCTGTGCAGATATCTGAGCTTGACCTTGACCTGACCCACTCACTTTGG 3582
QY 409 ----- 409
Db 3583 CACTGTGTAAAGTTGTGGGACCTCCTTCTTGTGTGGCCCTACACTAACCAGCCCTCCAG 3642
QY 409 ----- 409
Db 3643 GGGCCCCCTTCCCTTGGGAAGCCACCTAACCCAGGTAGTGTGTATCCTTTGCCCTCCA 3702
QY 409 ----- 409
Db 3703 CTGACCTCACTGACTACAAACCTGGGTGCTGGACTCTGCCCTTGAGGGCATGAAGTTGG 3762
QY 409 ----- 409
Db 3763 GGTGTCCCAAGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGA 3822
QY 409 ----- 409
Db 3823 AGACCTGCCCCCTGCGTCTCGTAGCACTTGAGGAGAGGAGTAGTAAGTTGCTAGCTGAGA 3882
QY 409 ----- 409
Db 3883 GGCTGGTTAACTGAGTAGTACTGCAGGGGTGAGAGGTATGGAGGGAGGGCTAAGT 3942
QY 409 ----- 409
Db 3943 TTTGGTTGGGGAGCCTGTGCTCCTGAGACCCCTGTTAGCCCCACTGATAACCTTCTTCAGC 4002
QY 409 ----- 409
Db 4003 CTTTCACTCTTCTGCTTGGCTGGGGCAGGGGGCTGGGCATCAGCGGCCAGGCCTGA 4062
QY 409 ----- 409
Db 4063 GTATGTGCTGCTGCCAGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGACC 4122
QY 409 ----- 409
Db 4123 ATGTCTGTCTCGGACCACCTCCAGACTCCAACTTCAGCGGACATTCCTTGGGGTGGCAGGC 4182

QY 409 ----- 409
Db 4183 AGGGAGGAAGTCTCTGGGAGGCCCTTCTTAACACAGCTGATGCGACACTTGGCACTG 4242
QY 409 ----- 409
Db 4243 CACGCTGTCTGCTGTCTCTTTGCCACCTTGTAGCTGCATGGTGAAGCCGTCTCC 4302
QY 409 ----- 409
Db 4303 CTGGTGTACGGTTTGAAGTCTGCCATGGCTCCACCTTCGAAATGCGAGCCAACTCAACTC 4362
QY 409 ----- 409
Db 4363 TTCTGCGATGGGACAATCTTGATAAGACCTGGCCCTTGTCTTAATAGAGGCTCTCG 4422
QY 409 ----- 409
Db 4423 GCCATCAGGGCAGGGGTTGGGGGATGGTTCGACCACTCACTCTGATCTAAGTCAGA 4482
QY 409 ----- 409
Db 4483 CAGCAGGAAGTAGAGAAGCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA 4542
QY 409 ----- 409
Db 4543 AGAGGGACATTCCTCTGCTTGGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGACA 4602
QY 409 ----- 409
Db 4603 AGGGAGCTCATGGCAGGGCAGCTACCTAGTGGCATCTGGACCCAGAGAGCAGAGCT 4662
QY 409 ----- 409
Db 4663 TCTCTGCACCGGCAATGAGGATTTCCAGATGTGGAGTGGAGGCGAGCAGGAAG 4722
QY 409 ----- 409
Db 4723 GTTAGGAGACCTCGCTGGGGTTTGGGCCATCAGGGGCCCTGCCCTGGCTTTGTCTCTC 4782
QY 409 ----- 409
Db 4783 TGTCTGTGCATCTCTTACCACCGTCTTCATTCCTTCTTCTTCTTCTTCTTCTTCTTCT 4842
QY 409 ----- 409
Db 4843 CTCTGTCTCTCTGATCTCTGTGATTTGTCTGTCTTACCTGTCTTCTTAAGAGGCT 4902
QY 409 ----- 409
Db 4903 AGAGGAGACCTAGACTTCTGGGTTTACATTTGTCCCCGCCCTACCCCTTACCTTCTCTCC 4962
QY 409 ----- 409
Db 4963 CACTCTGAGGAAGGTCCTGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCCT 5022
QY 409 ----- 409
Db 5023 GCTCCTGATTCATGAAGTCCCATTTGCCCTGGGATGGAGGCAAGGCTCTGTCTCTACA 5082
QY 409 ----- 409
Db 5083 GCTGGGTGGTCCAGTGTGGGTACACACCTGTCTCTTCCCTTTTCTTCCCTCTCT 5142
QY 410 ----- PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
Db 5143 GCCTTAGGTTCTCTGCCAAATACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACAG 5202
QY 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
Db 5203 CCTGATGACCACTTCTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACAGT 5262

QY 446 lGlyAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCy 466
 Db 5263 GGGTGTGGAGGAGTGGCTGTCCACCTCCACCGCGCTGTGGGGCCCTCTGCCCTG 5322
 QY 466 sAspValSerValArgValValGlyGluProThrGluAlaArgValValProGlyAr 486
 Db 5323 TGATGTCTCGTACGTGTGTGTGGGTGAGCCACCGAGCGGTGTTCCGGGCGG 5382
 QY 486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
 Db 5383 GGGCATCTGGCTGGACTGCCATCTGGATAGTGGCTTCTCTGTCCAGGTGCCCC 5442
 QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
 Db 5443 ATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTGTGTCACTGCCTATATGTGTC 5502
 QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleIleTyrPheAlaThrGlnValValPheAspLysSe 546
 Db 5503 TGCCGAGGCGCTGGGTCTGGTCCCATTTACTTTGCTACACAGGTAGTATTTACAAGAG 5562
 QY 546 rAspLeuAlaLysTyrSerAla 553
 Db 5563 CGACTTGGCCAAATACTACGG 5584
 RESULT 26
 ID AAS64039
 XX AAS64039 standard; cDNA; 2904 BP.
 AC AAS64039;
 XX 29-JAN-2002 (first entry)
 DE Human prostate cDNA P553S splice variant #2.
 KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
 OS Homo sapiens.
 XX WO200173032-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-US09919.
 XX 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX (CORI-) CORIXA CORP.
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX WPI; 2001-639232/73.
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 XX Claim 1; Page 482-483; 579pp; English.
 XX The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of

CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 XX Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.52e-143 Length: 2904
 Score: 1920.50 Matches: 390
 Percent Similarity: 77.23% Conservative: 0
 Best Local Similarity: 77.23% Mismatches: 1
 Query Match: 67.13% Indels: 115
 DB: 22 Gaps: 1
 US-09-593-793A-113 (1-553) x AAS64039 (1-2904)
 QY 163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
 Db 1 GTCTATGCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCTGCTGCTGAC 60
 QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
 Db 61 TGGGACACCAAGTGGCTGGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCCTG 120
 QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
 Db 121 CTCACCTCATCTTCTCCTACCTGCTGAGCAGCCACACTGCTGGTGGCTGAGGAGGAGCG 180
 QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
 Db 181 CTGGGCCCCACCGAGCAGCAGAAAGGCTGTGGGCCCTCTCTGCGCCCCACTGCTGT 240
 QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyValAlaLeuLeuProArgLeuHisGln 262
 Db 241 CCATGCGCGGCGCGCTTGGCTTTCGGAACCTTGGGCGCCCTGCTTCCCGGGCTGCACAG 300
 QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
 Db 301 CTGTGTGCGCGATGCCCGCACCTCTGCGCGGCTCTTGGCTGCTGCTGCTGCTGCTG 360
 QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValClyGlyLeuTyrGln 302
 Db 361 ATGGCACTCATGACCTTACCGCTGTTTACAGGATTTCTGGGCGAGGGGCTGTACCAG 420
 QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlyValVal 321
 Db 421 GCGTGGCCAGAGCTGAGCGGCGCACCGAGGCGCGGAGACACTATGATGAGGAAG-GCC 479
 QY 321 ----- 321
 Db 480 TCTGGTGTCTAGGAGTCTGATCAGAGTCTTGTGCCCTTGTACAGAAGAAAGGCGG 539
 QY 321 ----- 321
 Db 540 AGCTTATTCAAAGTCTAGAGGAGTGAAGGCTGAAGGCTGATTCAGATCTGCTGGT 599
 QY 321 ----- 321
 Db 600 TCCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCACAAATATCTCACCAGCGCT 659
 QY 321 ----- 321
 Db 660 TCCAGCTCAGCGCTCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGCTCTTGTGTCCCT 719
 QY 321 ----- 321
 Db 720 CTCACCGCGCTGTCTCTACAGCTGAGACTCCAGGAAACCTTCAGACTTACCTCTCTG 779

Db 421 GCGCTGCCAGACTCAGCGGGCACCAGCGCCGGAGACACTATGATGAAGAAG-GCC 479
QY 321 ----- 321
Db 480 TCTGGCTGCTTAGGAGTCTGATCAGAGTCTGTGCCCGAGTTTGACAGAAGGAAGCGG 539
QY 321 ----- 321
Db 540 AGCTTATCAAGTCTAGAGGGAGTGGAGAGTTAAGGCTGGATTTCAGATCTGCCTGT 599
QY 321 ----- 321
Db 600 TCCAGCGGAGTGGCCCTCTGCTCCCAACAGACTTTCCTCAATAATCTCACCAGGCGCT 659
QY 321 ----- 321
Db 660 TCCAGCTCAGGCGTCTAGAGGCTCTTGAAGCCTATGCCAGCTGTCTTTGTGTCCCT 719
QY 321 ----- 321
Db 720 CTCACCGGCTGTCTCTCAGAGCTGAGACTCCAGGAACCTTCAGACTACCTTCTCTCTGC 779
QY 322 -----ArgMetGlySerLeuGlyLeu 328
Db 780 CTTTACAAGGGCGGTGGCCACATCTCTGAGGGCGTTTCGATGGCGAGCCTGGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTCTGTCAGTGGCCATCTCCCTGCTCTCTGCTGTCATGGACCGGCTGGTGACGCA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTGGGCACTCGAGCAGCTATTGTCAGCTGTGGCAGCTTTCCTGCTGGCTGCGGGTGC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
Db 960 ACATGCTCTGCCACAGTGTGGCGGTGGAGAGCTTCAGCGCGCTCACCAGGGTTTCACC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlnGlyGln 408
Db 1020 TTCTCAGCCCTCAGATCTGCCCTACACACTGGCTCCCTCTACCCAGCGGAGAGCAG 1079
QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMet 428
Db 1080 GTGTTCTGCCCAATACCGAGGGACACTGGAGGTGTAGCAGTGAGGACAGCCTGATG 1139
QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACACGCTGGTGT 1199
QY 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGGAGTGGCTGCTCCACCTCCACCGCGCTCTGGGGGCTCTGCTGCTGTATGTC 1259
QY 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
Db 1260 TCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeu 508
Db 1320 TGCCCTGGACCTGCCATCTGGATAGTGCCTTCTGCTGCCAGGTGGCCCGCCATCCCTG 1379
QY 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
Db 1380 TTTATGGGCTCCATGTCTCAGCTCAGCCAGCTGTGACCTGCTATGCTGTGCTGCCGA 1439
QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
Db 1440 GGCCTGGGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1499
QY 549 AlaLysTyrSerAla 553
Db 1500 GCCAAATACTCAGCG 1514

RESULT 28

ABL95410

ID ABL95410 standard; cDNA; 2904 BP.

XX ABL95410;

AC ABL95410;

XX 19-JUL-2002 (first entry)

XX Human P553S splice variant SEQ ID NO 703.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;

KW gene therapy; gene; ss.

XX Homo sapiens.

XX US2002022248-A1.

XX 21-FEB-2002.

XX 12-JAN-2001; 2001US-0759143.

XX 25-FEB-1997; 97US-0806099.

XX 01-AUG-1997; 97US-0904804.

XX 09-FEB-1998; 98US-0020956.

XX 25-FEB-1998; 98US-0030607.

XX 14-JUL-1998; 98US-0115453.

XX 23-SEP-1998; 98US-0159812.

XX 15-JAN-1999; 99US-0232149.

XX 09-APR-1999; 99US-0288946.

XX 13-JUL-1999; 99US-0352616.

XX 12-NOV-1999; 99US-0439313.

XX 18-NOV-1999; 99US-0443686.

XX 14-JAN-2000; 2000US-0483672.

XX 27-MAR-2000; 2000US-0536857.

XX 09-MAY-2000; 2000US-0568100.

XX 12-MAY-2000; 2000US-0570737.

XX 13-JUN-2000; 2000US-0593793.

XX 27-JUN-2000; 2000US-0605783.

XX 10-AUG-2000; 2000US-0636215.

XX 29-AUG-2000; 2000US-0651236.

XX 06-SEP-2000; 2000US-0657279.

XX 02-OCT-2000; 2000US-0679426.

XX 10-OCT-2000; 2000US-0685166.

XX (XUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI: 2002-255649/30.

XX New prostate-specific polynucleotides for diagnosing and treating

PT diseases, in particular prostate cancer, and as markers for the

PT progression of cancer

XX

PS Claim 1; SEQ ID NO 703; 87pp; English.
 XX The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. the present sequence is a cDNA
 CC described in the invention.
 XX

SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:

Pred. No.: 1.52e-143 Length: 2904
 Score: 1920.50 Matches: 390
 Percent Similarity: 77.23% Conservative: 0
 Best Local Similarity: 77.23% Mismatches: 1
 Query Match: 67.13% Indels: 115
 DB: 24 Gaps: 1

US-09-593-793A-113 (1-553) x ABL95410 (1-2904)

Qy 163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
 Db 1 GTCTATGCTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCCATTGAC 60
 Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
 Db 61 TGGGACACAGTGCCCTGGCCCTACCTGGGCACCCAGGAGAGTGCCTCTTTGGCCTG 120
 Qy 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
 Db 121 CTCACCTCATCTTCTTCCCTGCTAGCAGCACACACACACACACACACACACAC 180
 Qy 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
 Db 181 CTGGGCCCCACGACCCAGCAGAGGGCTGTGGGCCCTCTCTTGTGCCCCACCTGCTGT 240
 Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
 Db 241 CCATGCCGGGCGCGTGGCTTCCGGAACTTGGCGGCCCTGCTTCCCGCGGTGCACCA 300
 Qy 263 LeuCysCysArgMetProArgThrLeuArgLeuArgLeuPheValAlaGluLeuCysSerTrp 282
 Db 301 CTGTGCTCGCGCATGCCCGCACCTGCGCGGCTCTTCGTGGCTGAGCTGTGACGTGG 360
 Qy 283 MetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeuTyrGln 302
 Db 361 ATGGCACTCATGACCTTACGCTGTTTACAGGATTTCTGGGGGAGGGCTGTACCA 420
 Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal --- 321
 Db 421 GCGGTGCCACAGCTGAGCCGGCACCGAGGCGCCGAGACACATATGATGAAGGAAG-GCC 479
 Qy 321 ----- 321
 Db 480 TCTGCTGCTTAGAGAGTCTGATCAGAGTGTGTCGCCCATTTTGACAGAAAGCGG 539
 Qy 321 ----- 321
 Db 540 ACCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGCTGGATTCAGATTCGCTGGT 599
 Qy 321 ----- 321
 Db 600 TCCAGCCGAGTGTGCCCTGTCTGCCACGACGACTTCCAAATAATCTCACACGCGCT 659
 Qy 321 ----- 321
 Db 660 TCCAGCTCAGGCGTCTAGAGCGTCTTGAAGCCCTATGGCCAGCTGTCTTTGTTCCT 719
 Qy 321 ----- 321
 Db 720 CTCACCCGCTCTCTCACAGCTGAGACTCCCGAGAAACCTTCAGACTACCTTCCTCTGC 779
 Qy 322 -----ArgMetGlySerLeuGlyLeu 328
 |||||||

Db 780 CTTACAGAAAGGGCGTTGCCACATCTCTGAGGCGTTTCGATGGCAGCGCTGGGCTG 839
 Qy 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
 Db 840 TTCTTGCAGTGGCGCATCTCCCTGGTCTCTCTGCTGATGACCGGCTGGTGGAGGA 899
 Qy 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
 Db 900 TTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCC 959
 Qy 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
 Db 960 ACATGCTCTGCTCCACAGTGTGGCGTGTGAGCAGCTTCAGCGCCCTCACCGGGTTCAC 1019
 Qy 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
 Db 1020 TTCTCAGCCCTGCAGATCTTCCCTACACACTGGGCTCTCCCTACACCGGAGAACGAG 1079
 Qy 409 ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet 428
 Db 1080 GTGTTCTTCCCAATACCGAGGGCAGCTGGAGGTGTAGCAGTGAGCAGCAGCTGATG 1139
 Qy 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
 Db 1140 ACCAGCTTCTTCCAGGCGCTAAGCTGGAGCTCCCTTCCCTTAATGGACACGTGGGTGCT 1199
 Qy 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerSerGluAspVal 468
 Db 1200 GGAGCAGTGGGCTCTCCACCTCCCGCGCTCTGCGGGGCTCTGCTGTGATGTGTC 1259
 Qy 469 SerValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
 Db 1260 TCCGTACGTGTGGTGGTGGAGCCACCGAGGCGAGGTGGTTCGCGCGCGGCGCATC 1319
 Qy 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
 Db 1320 TGCCTGGACCTCGCCATCTGTGATAGTGCCTTCTGCTGTCCAGGTGGCCCATCCCTG 1379
 Qy 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
 Db 1380 TTTATGGGCTCCATGTCCAGCTCAGCCAGCTGTGCTATATGCTGTCTGCCCA 1439
 Qy 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
 Db 1440 GGCCTGGTCTGGTGGCCATTTACTTTCTACACAGTAGTATTTGACAGAGGACCTTG 1499
 Qy 549 AlaLysTyrSerAla 553
 Db 1500 GCCAAATACACGCG 1514
 RESULT 29
 ABA91284
 ID ABA91284 standard; DNA; 1593 BP.
 XX
 AC ABA91284;
 XX
 DT 08-APR-2002 (first entry)
 XX
 DE Thioredoxin-ubiquitin-P501S(aal-320)His triple gene fusion.
 KW Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
 KW cancer; vaccine; therapy; human; gene; ds.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Escherichia coli.
 FH Key Location/Qualifiers
 FT 1..1593
 FT /*tag=
 FT /transl_except= (pos:607..609,aa:Xaa)
 FT /note= "Xaa not given in amino acid sequence of
 FT Figure 12b (AAM50662), which has a Val
 FT residue at amino acid position 208 not

not encoded by the present sequence"

FT XX PN W0200200892-A1.
XX PD 03-JAN-2002.
XX PF 19-JUN-2001; 2001WO-EP06952.
XX PR 26-JUN-2000; 2000GB-0015619.
XX PR 30-OCT-2000; 2000GB-0026484.
XX PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Cabezón Silva TEV, Delisse AEF;
XX DR P-PSDB; AAM50662.
XX PT Novel DNA sequence encoding triple fusion protein comprising ubiquitin
PT fused between thioredoxin and polypeptide of interest, useful for
PT producing recombinant polypeptide of interest suitable for medicinal
PT use .
XX PS Example 8; Fig 12b; 87pp; English.
XX CC The present sequence is that of a triple gene fusion comprising,
CC from the 5' end, the trxA thioredoxin gene from Escherichia coli,
CC the human ubiquitin coding sequence, the prostate antigen P501S
CC (amino acids 1-320) coding sequence, and DNA encoding a histidine
CC tail. The triple fusion was constructed in plasmid pRIT15115,
CC under the control of the lambda pL promoter. Triple fusion
CC protein (see AAM50662) was produced in E. coli G1724 transformants.
CC This is an example of the production of triple fusion proteins of
CC the invention comprising ubiquitin fused between thioredoxin and a
CC protein of interest, in this case P501S(aal-320). A claimed method
CC of producing a recombinant protein of interest involves: culturing
CC a host cell (preferably E. coli) under conditions which allow
CC for co-expression of the triple fusion and a ubiquitin-specific
CC endoprotease (especially Upl from Saccharomyces cerevisiae);
CC and recovering the recombinant protein directly from the bacterial
CC cells after it has been subjected to the action of the
CC ubiquitin-specific endoprotease in vivo. In the present case,
CC expression was controlled by addition of tryptophan. The
CC recombinant protein can be used as a vaccine for cancer therapy.
XX SQ Sequence 1593 BP; 308 A; 472 C; 461 G; 352 T; 0 other;

Alignment Scores:
Pred. No.: 5,84e-126 Length: 1593
Score: 1696.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.28% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABA91284 (1-1593)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
DB 604 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGGCGACCGGAAAGCCAGCTCTGCG 663

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
DB 664 GTCAACCTGCTAACTTTGGCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCG 723

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 724 CTTCTGCTGCTGGAAGTGGGGGTAGAGGAAGTTTCATGACCATGGTGGCGCATTTGT 783

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 784 CCAGTGTGGGCTGGTCTGTCCCGCTCCTAGGCTACGCCAGGACCATGCGGTGGA 843

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 844 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCTGCTGAGCCTC 903

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 904 TTTTCATATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCGATCCAGGCCCTTG 963

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 964 GAGCTGGCAGCTGCTCATCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 1023

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheAspProAspHisCysArgGlnAla 160
DB 1024 ACTCCACTGGAGCCCTGCTCTGACCTCTTCGCGGACCCGACCATGTGCCAGGCC 1083

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
DB 1084 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCTGC 1143

QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
DB 1144 ATTGACTGGGACACCATGTCCTGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTTT 1203

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
DB 1204 GGCTGCTCACCTCATCTTCCTACCTGCTAGCAGCCACACTGCTGTGCTGAGGAG 1263

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 1264 CGAGCGCTGGGCGCCACCGAGCCAGCAGAAAGGCTGTCCGCCCTCTCTGTCGCCAC 1323

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyValAlaLeuLeuProArgLeu 260
DB 1324 TGCTGTCCATGCGCGCGCGCTTGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1383

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1384 CACGAGCTGTGCTGGCGATGCCCGACCTGCGCGGCTCTCTGCTGGCTGAGCTGTGC 1443

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrLeuPheThrAspPheValGlyLeu 300
DB 1444 AGCTGGATGGCAGCTCATGACCTTCACGCTGTTTACAGGATTTCTGGGCGAGGGCTG 1503

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTrpAspGluGly 320
DB 1504 TACCAGGGGCTGCCAGAGCTGAGCGGGCACCCGAGGCCCGGAGACACTATGATGAGGC 1563

RESULT 30
ABN81320
ID ABN81320 standard; cDNA; 3663 BP.
XX
AC ABN81320;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human mast cell related gene MC14 SEQ ID NO 3.
KW Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
KW vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 294..746
FT /*tag= a
FT /product= "MC14-1"
FT 1238..2218
FT /*tag= a
FT /product= "MC14-2"
XX
PN W0200246389-A2.

XX 13-JUN-2002. 57
 XX 07-DEC-2001; 2001WO-US46180. 57
 XX 08-DEC-2000; 2000US-251835P. 57
 XX 14-MAR-2001; 2001US-275479P. 57
 XX 28-MAR-2001; 2001US-279115P. 57
 XX 02-APR-2001; 2001US-280143P. 57
 XX (UNIO) UCB SA. 57
 XX Nocka K, Pirozzi G, Einstein R; 57
 XX WPI; 2002-508560/54. 57
 XX P-PSDB; ABB77570, ABB77571. 57
 XX Novel isolated nucleic acids that are differentially expressed in mast 57
 XX cells in patients with allergic hypersensitivity, encoding proteins 57
 XX associated with mast cell degranulation and allergic hypersensitivity 57
 XX Claim 1; Page 98-102; 119pp; English. 57
 XX The invention relates to isolated nucleic acid (ABN81319-ABN81324), 57
 XX corresponding to genes differentially expressed in mast cells following 57
 XX activation or in patients with allergic hypersensitivity disease, (I) 57
 XX that encodes proteins (ABN7569-ABN7575) (II) or a protein fragment of 57
 XX (II) if at least 6 amino acids. (II) is useful for identifying binding 57
 XX partners. (I) or (II) is useful for diagnosing or treating a disease 57
 XX state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma, 57
 XX urticaria or atopic dermatitis or mastocytosis) in a subject which 57
 XX involves determining the level of expression of (I) or (II). A computer 57
 XX system, comprising a database containing information identifying the 57
 XX expression level in a tissue or at least one mast cell of (I), is useful 57
 XX for presenting information to identify the relative expression level of 57
 XX (I). (II) is used as a marker to detect, diagnose or identify an allergic 57
 XX response in a patient. The protein can also serve as a target that 57
 XX modulate gene expression or activity and as an antigen to raise 57
 XX polyclonal or monoclonal antibodies. (II) is useful for identifying 57
 XX agents that modulate expression of the protein or agents, such as 57
 XX agonists or antagonists. The agonists or antagonists are useful for 57
 XX modulating biological activity and function of (II) and thus are useful 57
 XX for alleviating disease conditions such as allergic hypersensitivity, 57
 XX seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis. 57
 XX Sequence 3663 BP; 740 A; 1058 C; 985 G; 880 T; 0 other; 57
 SQ Alignment Scores: 3663 Length: 3663
 Pred. No.: 3,78e-118 Matches: 3663
 Score: 1604.00
 Percent Similarity: 43.11% Conservative: 0
 Best Local Similarity: 43.11% Mismatches: 2
 Query Match: 56.06% Indels: 479
 DB: 24 Gaps: 2
 US-09-593-793A-113 (1-553) x ABN81320 (1-3663)
 Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
 Db 294 ATGGTCACAGAGGCTGTGGGTGAGCGCGCTGTGGCGCACCGGAAAGCCAGCTCTTGCTG 353
 Qy 21 ValAsnLeuLeuThrPheGlyValGluValCysLeuAlaGlyIleThrTyrValPro 40
 Db 354 GTCACACCTGCCTTGGCGCTGGAGGTGTGGTGGCGGAGGATCATACATATGTGGCG 413
 Qy 41 ProLeuLeuGluValGlyValGluValCysLeuAlaGlyIleThrTyrValPro 40
 Db 414 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGAGTTCATGACCATGGTGCT--GGGTGAGTC 472
 Qy 57 ----- 57
 Db 473 ACTACATCCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 532

Qy 57 ----- 57
 Db 533 CCTCTGCCCTGGAGCTGCTTGGAGGGAGAGGTGGTCTGCTGGNAGGCATTGCTGGGCA 592
 Qy 57 ----- 57
 Db 593 GGAGGGTGACCTGGCTGGGCTGAGGGGGCACACCAAGAGAAAGAGAATACCAAGACATA 652
 Qy 57 ----- 57
 Db 653 CCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 712
 Qy 57 ----- 57
 Db 713 AAATGCTCTTAACCTTTGGCTAGCCCTTTTATATATAGGATTAATCTATTATATGC 772
 Qy 57 ----- 57
 Db 773 TTACAACCAACCATTTGAGGTGATCCATTTTACAGAGAAGGAGAGAGGCTTTTAAAGAG 832
 Qy 57 ----- 57
 Db 833 TTAGGTAACTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCA 892
 Qy 57 ----- 57
 Db 893 GGTCTCCAGCGGAGCTTGTCTTACCCCTAGGACAAAGGGTGGACTCTGACTCTGCA 952
 Qy 57 ----- 57
 Db 953 GATAAATTTACAAAAGCCACAGAAGCAAGTAGTAACCATTTGTGTGACACCCCTCACC 1012
 Qy 57 ----- 57
 Db 1013 CCCAGGAAGAGGGGCCCTGTGAGGATTTGCAGGCTCTGGAGTCACTGCTTGTGTAAC 1072
 Qy 57 ----- 57
 Db 1073 GCTGCCCTTACCCTCCCTAGGTCTGGCCCTTTGNAATAGTATCACTTCTTAGTTGCTCC 1132
 Qy 57 ----- 57
 Db 1133 ATGCTCAGTTTGTCCATCTGAAATGGGGCATCTGTAATGCCTGTGTATGAGGAGTA 1192
 Qy 57 ----- 57
 Db 1193 AATTACAGCATCCCTGTGAAGACGCTAGCACAGTGTCCAGTACGGAATGTTATTTCCATPC 1252
 Qy 57 ----- 57
 Db 1253 TTCTCACGGAGCTTGGTTCCCTTCCCTTCCCTTGTCTTGTCCCAGCCATTGACTCAT 1312
 Qy 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
 Db 1313 ACTACTTCCCTTCTTGCAGGCATTTGGTCCAGTGTGGGCTGGTCTGTGTCCTCCTA 1372
 Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
 Db 1373 GGCTCAGCCAGTGACCACTGGCGTGGAGCGTATGGCGCCGCCGCCCTTCATCTGGGCA 1432
 Qy 92 LeuSerLeuGlyIleLeuLeuSerPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
 Db 1433 CTGTCTTGGGCATCTCTGCTGAGCCTCTTCTCATCCCAAGGGCGGCTGGCTAGCAGG 1492
 Qy 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeu 131
 Db 1493 CTGCTGTGGCGGATCCAGGCCCTTGAGCTGGAGCTGCTCATCTCTGGGCGTGGGCTG 1552
 Qy 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
 Db 1553 CTGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTTTC 1612

QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
DB 1613 CGGGACCCGACCACTGTGCGCAGGCTACTCTGTATGCTTATGATCATGCTTTGGG 1672
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
DB 1673 GGTGCTGGCTTACCTCTGCTGCAATGACTGGGACACAGTGCCCTGGCCCTTAC 1732
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
DB 1733 CTGGGCACCCAGGAGTGCCCTTTTGGCTGCTCACCTCATCTTCTCCTCGGTA 1792
QY 212 AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
DB 1793 GCAGCCACACTGCTGTGCTGAGGAGCAGGCTGGGCCCCACCGCAGCAGAGGG 1852
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaAlaArgLeuAlaPheArg 251
DB 1853 CTGTGCGCCCTCTGCTGTGCGCCCACTGCTGTCCATGCCA----- 1893
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
DB 1893 ----- 1893
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
DB 1893 ----- 1893
QY 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
DB 1893 ----- 1893
QY 312 GluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGln 331
DB 1893 ----- 1893
QY 332 CysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThr 351
DB 1893 ----- 1893
QY 352 ArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeu 371
DB 1893 ----- 1893
QY 372 SerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAla 391
DB 1893 ----- 1893
QY 392 LeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeu 411
DB 1893 ----- 1893
QY 412 ProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPhe 431
DB 1893 ----- 1893
QY 432 LeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySer 451
DB 1894 -----GGCCCTAAGCCTGGACCTCCCTTCCCTANTGGACAGTGGTGGTGGAGCAGT 1947
QY 452 GlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArg 471
DB 1948 GGCCGTGCTCCCACTCCACCCCGCTGCTGGGGGCTGCTGCTGTGATGCTCTCCGTAGT 2007
QY 472 ValValValGlyGluProThrGluAlaArgValValProGlyArgGlyLeuCysLeuAsp 491
DB 2008 GTGGTGGTGGGTGGACCCACCGAGCGGAGGTGGTTCGGGGCGGGGATCTGCTGGAC 2067
QY 492 LeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGly 511
DB 2068 CTCGCCATCCTGGATAGTGCCTTCTGCTGCTCCAGGTGGCCCATCCTGTTATGGGC 2127
QY 512 SerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGly 531

DB 2128 TCCATTGTCAGCTCAGCCAGTCTGTCACTGGCTATATGTTCTGCCGACGCTGGGT 2187
QY 532 LeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyr 551
DB 2188 CTGGTGGCCATTACTTTGCTACACAGGATAGTATTGTACACAGGACTTGGCCAATAC 2247
QY 552 SerAla 553
DB 2248 TCAGCG 2253
RESULT 31
AAS64153
ID AAS64153 standard; cDNA; 1203 BP.
XX
AC AAS64153;
XX 29-JAN-2002 (first entry)
XX Human /M. tuberculosis fusion protein RA12-P50IS-E2 cDNA.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Chimeric - Homo sapiens.
OS Chimeric - Microbacterium tuberculosis.
XX WO200173032-A2.
XX 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US09919.
PR 07-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI: 2001-639232/73.
DR P-PSDB; AAU69907.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Example 17; Page 542-543; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.
SQ Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;


```
Alignment Scores:
Pred. No.: 9.07e-103 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 22 Gaps: 1

US-09-593-793A-113 (1-553) x AAS64153 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----lleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCCGAGGACCCCGCCGGAATTCATCACCATTGTCGCCCTCTGCTGTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGTAGAGGAGAGTTTCATGACCATGGTGTGGGCATTGGTCCAGTGGTGGC 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyTyrGlyArg 84
Db 499 CTGGTCTGTGTCGCCCTCTAGGCTCAGCCAGTGCAGCTGGCGTGGAGCGTATGGCCGC 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTCATCTGGGCACCTGCTTGGGCATCTCTGTCGACCTCTTTCTCATCCCA 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGCCGGCTGCTAGCAGGCTGCTGTGCCCGGATCCAGCGCCCTGGAGCTGGCAGCTG 678
Qy 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCTGGCGTGGGCTCTGGACTCTGTGCCAGGTGTGCTTCACTCCACTGGAG 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGTCTCTGACCTCTCCGGACCCGACCACTGTCCACAGGCTACTCTGTCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATGATCAGTCTTGGGGGTGCTGTGGCTACCTTCCTGCTGCCATTGACCTGG 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTTGCCCTACCTGGCACCCAGGAGGAGTGCCTTTTGGCTGCTCAC 918
Qy 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAlaLeuGly 224
Db 919 CTCATCTTCTCAGCTGGTACGACACACTGTGTGTGGTGGTGGAGGAGCGCTGGC 978
Qy 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAGAGGCTGTGCGCCCTTGTGTGTCGCCCTCTGCTGTCCATG 1038
Qy 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGCGCCGCTTGGCTTCCGGAACCTGGCGCCCTGTCTCCCGGCTGCACCGCTGTC 1098
Qy 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGCCGCATGCCCGCACCTCGCGCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGCA 1158
Qy 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTTTACACGAGATTCGTGGCGGAG 1200

RESULT 32
AAH93917
ID AAH93917 standard; cDNA; 1203 BP.
XX
AC AAH93917;
XX
DT 04-OCT-2001 (first entry)

XX
DE Ra12-P501s-E2 construct cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 8; Page 504; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;

Alignment Scores:
Pred. No.: 9.07e-103 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 22 Gaps: 1

US-09-593-793A-113 (1-553) x AAH93917 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----lleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCCGAGGACCCCGCCGGAATTCATCACCATTGTCGCCCTCTGCTGTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGTAGAGGAGAGTTTCATGACCATGGTGTGGGCATTGGTCCAGTGGTGGC 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyTyrGlyArg 84
Db 499 CTGGTCTGTGTCGCCCTCTAGGCTCAGCCAGTGCAGCTGGCGTGGAGCGTATGGCCGC 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTCATCTGGGCACCTGCTTGGGCATCTCTGTCGACCTCTTTCTCATCCCA 618
```


Db 559 GCGCGGCCCTTCACTGGGCACTGTCCTTGGGCATCTCCGCTGAGCCCTCTTCTCATCCCA 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGCGCGCTGGCTAGCAGGCTGCTGTGCCGGATCCAGGCCCTCGAGCTGGCACTG 678
Qy 125 LeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCTCTGGCGCTGGCTGCTGACTTCTGTGCCAGGTGTGCTTCACTCCACTGGAG 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGTGACCTCTCCGGAGCCCGACCACTGTCCGAGCCCTACTCTGTCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCCTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTCTGCTGCCATTTGACTGGAC 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTTGGCCCTTACCTGGGCACCCAGGAGGAGTGCTCTTTGGCTGCTCACC 918
Qy 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaLeuGly 224
Db 919 CTCATCTCTCTACCTGCTGTAGCAGCCACACTGCTGTGTGGTGGAGGAGCGCTGGGC 978
Qy 225 ProThrGluProAlaGluLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAGAGGCTGTGGCCCCCTCTTGTGCCCCACTGCTGTCCATGC 1038
Qy 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGCGCGCTGGCTTCCGGAACCTGGCGCCCTGCTTCCCGGCTGCACCACTGTGC 1098
Qy 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGGCGCATGCCCGCCACCTCGCGCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGCA 1158
Qy 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTGTTTACAGGATTCGTGGCGCAG 1200
RESULT 34
AAC64928
ID AAC64928 standard; DNA; 2133 BP.
XX
AC AAC64928;
XX
XX 07-FEB-2001 (first entry)
XX Human prostate-related PS108 partial coding sequence SEQ ID NO: 16.
XX Human: prostate cancer; PS108; antibody; tumour; metastasis; ds.
XX Homo sapiens.
XX US6130043-A.
XX 10-OCT-2000.
XX 01-MAY-1998; 98US-00711710.
XX 02-MAY-1997; 97US-0850713.
XX (ABBO) ABBOTT LAB.
XX Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
PI Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
PI Kratochvil JD, Russell JC, Hodges SC;
XX WPI; 2000-655655/63.
XX
XX Methods for detecting target prostate-specific polynucleotides or

PT diseases of the prostate (e.g. prostate cancer), comprising detecting
PT the presence of any of PS108 nucleic acid sequences in a test sample -
XX Claim 1; Column 77-80; 55pp; English.
XX
CC The present invention is related to a number of partial coding and
CC protein sequences for the human prostate tissue protein PS108. These
CC sequences can be used in the diagnosis and prognosis of prostate
CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.
XX
SQ Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;

Alignment Scores:
Pred. No.: 3,78e-93 Length: 2133
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
Gaps: 0
DB: 21

US-09-593-793A-113 (1-553) x AAC64928 (1-2133)
Qy 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACCAAGGGCTGCCAGAGCTGAGCGGGCAGGCGGAGACATATCAT 61
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGCTCGGATGGGCGAGCTGGGGCTGTCTCTGTCAGTGGCCATCTCCCTGGCTCTC 121
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGCTGGTGCAGGATTCGACATCGAGCAGTCTATTGGCCAGT 181
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
Db 182 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCACATGCCTGTCCACAGTGTGGCGTGGTG 241
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCGCTCCACGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 301
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCAACCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACT 361
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGTGCTAGCAGTGAGGACAGCTGATGACAGCTTCTGCCAGGCCCTTAAGCCTGGA 421
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTTAATGGACACGTGGTGTGGAGCAGTGGCTGTCTCCACCTCCACCC 481
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 482 GCGCTCTCGGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGGGAGCCCAACC 541
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGTGGTTCGGGGCGGGGCATCTGCTGGAGCTGCCATCTCGATAGTGCC 601
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCCTGTGTCCAGGTGGCCCATCTCTGTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCTATATGGTGTCTGCCGAGGCTGGGTCTGGTCGCCATTTACTTTGCT 721
Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 2..769
 FT /*tag= a
 FT
 XX
 PN WO9850567-A1.
 XX
 XX
 PD 12-NOV-1998.
 XX
 PF 01-MAY-1998; 98WO-US08930.
 XX
 XX 02-MAY-1997; 97US-0850713.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 XX WPI; 1999-034731/03.
 DR P-PSDB; AAW85068.
 DR
 XX New isolated prostate-specific polynucleotides - used to develop
 PT products for the diagnosis and treatment of prostate diseases, e.g.
 PT benign hyperplasia, prostatic or prostate cancer
 XX
 PS Claim 1; Fig 1A-B; 122pp; English.
 XX
 CC The present sequence represents the consensus sequence for a PS108
 CC gene. The sequence is derived from overlapping clones AAV71166-79. The
 CC clone sequences are PS108 gene-specific. They are used in the method
 CC of the invention. The specification describes a method for detecting the
 CC presence of a target PS108 polynucleotide in a test sample. The method
 CC comprises contacting the test sample with at least 1 PS108-specific
 CC polynucleotide or complement, and detecting the presence of the target
 CC PS108 polynucleotide. The products can be used for detecting,
 CC diagnosing, staging, monitoring, prognosticating, in vivo imaging,
 CC preventing or treating, or determining predisposition to diseases or
 CC conditions of the prostate such as benign prostatic hyperplasia (BPH),
 CC prostatitis, prostatic intraepithelial neoplasia (PIN) and cancer. In
 CC particular the products can be used in drug screening and gene therapy.
 XX
 SQ Sequence 2152 BP; 419 A; 622 C; 569 G; 542 T; 0 other;

Alignment Scores:
 Pred. No.: 3.83e-93 Length: 2152
 Score: 1287.00 Matches: 255
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 44.98% Indels: 0
 DB: 20 Gaps: 0

US-09-593-793A-113 (1-553) x AAV71181 (1-2152)

QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
 Db 2 GGGCTGTACACAGGGCGTGCCAGAGCTGAGCGGGCCGACCGAGCGCCGGAGACATATGAT 61
 QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
 Db 62 GAAGCGTTCGGATGGCAGCGCTGGGGCTGTTCCTGTCAGTGGCCATCTCCCTGGCTTC 121
 QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
 Db 122 TCTCTGGTCATGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTATTTTGGCCAGT 181
 QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
 Db 182 GTGGCAGCTTCCCTGTGGCTGGCTGCCACATGCCCTGTCCACAGTGTGGCCGTGGTG 241
 QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
 Db 121

Db 242 ACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTCGAGATCTGCCCTACACA 301
 QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
 Db 302 CTGGCCTCCCTCTACACCGGAGAGAGGAGGTTCCTCCCAATACCGAGGGGACACT 361
 QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
 Db 362 GGAGGTGTAGCAGTGAGGACAGCCTGATGACCACTTCTCCAGGCCCTAAGCCTGGA 421
 QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
 Db 422 GCTCCCTTCCCTAATGGACACCGTGGGTGCTGGAGGACGTGGCTGCTCCACCTCCACC 481
 QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValAlaGluValValGlyGluProThr 478
 Db 482 GGGCTGTGGGGGCTCTGCCCTGTGATGTCCTCCGACGTGTGGTGGTGGAGCCACC 541
 QY 479 GluAlaArgValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
 Db 542 GAGGCCAGGTGTTCCGGCGCGGGCATCTCGCTGGACCTCGCCATCTCGATAGTGC 601
 QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
 Db 602 TTCTCTGCTGTCCAGGTGGCCCATCCCTGTTTATGGGTCCATTGTCAGTCCAGCCAG 661
 QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
 Db 662 TCTGTACCTGCTATATGTGTCTCCGAGCGCCCTGGGTCTGGTCCCATTTACTTTGCT 721
 QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
 Db 722 ACACAGGTAGTATTGTGACAAAGACGACATGGGCCAAATACTCAGCG 766
 RESULT 37
 AAC64927
 ID AAC64927 standard; DNA; 2124 BP.
 XX
 AC AAC64927;
 XX
 XX 07-FEB-2001 (first entry)
 DT Human prostate-related PS108 partial coding sequence SEQ ID NO: 15.
 DE Human; prostate cancer; PS108; antibody; tumour; metastasis; ds.
 KW Homo sapiens.
 OS US6130043-A.
 PN 10-OCT-2000.
 PD 01-MAY-1998; 98US-0071710.
 PF 02-MAY-1997; 97US-0850713.
 PR (ABBO) ABBOTT LAB.
 PA Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
 PI Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
 PI Kratochvil JD, Russell JC, Hodges SC;
 DR WPI; 2000-655655/63.
 XX Methods for detecting target prostate-specific polynucleotides or
 PT diseases of the prostate (e.g. prostate cancer), comprising detecting
 PT the presence of any of PS108 nucleic acid sequences in a test sample -
 PS Claim 1; Column 75-78; 55pp; English.
 XX The present invention is related to a number of partial coding and
 CC protein sequences for the human prostate tissue protein PS108. These
 CC sequences can be used in the diagnosis and prognosis of prostate

CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.

XX SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:

Pred. No.: 8.56e-92 Length: 2124
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AAC64927 (1-2124)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
DB 3 CAGGGCGTCCCGAGAGCTGAGCGGGCAGCGAGCGCCGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
DB 63 CGGATGGGAGCTGGGGCTGTCTTCGACAGTGGCCATCTCCCTGGTCTCTCTCGTTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
DB 123 ATGGACCGGCTGGTGCAGGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
DB 183 TTCCTGTGGTGGCGGTGCCATATCCCTGTCCACAGTGTGGCGGTGGACAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
DB 243 GCGCCCTCACCGGTTCACCTTCTCAGCCCTGCACATCTGCCCTACACACTGGCGCTCC 302
QY 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
DB 303 CTCTACACCGGAGAAGCAGGTGTCTCTGCCAAATACCGAGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProphe 441
DB 363 AGCAGTGGAGACAGCTGATGACCACTTCTCCTGCCAGGCCCTAAAGCTGGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlyLysSerGlyLeuLeuProProProAlaLeuCys 461
DB 423 CCTAATGGACAGCTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
DB 483 GGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
DB 543 GTGTTTCCGGGGCGGGCATCTGCTTGGACCTGGCCATCTGGATAGTCCCTTCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
DB 603 TCCAGGTGGCCCATCTCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAGCTGTCAC 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
DB 663 GCCTATATGGTGTCTGCCGAGCGCTGGGTCTGGTGGCCATTACTTTGCTACACAGGTA 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 723 GTATTTGACAAGAGCAGCTTGGCCAAATACTCAGCG 758
RESULT 38
AA507601
ID AA507601 standard; cDNA; 2124 BP.
XX
AC AA507601;

XX DT 23-OCT-2001 (first entry)
XX DE Prostate gene PS108-specific cDNA clone 1711346IH.
DE KW Prostate; PS108; immunogen; drug screening; image localisation;
KW diagnostic; therapeutic; prostate tissue disease; cancer; metastasis;
KW expressed sequence tag; EST; ss.
XX OS Homo sapiens.
XX PN US6252047-B1.
XX PD 26-JUN-2001.
XX PF 15-MAR-2000; 2000US-0525397.
XX PR 01-MAY-1998; 98US-0071710.
PR 02-MAY-1997; 97US-0850713.
XX (ABBO) ABBOTT LAB.
XX PA Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD, Yu H;
XX WPI: 2001-424488/45.
XX PT Novel PS108 polypeptide useful in assays for detecting antibodies to
PT prostate tissue, and as immunogens to produce PS108 antibodies -
XX Example 1; Fig 1; 55pp; English.
XX CC The sequence represents the coding sequence of prostate gene PS108 -
CC specific expressed sequence tag (EST) cDNA clone 1711346IH. The sequence
CC was used along with other overlapping cDNA clones to produce a full
CC length consensus sequence (see AA507155). This sequence could then be
CC used to produce PS108 polypeptides which are useful in assays for
CC detecting antibodies to prostate tissue, and as immunogens to produce
CC antibodies. The polypeptide is useful for screening compounds which
CC specifically bind to the polypeptide and for screening for drugs,
CC compounds, or any other agent which can be used to treat diseases
CC associated with PS108. The antibody is useful to detect, or for image
CC localisation of PS108 antigen in a patient, for detecting or diagnosing a
CC disease or condition, as delivery agents for therapeutic agents as well
CC as for diagnostic tests and for screening for diseases or conditions
CC associated with PS108, especially cancer. The antibody is also useful for
CC generating chimeric antibodies for therapeutic use, for inhibiting the
CC biological activity of PS108, in therapy (for e.g. to treat prostate
CC tissue disease including prostate cancer and its metastases), and to
CC detect the presence of any polypeptide in a test sample which shares one
CC or more antigenic determinants with the PS108 polypeptide.
XX SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:

Pred. No.: 8.56e-92 Length: 2124
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AA507601 (1-2124)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
DB 3 CAGGGCGTCCCGAGAGCTGAGCGGGCAGCGAGCGCCGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
DB 63 CGGATGGGAGCTGGGGCTGTCTTCGACAGTGGCCATCTCCCTGGTCTCTCTCGTTC 122

OY 342 MetAspArgLeuValGlnAArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
 DB 123 ATGGACCGGCTGGTCAGCGATTCCGGCACTCGAGCAGTCTATTTCGCCAGTGTGGCAGCT 182
 OY 362 PheProValAlaAlaGlyAlaValThrCysLeuSerHisSerValAlaValValThrAlaSer 381
 DB 183 TTCCTGTGGCTGGCGGTGGCACATGCTGCTCCACAGTGTGGCGGTGGTGCACAGCTTCA 242
 OY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
 DB 243 GCCGCCCTCACCGGCTTCCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCC 302
 OY 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
 DB 303 CTCTACCAACCGGGAGAGAGCGTGTCTCTGCCAATACCGAGGGGACACTGGAGGTGCT 362
 OY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
 DB 363 AGCAGTAGGACAGCTGATGACCACTCTCTCCAGCGCCCTTAAGCCTGGAGCTCCCTTC 422
 OY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
 DB 423 CCTAATGGACAGCTGGGTGCTGGAGGCACTGGCTCCACCTCCACCGCGCTCTGC 482
 OY 462 GlyAlaSerAlaCysAspValSerValArgValValValValGluProThrGluAlaArg 481
 DB 483 GGGGCTCTGCTGTGATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 542
 OY 482 ValValProGlyArgGlyGlyCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
 DB 543 GTGGTTCGGGCGGGGATCTGCTGGACCTCGCCATCTCCGATAGTGGATTCCTGCTG 602
 OY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
 DB 603 TCCAGAGTGGCCCATCCCTGTTATGGCTCCATTGTCCAGCTCAGCAGCTGTCTACT 662
 OY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
 DB 663 GCCTATATGGTGTCTGCGCGCAGCGCTGGGTGCTGGTGGTGGTGGTGGTGGTGGTGGT 722
 OY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
 DB 723 GTATTGACAGAGCGACTTGCCCAATACTACGCG 758
 RESULT 39
 AAV71180
 ID AAV71180 standard; cDNA; 2143 BP.
 XX
 AC AAV71180;
 XX
 DT 12-FEB-1999 (first entry)
 XX
 DE Clone 1711346IH, the PS108 gene contig full length sequence.
 XX
 KW PS108 gene; prostate disease; benign prostatic hyperplasia; BPH;
 RW prostatitis; prostatic intraepithelial neoplasia; PIN; cancer;
 XX drug screening; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FN W09850567-A1.
 XX
 PD 12-NOV-1998.
 XX
 PF 01-MAY-1998; 98WO-US08930.
 XX
 FR 02-MAY-1997; 97US-0850713.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI; 1999-034731/03.
 DR
 XX New isolated prostate-specific polynucleotides - used to develop
 PT products for the diagnosis and treatment of prostate diseases, e.g.
 PT benign hyperplasia, prostatic or prostate cancer
 XX
 PS Claim 1; Fig 1A-E; 122pp; English.
 XX
 CC The present sequence represents the full length contig of the PS108
 CC gene, as represented by clone 1711346IH. This clone is the contig of
 CC overlapping clones AAV71166-79. The clone sequences are PS108
 CC gene-specific. They are used in the method of the invention. The
 CC specification describes a method for detecting the presence of a
 CC target PS108 polynucleotide in a test sample. The method comprises
 CC contacting the test sample with at least 11 PS108-specific polynucleotide
 CC or complement, and detecting the presence of the target PS108
 CC polynucleotide. The products can be used for detecting, diagnosing,
 CC staging, monitoring, prognosticating, in vivo imaging, preventing or
 CC treating, or determining predisposition to diseases or conditions of
 CC the prostate such as benign prostatic hyperplasia (BPH), prostatitis,
 CC prostatic intraepithelial neoplasia (PIN) and cancer. In particular the
 CC products can be used in drug screening and gene therapy.
 XX
 SQ Sequence 2143 BP; 418 A; 621 C; 563 G; 541 T; 0 other;
 Alignment Scores:
 Pred. No.: 8.66e-92 Length: 2143
 Score: 1270.00 Matches: 252
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 44.39% Indels: 0
 DB: 20 Gaps: 0
 US-09-593-793a-113 (1-553) x AAV71180 (1-2143)
 OY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
 DB 3 CAGGGCGTGGCCAGAGCTGAGCGGGCACCGAGGGCCGGAGACACTATGATGAAGCGCTT 62
 OY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
 DB 63 CGGATGGGCGAGCGTGGGCTGTCTCTGAGTGGCGCATCTCCCTGGTCTCTCTGTGTC 122
 OY 342 MetAspArgLeuValGlnAArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
 DB 123 ATGGACCGGCTGGTCAGCGATTCCGGCACTCGAGCAGTCTATTTCGCCAGTGTGGCAGCT 182
 OY 362 PheProValAlaAlaGlyAlaValThrCysLeuSerHisSerValAlaValValThrAlaSer 381
 DB 183 TTCCTGTGGCTGGCGGTGGCACATGCTGCTCCACAGTGTGGCGGTGGTGCACAGCTTCA 242
 OY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
 DB 243 GCCGCCCTCACCGGCTTCCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCC 302
 OY 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
 DB 303 CTCTACCAACCGGGAGAGAGCGTGTCTCTGCCAATACCGAGGGGACACTGGAGGTGCT 362
 OY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
 DB 363 AGCAGTAGGACAGCTGATGACCACTCTCTCCAGCGCCCTTAAGCCTGGAGCTCCCTTC 422
 OY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
 DB 423 CCTAATGGACAGCTGGGTGCTGGAGGCACTGGCTCCACCTCCACCGCGCTCTGC 482
 OY 462 GlyAlaSerAlaCysAspValSerValArgValValValValGluProThrGluAlaArg 481
 DB 483 GGGGCTCTGCTGTGATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 542
 OY 482 ValValProGlyArgGlyGlyCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501

XX AAV61144;
 XX 06-JAN-1999 (first entry)
 XX 3' cDNA sequence of prostate tumour clone L1-12.
 DE Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
 KW Homo sapiens.
 XX WO9837093-A2.
 XX 27-AUG-1998.
 XX 25-FEB-1998; 98WO-US03492.
 XX 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1997; 97US-0806596.
 PR 01-AUG-1997; 97US-0904804.
 XX (CORI-) CORIXA CORP.
 XX Dillon DC, Xu J;
 PI WPI; 1998-609886/51.
 DR Polypeptides comprising immunogenic portions of prostate proteins -
 PT used in a vaccine for the treatment of prostate cancer
 XX Claim 3; Page 38-39; 130pp; English.
 PS The present sequence is a new DNA which encodes an immunogenic portion
 XX of a prostate tumour protein. The encoded immunogen, or the DNA itself,
 CC can be used as a vaccine for the treatment of prostate cancer. The DNA
 CC was identified by analysis of a subtracted cDNA library obtained by
 CC subtracting a prostate tumour cDNA expression library with a normal
 CC tissue cDNA library.
 XX Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
 SQ

Alignment Scores:
 Pred. No.: 2,49e-64 Length: 789
 Score: 919.00 Matches: 192
 Percent Similarity: 96.50% Conservative: 1
 Best Local Similarity: 96.00% Mismatches: 7
 Query Match: 32.12% Indels: 2
 DB: 19 Gaps: 0

US-09-593-793A-113 (1-553) x AAV61144 (1-789)

OY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
 Db 3 GTCATNTGGCCAGTGGCAGCTTCCCTGTGGCTGGCCGTCACATGCTGTCCAC 62

OY 374 SerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
 Db 63 AGTGTGGCCGGTGGACAGCTTCACCGCCCTCACCAGGTTCACCTTCTCAGCCCTGCAG 122

OY 394 lleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
 Db 123 ATCCCTGCCCTACACTGGCCTCCCTACCACCGGGAGAGCAGGTCTCTCGCCCAA 182

OY 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
 Db 183 TACCAGGGGACACTGGAGGTGTAGCAGTAGGACAGCCCTGATGACAGCTTCTCGCA 242

OY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
 Db 243 GCCCTTAAGCCTGGAGCTCCCTTCCCTAATGACACGTGGGTGGAGGAGTGGCCGTG 302

OY 454 LeuProProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
 DB: |||||||

Db 303 CTCCACCTCCACCGCGCTCTGCGGGCGCTCTGCTGTGATGTCTCCGTAGTGTGGT 362
 OY 474 ValGlyGluProThrAlaAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
 Db 363 GTGGGTGAGCCACCGANGCAGGTGGTTCGGGCCGGGGCATCTGCTGGACCTCGCC 422
 OY 494 lleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
 Db 423 ATCCCTGGATAGTC-TTCTCTGCTGCCANGTGGCCCATCCCTCTTTATGGCTCCATT 481
 OY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
 Db 482 GTCCAGCTCAGCCAGCTGTCTCACTATATGTTGTTGCGCGAGGCTGGGTCTGTC 541
 OY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
 Db 542 CC-ATTTACTTGTGTACACAGGTANTATTGACAAGACAGTGGCCCAATACTACGCG 600

RESULT 42
 AAV58487
 ID AAV58487 standard; cDNA: 789 BP.
 XX
 AC AAV58487;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE 3' fragment of prostate tumour specific gene L1-12.
 XX Prostate tumour specific gene; human; prostate cancer; detection;
 KW therapy; ss.
 XX Homo sapiens.
 XX WO9837418-A2.
 XX 27-AUG-1998.
 XX 25-FEB-1998; 98WO-US03690.
 PR 09-FEB-1998; 98US-0904809.
 PR 25-FEB-1997; 97US-0806596.
 PR 01-AUG-1997; 97US-0904809.
 XX (CORI-) CORIXA CORP.
 XX Dillon DC, Xu J;
 XX WPI; 1998-480805/41.
 XX Novel human prostate specific tumour protein and fragments - useful
 PT for detecting and treating prostate cancers
 XX Claim 1; Page 39; 141pp; English.
 XX This sequence represents a human prostate tumour specific gene, and can
 CC be used in the method of the invention. The method is for detecting
 CC prostate cancer comprises contacting a biological sample with an agent
 CC able to bind an immunogenic portion of a prostate protein (such as
 CC encoded by this sequence). An antibody which binds to an immunogenic
 CC portion of the prostate protein, and the method can be used to detect,
 CC monitor progression of, or treat prostate cancers. The antibody may
 CC also be conjugated to a therapeutic agent for use in therapy of prostate
 CC cancers.
 XX Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
 SQ

Alignment Scores:
 Pred. No.: 2,49e-64 Length: 789
 Score: 919.00 Matches: 192
 Percent Similarity: 96.50% Conservative: 1
 Best Local Similarity: 96.00% Mismatches: 7
 Query Match: 32.12% Indels: 2
 DB: 19 Gaps: 0

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US-09-593-793A-113 (1-553) x AA058487 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGCCAGTGGCAGCTTTCCCTGTGGCTGGCGTGGCCACATGCTGCCCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTACAGCTTTCAGCGCCCTCAGCGGCTTCCACCTTCTCAGCGCTGCGAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlnValPheLeuProLys 413
Db 123 ATCTTCCCTACACACTGGAGCTGCTTACACCGCGGAGAGCAGGTGTCTGCCCCAAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGCTAGCAGTAGGACAGCCTGATGACCAGCTTCTCGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTTAAGCTGGAGCTTCCCTTCCCTATATGACACGTGGGTGCTGGAGGAGTGGCCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCCACTCCACCGCGCTCTCGGGGCTCTGCGTGTGATGCTCTCCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGCTGCTGGCGCGGGGATGCTGCTGGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCCTGGATAGTGC-TTCCTGTGTCCTCCANGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTACTGCTATATGGTGTCTGCGCGAGGCTGGGTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAlaAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTCTACACAGGTANTATTGACAGACGANTTGGCCAAATACTCAGCG 600

RESULT 43
AAA06250
ID AAA06250 standard; cDNA; 789 BP.
XX AC
XX AC AAA06250;
XX DT 13-JUN-2000 (first entry)
XX DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:10.
XX KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX KW immunogenic; cytostatic; vaccine; ss.
XX OS Homo sapiens.
XX PN WO200004149-A2.
XX PD 27-JAN-2000.
XX PF 14-JUL-1999; 99WO-US15838.
XX PR 14-JUL-1998; 98US-0115453.
XX PR 14-JUL-1998; 98US-0116134.
XX PR 23-SEP-1998; 98US-0159812.
XX PR 23-SEP-1998; 98US-0159822.
XX PR 15-JAN-1999; 99US-0232149.
XX PR 15-JAN-1999; 99US-0232880.
XX PR 09-APR-1999; 99US-0288946.
XX PA (CORI-) CORIXA CORP.
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XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX PT New polypeptide useful for treating and diagnosing prostate cancer
XX PT comprises an immunogenic portion of prostate tumor protein -
XX PS Claim 1; Page 99; 263pp; English.
XX CC The present invention describes isolated polypeptides, comprising an
XX CC immunogenic portion of a prostate tumour protein (ptp). The polypeptides
XX CC and polynucleotides encoding them have cytostatic activity and can be
XX CC used in vaccines and in gene therapy. The polypeptides and
XX CC polynucleotides encoding them, antigen presenting cells which express
XX CC the polypeptides, antibodies against the polypeptides and vaccines
XX CC comprising them can be used for inhibiting the development of prostate
XX CC cancer in a patient. The polypeptides can be used to generate antibodies
XX CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
XX CC the polynucleotides encoding the polypeptides can be used as a probe or
XX CC to modulate the expression of the polypeptides. AAA06241 to AAA0691 and
XX CC AA082000 to AA082020 represent sequences used in the exemplification of
XX CC the present invention.
XX SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:
Pred. No.: 2,49e-64 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AAA06250 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGCCAGTGGCAGCTTTCCCTGTGGCTGGCGTGGCCACATGCTGCCCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTACAGCTTTCAGCGCCCTCAGCGGCTTCCACCTTCTCAGCGCTGCGAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlnValPheLeuProLys 413
Db 123 ATCTTCCCTACACACTGGAGCTGCTTACACCGCGGAGAGCAGGTGTCTGCCCCAAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGCTAGCAGTAGGACAGCCTGATGACCAGCTTCTCGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTTAAGCTGGAGCTTCCCTTCCCTATATGACACGTGGGTGCTGGAGGAGTGGCCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCCACTCCACCGCGCTCTCGGGGCTCTGCGTGTGATGCTCTCCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGCTGCTGGCGCGGGGATGCTGCTGGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCCTGGATAGTGC-TTCCTGTGTCCTCCANGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTACTGCTATATGGTGTCTGCGCGAGGCTGGGTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAlaAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTCTACACAGGTANTATTGACAGACGANTTGGCCAAATACTCAGCG 600
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Db 542 CC-ATTTCATTGTACACAGGTANTATTGACAGAAGCAGTTTGCCCAATACTCAGCG 600
AAS63458

RESULT 44

ID AAS63458 standard; cDNA; 789 BP.

AC AAS63458;

DT 29-JAN-2002 (first entry)

DE Human prostate cDNA sequence #10.

XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

XX WO200173032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US09919.

XX 27-MAR-2000; 2000US-0536857.

XX 09-MAY-2000; 2000US-0568100.

XX 12-MAY-2000; 2000US-0570737.

XX 13-JUN-2000; 2000US-0593793.

XX 27-JUN-2000; 2000US-0605783.

XX 10-AUG-2000; 2000US-0636215.

XX 29-AUG-2000; 2000US-0651236.

XX 06-SEP-2000; 2000US-0657279.

XX 02-OCT-2000; 2000US-0679426.

XX 10-OCT-2000; 2000US-0685166.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 232-233; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.

XX SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:

Pred. No.: 2,49e-64 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS63458 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCATNTGGCCAGTGTGGCAGCTTTCCCTCTGGCTGCCGTGCACATGCTGTCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGCCCGTGGTGACAGCTTCAGCCGCCCTCACCAGGTTTCACCTCTCTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCTCCCTACACACTGGCCCTCTACCCACCGGAGAGCAGGTGTTCTCTGCCCAAA 182
QY 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTGCTAGCAGTGCAGGACAGCCTGATGACAGCTTCTCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGCTGGAGGAGTGGCCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCCACCTCCACCCGCCCTCTCGGGGCCCTCTGCTGTGATGCTCTCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGTGAGCCACCGAGGCCAGGTGGTTCGGGCCGGGCATCTGCCTGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGTGATAGTGC-TTCCTGCTGTCCCANGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyValVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTCACTGCCCTATATGTTGTTCTGCCGAGGCTGGGTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTTCATTGTGTACACAGGTANTATTGACAGAAGCAGTATGGCCAAATACTCAGCG 600

RESULT 45

AAS10009

ID AAS10009 standard; cDNA; 789 BP.

XX AAS10009;

XX 24-OCT-2001 (first entry)

XX Human prostate tumour cDNA L1-12 #1.

XX Human; prostate tumour protein; prostate cancer; ss.

XX Homo sapiens.

XX US6262245-B1.

XX 17-JUL-2001.

XX 25-FEB-1998; 98US-0030607.

XX 25-FEB-1997; 97US-0806099.

XX 01-AUG-1997; 97US-0904804.

XX 09-FEB-1998; 98US-0020956.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC;

XX WPI; 2001-440862/47.

XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient -

yy

PS Example 1; Column 32-33; 105pp; English.

XX

The sequence is a human prostate tumour cDNA which encodes a partial tumour protein. The DNA is useful for inhibiting the development of prostate cancer or for treating prostate cancer in a patient.

XX

SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:

Pre

Score:	919.00	Matches:	192
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Alignment Scores:

Pred. No.:	2,498-64	Length:	789
Score:	919.00	Matches:	192
Percent Similarity:	96.5%	Conservative:	1
Best Local Similarity:	96.0%	Mismatches:	7
Query Match:	32.1%	Indels:	2
DB:	22	Gaps:	0

Score:	919.00	Matches:	192
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Percent Similarity:	Conservative:
96.50%	

Best Local Similarity:	96.00%
Mismatches:	22/128

Query Match: 32.12%
Indels: 22
Caus: 22

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DB: 27
Gaps: 0
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US-09-593-793A-113 (1-553) x AAS10009 (1-789)

Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373

Db 3 GTCTATNTGGCCAGTGTTGGCAGCTTTCCTGTGGCTGCCGGTGCCACATGCCCTGTCCCAC 62

Qv 374 SerValAlaValValThrAlaSerAlaAlaLeuThrGlypHeThrPheSerAlaLeuGln 393

[illegible]

Db 63 AGTGTGCCGTGGTGACAGCTTCAGCCGCCCTCACGGGTTACCTTCTCAGCCCTGCAG 122

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QY 394 I I e L e u p r o t y r t h r l e u a l a s e r l e u t y r h i s a r g g l u l y s g l n v a l p h e l e u p r o l y s 413

Db 123 ATCCTGCCCTACACACTGGGCTCCCTCTACCCACGGGAGAGCAGGTGTTCCGTGCCCAA 182

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Qy 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeupro 433

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DB I83 TACCGAGGGACAC TGGAGGTGCTAGCAGT GAGGACAGCC T GATGACCAGCTT CCTGCCA 242

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Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCCTG 302

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Db 303 CTCCACCTCCACCCGGCTCTGCGGGCCTCTGCCGTGATGTCTCCGTACGTGTGGTG 362

Search completed: February 19, 2003, 03:53:21
Job time : 353 secs

Job time : 353 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:49:54 ; Search time 53 Seconds
(without alignments)
3199.854 Million cell updates/sec

Title: US-09-593-793a-113
Perfect score: 2861
Sequence: 1 MVORLWVSRLLRKQAQLL.....AIYFATQVWFDSKLAKYSA 553

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.spool/US09593793/runat_13022003_161309_21582/app_query.fasta_1.711
-DB=Issued_Patents_NA -QPMF=fastap -SUFFIX=tni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=45
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Database : Issued Patents_NA: *
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	100.0	3410	4	US-09-020-956-110
2	2861	100.0	3410	4	US-09-030-607-110
3	2861	100.0	3410	4	US-09-065-785-110
4	2861	100.0	3410	4	US-09-439-313-110
5	2861	100.0	3410	4	US-09-352-616A-110
6	2861	100.0	3410	4	US-09-602-877A-100
7	2861	100.0	3410	4	US-09-232-149A-110
8	2716.5	94.9	4034	4	US-09-605-785-704
9	2538.5	88.7	4894	4	US-09-605-785-702
10	2144	74.9	6976	4	US-09-605-785-705
11	1920.5	67.1	2904	4	US-09-605-785-703
12	1287	45.0	2152	3	US-09-071-710-16

13	1287	45.0	2152	4	US-09-525-397-16	Sequence 16, Appl
14	1270	44.4	2143	3	US-09-071-710-15	Sequence 15, Appl
15	1270	44.4	2143	4	US-09-525-397-15	Sequence 15, Appl
16	919	32.1	789	4	US-09-020-956-10	Sequence 10, Appl
17	919	32.1	789	4	US-09-030-607-10	Sequence 10, Appl
18	919	32.1	789	4	US-09-605-785-10	Sequence 10, Appl
19	919	32.1	789	4	US-09-439-313-10	Sequence 10, Appl
20	919	32.1	789	4	US-09-352-616A-10	Sequence 10, Appl
21	919	32.1	789	4	US-09-232-149A-10	Sequence 10, Appl
22	440	15.4	255	3	US-09-071-710-3	Sequence 3, Appl
23	440	15.4	255	4	US-09-525-397-3	Sequence 3, Appl
24	423	14.8	258	3	US-09-071-710-1	Sequence 1, Appl
25	423	14.8	258	4	US-09-525-397-1	Sequence 1, Appl
26	418	14.6	247	3	US-09-071-710-4	Sequence 4, Appl
27	418	14.6	247	4	US-09-525-397-4	Sequence 4, Appl
28	357	12.5	217	3	US-09-071-710-2	Sequence 2, Appl
29	357	12.5	217	4	US-09-525-397-2	Sequence 2, Appl
30	330	11.5	1773	1	US-08-356-340-3	Sequence 3, Appl
31	330	11.5	1773	2	US-08-786-555-3	Sequence 3, Appl
32	324.5	11.3	1969	1	US-08-356-340-1	Sequence 1, Appl
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c 42	123	4.3	1269	5	PCT-US96-10986-13	Sequence 13, Appl
c 43	123	4.3	5076	2	US-08-494-907-2	Sequence 2, Appl
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c 45	123	4.3	6170	2	US-08-494-907-4	Sequence 4, Appl
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c 52	120	4.2	7076	1	US-09-837-863-20	Sequence 20, Appl
c 53	120	4.2	7076	4	US-09-837-863-21	Sequence 21, Appl
c 54	120	4.2	7092	4	US-09-837-863-19	Sequence 19, Appl
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c 56	120	4.2	7573	4	US-09-837-863-27	Sequence 27, Appl
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c 58	119.5	4.2	6306	1	US-08-470-950-3	Sequence 3, Appl
c 59	119.5	4.2	6306	1	US-08-467-781-3	Sequence 3, Appl
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c 62	119.5	4.2	6306	5	PCT-US93-06160-3	Sequence 3, Appl
c 63	119.5	4.2	53526	3	US-08-658-136-2	Sequence 2, Appl
c 64	119.5	4.2	53577	3	US-08-658-136-1	Sequence 1, Appl
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c 66	118.5	4.1	4030	4	US-09-293-505-1	Sequence 1, Appl
c 67	118	4.1	1766	4	US-09-661-711A-13	Sequence 13, Appl
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c 73	115.5	4.0	3534	2	US-08-841-178-26	Sequence 26, Appl
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76	115.5	4.0	17612	3	US-08-911-853-29	Sequence 29, Appl
77	115.5	4.0	17612	4	US-09-479-409-29	Sequence 29, Appl
78	115.5	4.0	17612	4	US-09-479-453-29	Sequence 29, Appl
79	115	4.0	18994	1	US-08-459-586-4	Sequence 4, Appl
c 80	115	4.0	18994	2	US-08-282-696-4	Sequence 4, Appl
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c 82	114.5	4.0	4951	2	US-08-752-307B-1	Sequence 1, Appl
c 83	114.5	4.0	4951	4	US-09-707-802-1	Sequence 1, Appl
c 84	114.5	4.0	4951	4	US-09-991-326-1	Sequence 1, Appl
85	113	3.9	4403765	4	US-09-103-840A-2	Sequence 2, Appl

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c 89 112.5 3.9 4833 4 US-09-513-783A-21 Sequence 21, Appl
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91 110 3.8 2571 4 US-09-336-643A-80 Sequence 80, Appl
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c 94 109 3.8 1765 2 US-08-282-696-15 Sequence 15, Appl
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c 98 109 3.8 2304 4 US-08-486-403-1 Sequence 1, Appli
99 109 3.8 111282 4 US-09-754-250-3 Sequence 3, Appli
c 100 108.5 3.8 35060 3 US-09-814-095-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
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; Sequence 110, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dilllin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-09-020-956-110
Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTrpValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGGATCATCATGTGCGC 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGCTAGAGGAGAGTTTCATGACCATGGTGTGGGCATTGCT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTGTGTCGCTGCTAGGCTCAGCCAGTGCACCATGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTCATCTGGGCACCTGCTCCTGGGCATCTGCTGAGCCTC 583
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Db 584 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCAGCTCTCATCTCGGGCGCTGGGCTGCTGGACTTCTGGCCAGGTGTCTTC 703
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QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
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Db 1184 TACCAAGGCGTGGCAGAGCTGAGCGGGCAGCCGAGCGCGCGCTGCTTCCCGGGCTG 1243
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QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTTGGCCAGTGTGGA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380

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Qy 381 SerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCAGGTTACCTTCTCAGGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
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Db 1484 TCCCTCTACCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGT 1543
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Db 1544 GCTAGCAGTGGAGACAGCTGTATGACCATCTCTCTGCCAGGCCCTTAAGCTGGAGCTGCC 1603
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Db 1604 TTCCTAATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCCACTCCACCCCGGCTC 1663
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Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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RESULT 2

US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-110
Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-030-607-110 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCGG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGTGGAGTGGGGTAGAGGAGAGTTTCATGACCATTGGTGTGGGCATTGGT 463
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Qy 81 ArgTyrGlyArgArgArgProPheIleThrPalaLeuSerLeuGlyIleLeuLeuSerLeu 100
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RESULT 3
US-09-605-785-110
; Sequence 110, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
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; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-785-110

Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-605-785-110 (1-3410)

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Db 1424 TCAGCGCGCTCACCGGTTTCACTTCTCAGCCCTGCAGATCCCTCCCTACACACTGCC 1483
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Db 1844 ACTGCCATATGTTGCTGCGCAGGCTGGGTCTGGTGGCCATTACTTTTGTCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGAAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 4

US-09-439-313-110
; Sequence 110, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-110

Alignment Scores:
Pred. No.: 9.55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-110 (1-3410)

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QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCCATATGTGTCTGCCGAGCGCTGGGTCTGGTGGCCATTACTTTTCTGTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 5
US-09-352-616A-110
; Sequence 110, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuyi
; APPLICANT: Xu, JiangChun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-110
Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-352-616A-110 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGTCGGCACCCGAAAGCCAGCTCTTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGCTTTGGCCGCGAGGCATCACCTATGTGCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CCTCTGCTGCTGGAGTGGGGGTAGAGGAGATTCATGACCATGCTGGCGCATTTGCT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGGCGCTGTGTCTGCCCTCCTAGGCTCAGCCAGTGCACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTCTGTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCGAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGGCACTGCTCATCTTGGGCGTGGGGCTGTGGACCTTCTGTGGCCAGGTGTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCGGGAGCCCGGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCTTTCATGATCATGCTTGGGGCTGTGGGTACCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCAAGTGGCCCTTGGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTT 883

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QY 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCTCATCTTCCTCAGCTGCTAGCAGCCACACCTGCTGGTGGCTGAGGAG 943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGGGCCCTCTCTGTGGCCCCAC 1003

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATCGCGGCCGCTGGCTTCCGGAACCTGGGGCGCTGCTCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGATGCGCCGACCCCTGCGCGCTCTTCGTGGCTGAGCTGTGC 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTTCTGGGGCAGGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGCGCCAGCGCCGAGACACTATGATGAAGC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGCGAGCTGGGGCTGTCTCTGCAGTGCGCCATCTCCCTGGCTCTCTCTG 1303

QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGCTATTGGCCAGTGGCA 1363

QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGCTGCGGTGCCACATGCCCTGCCACAGTGGCGGTGGTGACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProThrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTCCCTACACACTGGCC 1483

QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACCCAGCGGAGAGCAGGTGTCTTCGCCCAATACCGAGGGGACACTGGAGGT 1543

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTACAGTGAGCAGCCTGATGACCAGCTTCCTGCCAGGCCCTTAAGCCTGGAGCTCCC 1603

QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACAGCTGGGTGCTGGAGCAGTGGCTGTCCACCTCCACCCCGGCTC 1663

QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCTGTGATCTCCGTACGTGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1723

QY 481 ArgValValProGlyValGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCGGGGCGGGGCATCTGCCGTGGACCTGCCATCTCGATGATGCTTCCTG 1783

QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGCTGTGC 1843

QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTGCCCGAGCGCTGGGTCTGGTGGCCATTTACTTTGCTACACAG 1903

QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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RESULT 6

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US-09-602-877A-100
; Sequence 100, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-602-877A-100
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Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-602-877A-100 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGTGAGCGCTGTGTGGCGCACCGGAAAGCCAGCTTGTCTG 343

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGCGAGGATCACCTATGTGCG 403

QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CTTCTGCTGTGGAGTGGGGGTAGAGGAGAGTTCATGACCATTGGTGGCGCATTTGT 463

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTCTGCCCTCTCTAGCTCAGCCAGTACCCACTGGCGTGA 523

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCCGCCGCCCTTCATCTGGGCACCTGCTTGGGCATCCTGTGAGCCCTC 583

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTCTCATCCCAAGGCGGCTGGCTAGCAGGCTGTGTGCCGATCCCGAGGCCCTG 643

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGCTGGGCTGTCTGTGACTTCTGTGGCAGGTGTCTTC 703

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTCTCTGACCTCTCCGGGACCCGACACTGTGCGCAGGCC 763

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTCATGATCATCTTGGGGGCTGTCTGGGGCTACTCTCTGCTGCC 823

QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGACACAGTGCCTGCCCTTACCTGGGACCCAGCCAGGAGGTGCCTCTTT 883

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 884 GGCCTGCTCACCTCATCTTCTCACCCTGCGTAGCAGGCACACTGCTGTGCTGAGGAG 943
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Db 944 GCACGCGTGGCGCCACCAGCAGCCAGAGGCGCTGTCGGCCCGCTCTGTGCGCCACC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
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QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
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Db 1064 CACACGTGTGCTGCCGATGCCCGCCAGCCCTGCGCGGCTCTCTGTGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
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Db 1124 AGCTGGATGGCACTATGACCTTCACGCTGTTTACACGGATTCGCTGGCGGCGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
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Db 1184 TACCAGGGGTGCCAGAGCTGAGCGCGGCACCGAGGCGCGGAGACACTATGATGAAGC 1243
QY 321 ValArgMetClySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
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Db 1244 GTTCGGATGGCACGCTGGGCGTTCCTCCAGTGGCCATCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGTGTGTCAGCGATTTCGCGACCTCGACAGCTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCCTTCCCTGTGCTGCCGTGTCACATGCTGTCACAGTGTGGCGCTGTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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Db 1424 TCAGCGCCCTCACCGGTTACCTTCTCAGCCCTGCATCTCGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
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Db 1484 TCCTCTACACCGGAGAGCAGGTGTTCTGCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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Db 1544 GCTAGCAGTGAGGACAGCTGATGACAGCTTCTGCCAGCGCTTAAAGCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuProProProProAlaLeu 460
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QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
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Db 1664 TGGGGGCTCTGCCCTGTGATGTCCTCGTACGTGTGTTGGTGGTGGTGGCCAGGCTC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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Db 1724 AGGGTGTTCCGGCGCGGCGCATCTGCTGGACCTCGCCATCTCGCATAGTGTCTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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Db 1784 CTGTCCAGGTGGCCCATCTCCCTGTTTATGGGCTCATTTGTCAGCTCAGCCAGTGTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1904 GTAGTATTTGACAAGAGCGCACTTGGCCAAATACTCAGCG 1942
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RESULT 7

US-09-232-149A-110

; Sequence 110, Application US/09232149A

; Patent No. 6465611

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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-110
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Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-232-149A-110 (1-3410)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
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Db 344 GTCAACCTCTAACCTTTGGCTGGAGGTGTGTTGGCCGAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 404 CCTCTGCTCTGCTGAAAGTGGGGGTAGAGAGAGTTTCATGACCATGGTGTGGGCAT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTCTGGGCTGTGCTGTGTCCCGCTCCFAGGCTCAGCCAGTACCATGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Db 524 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACCTGTCTTGGGCATCTGCTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
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Db 644 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Db 704 ACTCCACTGGAGCCCTGCTCTGTGACCTCTCCCGGAGCCCGACCATGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
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Db 764 TACTCTGTATGCTTTCATGATCATGTCTGGGGGTGCTGTGGCTTACCTGTGCTGCTGC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
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Db 824 ATGACTGGGACACCATGTCCTTGGCCCTTACCTGGGCACCCAGGAGGAGTGCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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Db 884 GGCTGTCTACCCCTCATCTTCTCACCCTAGCAGGCACACTGTGCTGTGCTGCTGAGG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Db 944 GCAGCGCTGGGCCCCACCAGGACGACGAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003

Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAspLeuGlyAlaLeuLeuProArgLeu 260

Db 1004 TGCTGTCCATCGCGGCGCTGTGGCTTCCGGAACCTGGGCGCTGTCTCCCGGCTG 1063

Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280

Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCCCTGGCGCGCTCTTCGTGGCTGAGCTGTC 1123

Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300

Db 1124 AGTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCGTGGCGAGGGCTG 1183

Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

Db 1184 TACCAGGGCTGCCAGAGCTGAGCGGCGCAGGCGCGGAGACACTATGATGAGGC 1243

Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340

Db 1244 GTTCGGATGGCAGCCTGGGGCTGTCTCTGCAGTGCACATCTCCCTGTCTCTCTCTG 1303

Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360

Db 1304 GTCATGGACCGCTGGTGGCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGTGTGCA 1363

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380

Db 1364 GCTTTCCCTGTGGCTGCGGGTCCACATGCTTCCACAGTGTGGCGGTGGTACAGCT 1423

Qy 381 SerAlaLeuLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400

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Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420

Db 1484 TCCTCTACCCACCGGAGAGAGGAGGTGTTCTGCCCCAATACCGAGGGGACACTGGAGGT 1543

Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440

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Db 1664 TCGGGGGCTCTGCTGTGTATGTCCTCGGTACGTGTGGTGGTGGAGCCACCGAGGCC 1723

Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500

Db 1724 AGGGTGGTTCCGGCGGGGCATCTGCTGGACCTCGCCATCTCGATAGTGCCTTCTCTG 1783

Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520

Db 1784 CTGTCCCAAGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGTCCAGCCAGCTGTGTC 1843

Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540

Db 1844 ACTGGCTATATGGTGTCTGCCAGCGCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1903

Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553

Db 1904 GTAGTATTGACAAGCGCACTTGGCCAAATACTCAGCG 1942

RESULT 8

US-09-605-785-704
; Sequence 704, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-704

Alignment Scores:
Pred. No.: 8.19e-250 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 4 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-605-785-704 (1-4034)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGCTGCCGACCGAAGCCAGGCTCTTGCTG 340

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

Db 341 GTCAACCTGCTAACTTTGGCCTGGAGGTGTCTTTGGCGCAGGCATCACCTATGTGCGG 400

Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

Db 401 CCTCTGCTGCTGGAGTGGGGTAGAGGAGAGTTTCATGACCATGGTGGCATTTGGT 460

Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

Db 461 CCAGTGTGGGCTGTGTGTCTGCCGCTCTCCTAGGCTCAGCCAGTGACCACTGGCGTGA 520

Qy 81 ArgTyrGlyArgArgProPheIleThrPAlaLeuSerLeuGlyIleLeuSerLeu 100

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Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120

Db 581 TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGTGTGCCGATGCCAGGCCCTG 640

Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140

Db 641 GAGCTGGCACTGCTCATCTCTGGCGCTGGGGCTGTGGAGCTCTGTGGCCAGGTGTGCTTC 700

Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

Db 701 ACTCCACTGGAGGCGCTCTCTCTCACCTCTTCCGGGACCCGACCACTGTCCGAGGCC 760

Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180

Db 761 TACTCTGTATGCTTTCATGATCATGCTTTGGGGGCTGCTTGGGGTACCTCTCTGCTGCC 820

Qy	181	I	lea	Sp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Cys	Leu	Phe	200	
Db	821	A	TTG	ACT	GGG	CAC	ACG	TGCC	TGG	CCCC	CTAC	TCTGG	CAC	CCCA	CGAG	GAG	AGT	GGC	TCT	TTT	880		
Qy	201	G	ly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	220	
Db	881	G	GC	TG	CT	CAC	CC	TCA	TCT	TCT	CA	CC	TG	CTAG	CAG	CA	CA	CT	GT	GG	TG	940	
Qy	221	A	la	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	240
Db	941	G	C	AG	CG	T	GG	CCCC	AC	CC	AG	CC	CAG	CAG	AAG	GG	CTG	TG	CG	CC	CT	CT	1000
Qy	241	C	ys	Cys	Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	260
Db	1001	T	G	CT	GC	AT	CG	CG	CC	CG	CT	TG	CTT	TCC	GG	AAC	CTTGG	CG	CC	CT	CT	CT	1060
Qy	261	H	is	Gln	Leu	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala	Glu	Leu	Cys	280	
Db	1061	C	ACC	AG	CT	GT	GC	TGCC	AT	GCCC	GC	AC	CC	CTG	CG	CG	CT	CT	CG	TG	CT	CT	1120
Qy	281	S	er	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	300
Db	1121	A	GC	TG	AT	GG	CA	CT	CA	CT	TG	CT	TTT	TAC	CG	GA	TTT	CG	TG	GG	CG	AG	1180
Qy	301	T	yr	Cln	gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	---	319
Db	1181	T	ACC	AG	GG	CG	TG	CCCC	AG	AG	CT	GAG	CG	GC	ACC	GAG	CG	CC	GG	AG	CA	CT	1240
Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
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Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
Db	1301	G	CT	G	TG	TG	CT	GG	CT	GT	GC	T	CC	AT	C	T	G	S	C	C	C	C	1360
Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
Db	1361	A	TG	GA	CC	CC	AT	CT	GC	A	T	A	C	AC	G	CT	T	C	A	T	CT	CT	1420
Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
Db	1421	A	GG	A	GC	C	T	CT	GG	CT	CT	AG	AG	CT	GA	GC	AG	TC	GT	GC	CC	C	1480
Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
Db	1481	G	AA	AG	CG	G	AG	CT	TAT	T	CA	A	AG	CT	A	G	G	G	AG	T	A	A	1540
Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
Db	1541	C	TG	CC	T	GG	T	T	CC	AG	CC	GA	GT	G	GC	CT	GT	C	C	C	C	C	1600
Qy	319	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	319
Db	1601	C	C	AG	CG	C	T	T	CC	AG	CT	CT	TA	GA	AG	CG	CT	T	GA	GC	CT	AT	1660

Qy	320	-----GlyValArgMetGlySer	325
Dd	1901	CCTTCCCTCCAGGCCTGTGTCTATGGCCCCCTCCTCCCTCTGCAGGCGTTTCGGATGGGCGAC	1960
Qy	325	rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe	345
Dd	1961	CCTGGGCGCTTCTCTCGAGTGGGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACC GGCT	2020
Qy	345	uValGlnArgPheGlyThrArgAlaValTyrlLeuAlaSerValAlaAlaPheProValAl	365
Dd	2021	GGTGACAGATTGGCACACTGGACAGCTCATTTTGGCCAGTGTGGCAGCTTCCCCTGTGGGC	2080
Qy	365	aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh	385
Dd	2081	TGCCGGTGCCACATGCTGTGCCACAGTGTGCCCGTGGTGTGACAGCTTCAGCCGCCCTCAC	2140
Qy	385	rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrrThrLeuAlaSerLeuTyrrHisAr	405
Dd	2141	CGGGTTCACTTCTCAAGCCCTCGAGATCTGGCCCTACACACTGGCCTCCCTCTACCACCG	2200
Qy	405	gGluLyGlnValPheLeuProLysTyrrArgGlyAspThrGlyAlaSerSerGluAs	425
Dd	2201	GGAGAAGCAGGTGTCTCGCCAAATACCAGAGGGACACTGGAGGTGCTACAGTGAAGA	2260
Qy	425	pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi	445
Dd	2261	CAGCCTGATCAGCAGCTTCTGCCAGGCCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACA	2320
Qy	445	sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl	465
Dd	2321	CGTGGTGTGGAGGAGTAGTGGCTGCTCCACACTCCACCCGCGCTCTCGGGGGCTCTGC	2380
Qy	465	aCysAspValSerValArgValValGlyGluProThrGluAlaArgValValProGl	485
Dd	2381	CTGTGATGTCTCCGTAGTGTGGTGGGTGAGCCACCCAGGCCAGGGTGGTTCCGGG	2440
Qy	485	yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl	505
Dd	2441	CCGGGGCATCTGCCCTGGACCTCCCATCTCGATAGTAGTGCCTTCTGTCTGCCAGTGGC	2500
Qy	505	aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrrMetVa	525
Dd	2501	CCCATCTCTGTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTCTACTGCCTATATGTT	2560
Qy	525	IserAlaAlaGlyLeuGlyLeuValAlaIleTyrrPheAlaThrGlnValValPheAspLy	545
Dd	2561	GTCGTGGCCGAGGCGTGGGTCTGGTGCCCATTTACTTTGTACACAGGTAGTATTTGACA	2620
Qy	545	sSerAspLeuAlaLysTyrrSerAla	553
Dd	2621	GAGCGACTTGGCCAAATACTACGCG	2645
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US-09-605-785-702			
; Sequence 702, Application US/09605785			
; Patent No. 6321716			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiongchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqui			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriack			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			

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; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE INVENTION: DIAGNOSTICS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-605-785-702

Alignment Scores:
Pred. No.: 1,17e-232 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 4 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-605-785-702 (1-4894)
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCAACCTGCTAACCTTTGGCCGTGAGGTGTGTTTGGCGCGCAGCATCACCTATGTGCGG 393
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu 57
Db 394 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTCAATGACCATTGCTGCT-GGGTGAGTTC 452
QY 57 ----- 57
Db 453 ACTACATCCTCCTCTCCTTCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGATGA 512
QY 57 ----- 57
Db 513 COTCTGCCCTGGGAGCTGCTTGGAGGGAGAGGTGTCTGCTGGGAAGGCATTGCTGGGCA 572
QY 57 ----- 57
Db 573 GGAGGGTGACCTTGGCTGAGGGGSCACACCAGAGAAGAAGAAATACCAAGACATA 632
QY 57 ----- 57
Db 633 CCCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCTGGCTCATAGAGACACTGGAG 692
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Db 813 TTAGGTAAGTCTTAGCCAAAGCCAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
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Db 873 GGTCTCCCGCGGAGCTTGCTCTACCCCTAGGACAAAGGGTGGACTCTCTGACTCTGCA 932
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QY 57 ----- 57
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QY 57 ----- 57
Db 1053 GCTGCTCTTTACCCTCCCTAGTCTGCGCCTTTTGAATAGTATACACTTCTTAGTTGCTCC 1112
QY 57 ----- 57
Db 1113 ATGCCTCAGTTTGTCCATCTGAAATGGGGCATCTGTAATGCCTGTGTATGAGGAGTA 1172
QY 57 ----- 57
Db 1173 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTGAGTACGGAATGTTATTTCCATCC 1232
QY 57 ----- 57
Db 1233 TTCTCAGGAGCTTGGTTCCCTTCCCTTGTGCCCTTACTTGTCTCCAGCCATTGACTCAT 1292
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1293 ACTACTTCCCTTCTTGCAGGCATTGCTCCAGTGTGGGCTGGTCTGTGTCGCCGCTCTTA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
Db 1353 GGCTCAGCCAGTGACCACTGGCGTATGCGCGCGCCGCTTATCTCTGGGCA 1412
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QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
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QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
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QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
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QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
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QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGCGCCCTGCTTCCCGGCTGCACCATGTCTGCCGATGCCCGCACCCCTG 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CGCGGCTCTTCTGTGGCTGAGCTGTGCAGTGGATGGGACTCATGACCTTCACGCTGTTT 2012
QY 292 TyrThrAspPheValGlyGluLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
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QY 319 ----- 319
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QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
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QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTCTCCACAGTGTGGC 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
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QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgG1 416
Db 3033 CTACACACTGGCCCTCCCTCTACACCGGGAGAGCAGGTGTTCTTGCCCAATACCGAGG 3092
QY 416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGTATGACCACTTCTCTGCCAGGCCCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
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QY 456 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyG1 476
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QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCACCGAGGCGAGGCTGTTCGGGGCGGGGCATCTGCCTGGACCTGCCATCCTGGA 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
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QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536
Db 3393 CAGCCAGTGTCTCACTGCCCTATATGCTGTCTGCCGAGGCTGGGTCTGGTCGCCATTTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 10

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US-09-605-785-705
; Sequence 705, Application us/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-705
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Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservatives: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 4 Gaps: 3
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US-09-593-793A-113 (1-553) x US-09-605-785-705 (1-6976)

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Qy	112	LeuLeuCysProaspProArgProLeuGluLeuAlaLeuLeuLeuLeuLeuLeuValGlyLeu	131
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Qy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151
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Db	1604	CTGGGCACCCAGGAGAGTGCCTCTTTGGCTTGCTCACCTCATCTTCTCACTTGGCTA	1663
Qy	212	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly	231
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Qy	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe	291
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QY 319 ----- 319
Db 2624 TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCAGGCTCTGTCTGATGGCCCCTC 2683
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QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2804 GGCCAGTGTGGCAGCTTTCCTGTGGCTGCCGGTGCCACATGCCTGTCTCCACAGTGTGC 2863
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
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Db 2864 CGTGTGACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTTGCC 2923
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal ----- 409
Db 2924 CTACACACTGGCTCCCTCTACCACCGGAGAGCAGGT - ACTCATTTGCCAGTGGGTGG 2982
QY 409 ----- 409
Db 2983 AGTCAGGTGGAGGGTGGTCTGGGTTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT 3042
QY 409 ----- 409
Db 3043 CTGGCAAGCAACTTTGGAGATGCTTCTTTGAATCAGAGAAGAGCTTATCTAGCCCCA 3102
QY 409 ----- 409
Db 3103 GGCCACAGAGCTTGGCTGCAGAACAGTGTAGATTAGATTCTGGGAATGACTTCTCTGGGG 3162
QY 409 ----- 409
Db 3163 TCAGGACTGTAGACTTGAATGGATGATTCAGGNAATGCAAAATACGATAGTGGAA 3222
QY 409 ----- 409
Db 3223 TCCCGAAGGTCAGGCCACGAGGCCCTAGGCTTCTAGGCTGGTTGTCTATGGAGAGG 3282
QY 409 ----- 409
Db 3283 CAGGGCGCTGAATCAGTAGACCCCTGGGCCATTTCAGCCTCAGCAGCGGAGTGGGAATG 3342
QY 409 ----- 409
Db 3343 GTCCAGCCTTAGCAACACCTTTTTCAGGGAGCAGCAACCTGACTTAGCCCTGATCCTAC 3402
QY 409 ----- 409
Db 3403 TCTGGTCTGAGATGGGCGAGGCTCTTCTPACCCCTTTCTTCTGGCTTATTTTCT 3462
QY 409 ----- 409
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QY 409 ----- 409

Db 3523 TCCCTTCCCTTCCCTTCCCTGTGCAGATATCTGAGCTTGACACCTGACCCACTCACTTGG 3582
QY 409 ----- 409
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Db 3703 CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCTTTGAGGGGCATGAAGTTGG 3762
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Db 3943 TTTGGTTGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCACCTGATAACCTTCTTCAGC 4002
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Db 4063 GTATGTGCTGCTGCCAGGAAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGAGC 4122
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Db 4123 ATGCTGTCTCGGACCACCTCCAGACTCCAACCTCAGCGGACATTCCTGGGGTGGCAGGC 4182
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Db 4183 AGGGAGGAGAAGTCTCGGAGGCCCTTCCCTAACAGCAGCTGATGCGCAGACTTTGGCACTG 4242
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Db 4243 CACGCTGTGCTGCTGTTCTTGGCCACTTGTGTGAGCTGCATGGTGAGCCGTGGGTTC 4302
QY 409 ----- 409
Db 4303 CTGGTGTGAGGTTTGCAGCTCTGCCATGGCTCCCACTCGCAATGCAGCCAACCTCAACTC 4362
QY 409 ----- 409
Db 4363 TTCTGGCATGGGACAATGTTGGATAAGACCTGGCTTCTTCTTAAATAGGAGGCTCTGG 4422
QY 409 ----- 409
Db 4423 GCCATCAAGGCGAGGGTTGGGGGATGGTGTGCAGCAGTGCAGTCACTCTGATCTAAGTCA 4482
QY 409 ----- 409
Db 4483 CAGCAGGAAGGAAGTGAAGACCTTCAACATTTAGCACAGCTGGGCTGGGGAGGTGGGA 4542
QY 409 ----- 409
Db 4543 AGAGGGACATTCCTCTGCTGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGGACA 4602
QY 409 ----- 409
Db 4603 AGGGAGCTCATGGCAGGCAGCTACCCCTAGTGGCATCTGGGACCCAGAGAGCAGCT 4662

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Qy 409 ----- 409
Db 4663 TCTCTGACCGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGCGCAGGAGGAAG 4722
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Qy 409 ----- 409
Db 4783 TGTCTGTGCATCTTTACCAACCGCTTCATTTCCCCCTGTGTCTTTTCTTACCTTGGAG 4842
Qy 409 ----- 409
Db 4843 CTCCTGTTCTCTGATCTGTGATATTGAGTTGTGTGCTGCTTACCTGTTCTAAGAGGCT 4902
Qy 409 ----- 409
Db 4903 AGAGGAGACCTAGACTTCTGGGTTTCCATTTGTCCCGCCCTACCCCGTTACCCCTTCTCC 4962
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Db 4963 CACTCTCAGGAAGGCTCTGTTAGACTTGGACCAAGTAGGGTCTCOATCTTCTCTCT 5022
Qy 409 ----- 409
Db 5023 GCTCCTGATTCTCATGAAGTCCCATTTGCCCTGGGATGGAGGCAAGGCTGTCTTCACA 5082
Qy 409 ----- 409
Db 5083 GCTGGGGTGGTCCAGTCTGGGTACACACCTGTCTCTTCCCTTTTCTTACCCCTCT 5142
Qy 410 -----PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
Db 5143 GCCTTAGTGTTCCTGCCCAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG 5202
Qy 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
Db 5203 CCTGATGACCAAGTCTCTGCCAGGCCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACAGT 5262
Qy 446 lGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCy 466
Db 5263 GGGTGTGGAGGACGTGGCTGCTCCACCTCCACCCGCGCTCTGCGGGGCTCTGCGCTG 5322
Qy 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
Db 5323 TGATGTCCTCCGTAGCTGTGGTGGGTGGAGCCCAACCGAGGCCAGGGGTGTTCCGGGCGG 5382
Qy 486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaApr 506
Db 5383 GGGCATCTGCCTGGACCTCGCATCTCTGGATAGTGCCTTCTGCTGCCAGGTGGCCCC 5442
Qy 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
Db 5443 ATCCCTGPTTATGGGCTCCATTGTCCAGCTCAGCCAGCTGTCTACTGCTATATGGTGTG 5502
Qy 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
Db 5503 TGCCCGCAGGCTGGGTGTGGTGGCCATTCTTTGCTACACAGGTAGTATTGTGACAAGAG 5562
Qy 546 rAspLeuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCCAATACTCAGCG 5584
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RESULT 11

US-09-605-785-703
: Sequence 703, Application US/09605785
: Patent No. 6321716
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.

: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqui
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darriek
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C16
: CURRENT APPLICATION NUMBER: US/09/605,785
: NUMBER OF SEQ ID NOS: 835
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 703
: LENGTH: 2904
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-605-785-703

Alignment Scores:
Pred. No.: 6,94e-174 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 4 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-605-785-703 (1-2904)

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Qy 163 ValThrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
Db 1 GTCATATGCTTCATGATCAGTCTTGGGGGCTGCCCTGGGCTACCTCCTCGCTGCCATTGAC 60
Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
Db 61 TGGGACACACAGTGGCTTGGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCTG 120
Qy 203 LeuThrLeuIlePheLeuThrCysValAlaIleAlaThrLeuLeuValAlaGluAlaIa 222
Db 121 CTCACCTTCATCTTCTCCTCACCCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAGCAGCG 180
Qy 223 LeuGlyProThrGluProAlaGluClyLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGGCCCCACCGAGCCAGAGAGGGCTGTGGGCCCCCTCCTTGTGCCCCCACTGCTGT 240
Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
Db 241 CCATGCCGGGCGGCTTGGCTTTCGGAAACCTGGGGGCCCTGCTTCCCGGCTGCACCGAG 300
Qy 263 LeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGTGCTGCCCATGCCCCCGACCTTGGCGGGCTCTTTCGTGGGTGAGCTGTGACGTGG 360
Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
Db 361 ATGGCACTCATGACCTTCACCGCTGTTTACACGGATTTCTGGGGGAGGGGCTGTACCGAG 420
Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal--- 321
Db 421 GGCCTGCCCAAGAGCTGAGCCCGGACCGAGGCGCCCGGAGACACTATGATGAAGGAAG-GCC 479
Qy 321 ----- 321
Db 480 TCTGGTGTCTTAGGAGTCTGATCAGAGTCTGTGGCCCCAGTTTTCACAGAGGAAAGCGG 539
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QY 321 ----- 321
Db 540 AGCTTATCAAAGTCTAGAGGAGTGGAGAGTTAAGGCTGGATTTTCAGATCTGCTGGT 599
QY 321 ----- 321
Db 600 TCCAGCCGAGTGTGCCCTCTGCTGCCCAACGACTTTCCTCAATAATCTCACCAGGCGCT 659
QY 321 ----- 321
Db 660 TCCAGCTCAGCGCTCTAGAGCGTCTTGAAGCCTATGCCAGCTCTCTTTGTGTTCCCT 719
QY 321 ----- 321
Db 720 CTCACCCGCTGTCTCTACAGCTGAGACTCCCGAGAACTTTCAGACTACCTCTCTCTGC 779
QY 322 ----- ArgMetGlySerLeuGlyLeu 328
Db 780 CTTTCAGCAAGGGCGGTGCCCCACATTTCTGTAGGGCGTTTCGATGGCAGCGCTGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTCTTCGACGTGCCCATCTCCCTGCTCTCTCTGCTCATGGACCGGCTGTGTGACGCA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTCGGCAGCTCGAGCAGCTCTATTGTCAGTGTGGCAGCTTTCCTCTGTGCTGCCGTGCC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
Db 960 ACATGCTCTCCACAGTGTGCCGTGGTGACAGTTTCAGCGCCCTCACCGGGTTCACC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
Db 1020 TTCTCAGCCCTCGACATCTCCCTACACACTGGCTCCCTCTACCCCGGAGAGCAG 1079
QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMet 428
Db 1080 GTGTTCTCTCCCAATACCGAGGGGACACTGGAGGTGTAGCAGTGGAGCAGCGCTGATG 1139
QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTCTCTGCCAGGCCCTAAGGCTGGAGCTCCCTTCCCTAATGGACACGCTGGTGCT 1199
QY 449 GlyGlySerGlyLeuLeuProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGCAGTGGCTGCTCCACCTCCACCCGGCTCTGCGGGGCTCTGCTGTGTATGTC 1259
QY 469 SerValArgValValGlyGluProThrGluAlaArgValProGlyArgGlyIle 488
Db 1260 TCCGTACGTGTGTTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCGCGCGCGGCATC 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
Db 1320 TCCTGGAGCTCGCCATCTGATAGTGCCTTCCCTGCTGCCAGGTGGCCCGCCATCCCTG 1379
QY 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
Db 1380 TTTATGGGCTCATTTGTCCAGCTCAGCCAGCTGTGTACATGCCCTATATGGTGTCTCCGCA 1439
QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
Db 1440 GGCTTGGGTCTGCTGCCATTTACTTTGTACACAGGTAGTATTGTTGACAAAGGCGACTTG 1499
QY 549 AlaLysTyrSerAla 553
Db 1500 GCCAAATACTCAGC 1514

RESULT 12

US-09-071-710-16

; Sequence 16, Application US/09071710

; Patent No. 6130043

; GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-16
Alignment Scores:
Pred. No.: 1,76e-113 Length: 2152
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-16 (1-2152)
... QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACCAAGGGGTGCCAGAGCTGAGCGGGCCAGCGGCGGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGGCGTTCGGATGGCAGCGCTGGGGCTGTTCCTGTGAGTGGCCATCTCCCTGCTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGTGTCATGGACCGGCTGGTGGCAGGATTCGGCAGCTCGAGCAGTCTATTGTCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378

Db 182 GTGCAGCTTCCCTGGCTGCGGTGCCACATGCTGTCCACAGTGTGGCGGTGG 241
QY ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 301
QY LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCAACGGAGAGAGGTTCTCTCCCAATACCGAGGGGACACT 361
QY GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTAGGACACCTGATGACACAGCTTCTGCGAGCCCTAAGCCCTGGA 421
QY AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTAATGACACGTGGGTGCTGGAGGAGTGGGCTGCTCCACCTCCACCC 481
QY AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
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QY GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGTTGGTTCGGGCGGGGCATCTGCTGGACCTGCCATCTGGATAGTGCC 601
QY PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCCCTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATTTGCCAGTCCAGCCAG 661
QY SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTACATGCCTATATGTGTCTGCCGAGGCTGGGTCTGGTGCCTATTACTTTGCT 721
QY ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 13
US-09-525-397-16
; Sequence 16, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525.397

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-525-397-16
Alignment Scores:
Pred. No.: 1.76e-113 Length: 2152
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
DB: 4 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-525-397-16 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACACAGGCGGTGCCAGAGCTGAGCCGGGACCGAGGCCGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCCGATGGGACGCTGGGGCTGTCTCTGACGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTTCATGGACCGGCTGGTGCAGCATTCGGCAGCTCGAGCAGCTATTTTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCTGTGCTGCGGTGCCACATGCCGTGCCACAGTGTGGCGGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCTGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCAACGGAGAGAGGTTCTCTCCCAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTAGGACACCTGATGACACCTTCTGCCAGGCCCTAAGCCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTAATGACACCTGGGTGCTGGAGGAGTGGGCTGCTCCACCTCCACCC 481
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 482 GCGCTCTGCGGGGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGTTGGTTCGGGCGGGGCATCTGCTGGACCTGCCATCTCCCATAGTAGTCC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||

Db 602 TTCTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCATATATGTTGCTGCGCAGGCTGGGTCTGCTGCCATTTACTTGTCT 721
QY 539 ThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 766
RESULT 14
US-09-071-710-15
; Sequence 15, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-15
Alignment Scores:
Pred. No.: 7.38e-112 Length: 2143
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
Gaps: 3

US-09-593-793a-113 (1-553) x US-09-071-710-15 (1-2143)
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTCCCAAGAGCTGAGCGGGCCAGGAGCCCGGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCAGCCCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAa 361
Db 123 ATGGACCGGCTGTGTCAGCGATTTCGGCACTCGAGCAGTCTATTGTGCCAGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
Db 183 TTCCCTGTGGCTGCCGCTGCCACATGCCGTGCCACAGTGTGGCCGTGGTGACAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCGGCCCTCACCAGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCC 302
QY 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyAla 421
Db 303 CTCTACCAACCGGAGAGAGAGGTGTTCTGCCCAATACCGAGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGGAGCAGCCTGATGACCACTTCTTCCGCCAGGCCCTAAGCCTGGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 423 CCTAATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCCGGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluAlaArg 481
Db 483 GGGGCCCTCTGCCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCCAGG 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGCGGGGGCATCTGCTGGACCTCGCCATCCTGGATAGTGCCTTCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCCAAGTGGCCCATCCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGCTGTGCACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGTTGCTGCCGAGGCGCTGGGTCTGGTGGCCATTACTTTGCTACACAGGTA 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 758
RESULT 15
US-09-525-397-15
; Sequence 15, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE


```
US-09-593-793A-113 (1-553) x US-09-020-956-10 (1-789)
;
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ... US-09-030-607-10

Alignment Scores:
Pred. No.: 6,14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-030-607-10 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
DB 3 GTCTATNTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGGCGGTGCCAGATGCGCTGCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
DB 63 AGTGTGGCGGTGGTACAGCTTCACCGCCCTCACCGGTTCCACCTTCTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
DB 123 ATCTGTCCTTACACATGGCCCTCCCTCTACACCGGGAGAGCAGTGTCTCTGCCCAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
DB 183 TACCCAGGGGACACGTGGAGGTCTAGCAGTGAGACAGCCTGATGACCAGCTTCTGCCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
DB 243 GGCCTTAGCCTGGAGCTCCCTTCCCTATATGACACGTGGGTGGTGGAGCAGTGGCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
DB 303 CTCCCACTCCACCGCGCTCTCGGGGCTCTGCGGGCTCTGCTGTGATGCTCTCCGTAGCTGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
DB 363 GTGGGTGAGCCACCGAGGGGTGTCCGGCGGGGATCTGCTGGCCGGGATCTGCTGGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
DB 423 ATCTGGATAGTGC-TTCTCTGCTGCCANGTGGCCCATCCCTGTTTATGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyVal 533
DB 482 GTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCGCGCAGGCTGGGTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 542 CC-ATTACTTTGCTACACAGGTANTATTTGACAAGACGANTTTGCCAAATACTCAGCG 600

RESULT 17
US-09-030-607-10
; Sequence 10, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
```


APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605.785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-10

Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-605-785-10 (1-789)

Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCATATNTGGCCAGTGTGGCAGCTTCCCTGTGGCTGGCGTGCACATGCTGTCCAC 62
Qy 374 SerValAlaValThAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTACAGCTTACAGCCGCTTCCACCGGGTTTCACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTGCCCTACACTGGCCTTCCCTTACCACCGGGAGAGCAGGTGTCTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyGlyAlaSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGTAGCAGTGAGGACACCTGTAGTACACAGCTTCTCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTTCCCTTCCCTAATGGACACGCTGGGTGTGGAGGAGTGGCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCGCGCTCTGGGGGCTCTGCCGTGTGATGTCTCGTACGTGTGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGAGGTGTTCGGGGCGGGGCACTGTCTGGAGCTTCCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGGGATAGTC-TTCTGCTGTCCCACTGGCCCATCCCTGTATTATGGGTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTACCCAGTGTGTCTACCTGCCTATATGTGTGTCTGCCGAGGCTGGGTCTGTCT 541

Qy 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTGTACACAGGTANTATTGACAAGAAGCAGTTTGGCAAATACTCAGCG 600
RESULT 19
US-09-439-313-10
Sequence 10, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439.313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-10

Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-10 (1-789)

Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCATATNTGGCCAGTGTGGCAGCTTCCCTGTGGCTGGCGTGCACATGCTGTCCAC 62
Qy 374 SerValAlaValThAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTACAGCTTACAGCCGCTTCCACCGGGTTTCACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTGCCCTACACTGGCCTTCCCTTACCACCGGGAGAGCAGGTGTCTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyGlyAlaSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGTAGCAGTGAGGACACCTGTAGTACACAGCTTCTCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTTCCCTTCCCTAATGGACACGCTGGGTGTGGAGGAGTGGCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCGCGCTCTGGGGGCTCTGCCGTGTGATGTCTCGTACGTGTGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493

Db 363 GTGGGTGAGCCACCCAGCCAGGGTGGTTCGGGGCCGGGCGATCTGCCTGGACCTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
|||||
Db 423 ATCCCTGGATAGTGC-TTCCTGTCTGCCANGTGGCCCATCCTCTTTATGGGCTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCGAGGCTGGGTCTGGTC 541
Qy 534 AlaIleTyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTTGCTACAGGTANTATTGACAAGACGANTTGGCCAAATACTCAGCG 600
RESULT 20
US-09-352-616A-10
; Sequence 10, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-10
Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-352-616A-10 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGTGCAGCTTCCCTGTGGCTGCCGGTGCACATGCTGCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGTGACAGCTTCAGCCGCCCTCACC GG GTTACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCCCCACACAGTGTCCCTTACCACCGGGAGAGACAGGTGTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCAGGGGACACTGGAGGTGCTAGCAGTGAGGACGCTGATACACAGCTTCTCGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCTTAAGCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
|||||

Db 303 CTCACCCTCCACCCGCGCTCTCGGGGGCCCTCTGCCTGTGTGTCTCCGTACGTGTGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyLeuCysLeuAspLeuAla 493
|||||
Db 363 GTGGGTGAGCCACCCAGCCAGGGTGGTTCGGGGCCGGGCGATCTGCCTGGACCTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCCCTGGATAGTGC-TTCCTGTCTGCCANGTGGCCCATCCTCTTTATGGGCTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCGAGGCTGGGTCTGGTC 541
Qy 534 AlaIleTyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTTGCTACAGGTANTATTGACAAGACGANTTGGCCAAATACTCAGCG 600
RESULT 21
US-09-232-149A-10
; Sequence 10, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-10
Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-232-149A-10 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGTGCAGCTTCCCTGTGGCTGCCGGTGCACATGCTGCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGTGACAGCTTCAGCCGCCCTCACC GG GTTACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCCCCACACAGTGTCCCTTACCACCGGGAGAGACAGGTGTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCAGGGGACACTGGAGGTGCTAGCAGTGAGGACGCTGATACACAGCTTCTCGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCTTAAGCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCCTG 302

PRIOR APPLICATION DATA: 09/071,710
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: base_polymorphism
LOCATION: 215
OTHER INFORMATION: /note= " N' represents an A or G or
OTHER INFORMATION: T or C polymorphism at this position"
US-09-525-397-3

Alignment Scores:
Pred. No.: 7.37e-34 Length: 255
Score: 440.00 Matches: 83
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 15.38% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-3 (1-255)

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 2 ACAGCTTCAGCGCCCTCACCAGGCTGCACCTTCAGCCCTGCAGATCTGCCCTACACA 61
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 62 CTGGCTCCTCTACACCGGAGAGAGAGAGGTTCTGCTGCCCAATACCGAGGGACACT 121
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 122 GGAGGTGCTAGCAGTACGAGCAGCCTGATGACAGCTTCCTGCCAGGCCCTAAGCCTGGA 181
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
DB 182 GCTCCCTTCCCTTAATGGACACGTGGTGTGGANGAGTGGCTGCTCCACCTCCACCC 241
QY 459 AlaLeuCysGly 462
DB 242 GCGCTCTGCGGG 253

RESULT 24

US-09-071-710-1
Sequence 1, Application US/09071710
Patent No. 6130043
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
US-09-071-710-1
Alignment Scores:
Pred. No.: 3.17e-32 Length: 258
Score: 423.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.79% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-1 (1-258)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
DB 2 GGGCTGTACCGAGGGCTGCCAGAGCTGAGCGGGCAGCGAGCGGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 62 GAAGCGGTTCGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 122 TCTCTGTGTCATGGACCGGCTGTGCAGCGATTCGGCAGCTCGAGCAGCTCTATTTGGCCACT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
DB 182 GTGGAGAGCTTTCCTGTGGCTGCCCGTCCCATCCCTGTCCACAGTGTGGCCCGTGGTG 241
QY 379 ThrAlaSerAlaAla 383
DB 242 ACAGCTTCAGCGGCC 256
RESULT 25
US-09-525-397-1
Sequence 1, Application US/09525397
Patent No. 6252047
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083-US.P1
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-525-397-1

Alignment Scores:
Pred. No.: 3,17e-32 Length: 258
Score: 423.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.79% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-1 (1-258)

Qy 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACACAGGGCGTGCACAGCTGAGCGGGACCCGAGCGCCGAGACACTATGAT 61
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGGTTCGGATGGGAGCGCTGGGCGTGTCTCTGAGTCGCGCATCTCCCTGGTCTTC 121
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGCTGGTCAGGATTCGGCACTCGAGCAGTCTATTGGCCAGT 181
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGCAGCGTTTCCCTGTGGCTGGCGGTGCCACATGCCTGTCCACAGTGTCCCGGTGTGTG 241

Oy 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCGCC 256

RESULT 26

US-09-071-710-4
Sequence 4, Application US/09071710
Patent No. 6130043
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083-US.P1
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-4

Alignment Scores:
Pred. No.: 8.93e-32 Length: 247
Score: 418.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.61% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-4 (1-247)

Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1 GCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCTGCTCCACCTCCACCC 60

; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-2

Alignment Scores:
Pred. No.: 5.02e-26 Length: 217
Score: 357.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.48% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-2 (1-217)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGCGGTGCCAGAGCTGAGCGGCGCCAGGAGCCGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCGAGCGCTGGGCGTGTCTCGCAGTGGCCATCTCCCTGGTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaLa 361
Db 123 ATGGACCGGCTGTGTCAGCGATTCGGCACCTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGTGGCGGTGCCACATGCCTGTGCC 215

RESULT 29

US-09-525-397-2
; Sequence 2, Application US/09525397
; Patent No. 6252047

; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-2

Alignment Scores:
Pred. No.: 5.02e-26 Length: 217
Score: 357.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.48% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-2 (1-217)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGCGGTGCCAGAGCTGAGCGGCGCCAGGAGCCGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCGAGCGCTGGGCGTGTCTCGCAGTGGCCATCTCCCTGGTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaLa 361
Db 123 ATGGACCGGCTGTGTCAGCGATTCGGCACCTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGTGGCGGTGCCACATGCCTGTGCC 215

RESULT 30

US-08-356-340-3
; Sequence 3, Application US/08356340
; Patent No. 5608146
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; APPLICANT: RIESMEIER, Jorg
; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE
; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A
; TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND
; TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,340
; FILING DATE: 21-DEC-1994
; CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/EP93/01604
FILING DATE: 22-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 442 759.2
FILING DATE: 24-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1773 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORGANISM: Solanum tuberosum

FEATURE:

NAME/KEY: CDS

LOCATION: 5..1552

OTHER INFORMATION: /note= "Sucrose-Transporter"

US-08-356-340-3

Alignment Scores:

Pred. No.:	4,6e-22	Length:	1773
Score:	330.00	Matches:	132
Percent Similarity:	42.94%	Conservative:	93
Best Local Similarity:	25.19%	Mismatches:	194
Query Match:	11.53%	Indels:	106
DB:	1	Gaps:	20

US-09-593-793a-113 (1-553) x US-08-356-340-3 (1-1773)

Qy	4	ArgLeuThrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeu	23
Db	89	AGCATATGG-----AAATATAGTTGTAGCTTCC	118
Qy	24	LeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeu	43
Db	119	ATAGCTGCTGGTTCATTTGGTGGCTCTTCAGCTCTCTTTGGCTTACACTTATGTT	178
Qy	44	LeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGlyProValLeu	63
Db	179	CAATTGCTCGGAATTCCTCATAAATTTGCTCTTTTATTGGCTTTGTGACCGGATTTCT	238
Qy	64	GlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGly	83
Db	239	GGTATGATTGTCAGGCAGTTGCGGCTACTACAGTGAATAATGCTCCCTCCGCTTTCGGT	298
Qy	84	ArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIle	103
Db	299	CGCCGCGGCCCATTCATTGCCCGGAGCTGCACCTTGTATGATTCGCGTTCCTCATC	358
Qy	104	ProArgAlaGlyTrpLeuAlaGlyLeu-----LeuCysProAsp	116
Db	359	-----GGATTGCGCCGCCACCTTGTGTCACGCTCCGGTGCACACTCTCGGAAAGGA	409
Qy	117	ProArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGly	136
Db	410	TTTAGCCACCTGCCATTCGGTTTCGTCGCGGCTTTGGATCCTGATGTTGCTAC	469
Qy	137	GlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgProAsp---	155
Db	470	AACATGTTACAGGGCCCATGACAGACACTACTGGCTGATCTCTCGCGCGGAAATCCGCG	529
Qy	156	HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGly	175

Db	530	AGGATGAGAACACAGCAAAATGCTTTTCTCATCTTTCATGGCCGTCGGAACATCTCGGG	589
Qy	176	TyrLeuLeuProAlaIleAspTrp-----AspThrSerAla	187
Db	590	TAGCGCGCGGTTTCATATTTCTACCTCTTTAAAGTATTCCCCTTCTCAAAACCAAGCC	649
Qy	188	LeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe---GlyLeuLeuThrLeuIle	206
Db	650	TGGACATGCTACTGCGCAAAATCTGAAGAGTTGTTCTTCATCGCTATATCTCTTTACTC	709
Qy	207	PheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu---AlaAlaLeuGlyPro	225
Db	710	AGCTTAACAACCATACCTTAACCTTAGTCGCGGAAACAGAGCTCCCGGAGAAGACGAG	769
Qy	226	ThrGluProAlaGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg	245
Db	770	CAAGAAATCGACGAGAAATTAGCCGCGCGGGA-----AAA	805
Qy	246	AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys	265
Db	806	TCGAAAGTACCGTTT-----TTCGCTGAAATTTTGGGCTTTGAAGAATTA-----	853
Qy	266	ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu	285
Db	854	-----CCTCGACCGATGTGATTTCTTATTAGTAACCTGTTGAACCTGATCGCGTGG	907
Qy	286	MetThrPheThrLeuPheThrAspPheValGlyGluGlyLeuTyrGlnGlyValPro	305
Db	908	TTTCCCTTTTCTTATACGATACAGATTGGATGGCTAAGGAGGTTTTCGGTGA-----	961
Qy	306	ArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyValArgMetGlySer	325
Db	962	-----CAAGTCGGTGAT-----GCGAGGTGTACGATTTGGTGTACGCGTGTGCA	1009
Qy	326	LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu	345
Db	1010	ATGGGATTACTGTGCAATCTGTGTTCTAGGCTTTATCTCCTCGGTTGGATTTCTTA	1069
Qy	346	ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla	365
Db	1070	GGGAAGAAATTTGGT---GGTCTAAGAGTTATGGGAATTTTGAACITTTGTTTG---	1123
Qy	366	AlaGlyAlaThrCysLeuSerHisSerValAlaVal---	378
Db	1124	-----GCTATTGCTTGGCTATGACCATTTTGGTCACCAAAATGCCGAGAAATCTCGC	1177
Qy	379	-----ThrAlaSerAlaAlaLeuThrGlyPheThr---	388
Db	1178	CAGCAGACCCCGCGGCACACTTATGGGCGCACGCTTGGTGTAAATCGGTGCTTGG	1237
Qy	389	-----PheSerAlaLeuGlnIle-----LeuProTyrThrLeu	399
Db	1238	CYTCTCTTTGCGCCCTTGGTATTCCTCTGCGGCAACTTTTAGTATTCCATTTGCTTG	1297
Qy	400	AlaSerLeuTyrHisArgGluLys-----	407
Db	1298	GCATCTATATTTCTAGTAATCGTGGTTCAGGACAAGTTTGTCTACTAGAGTGCCTCAAT	1357
Qy	408	---GlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSer	426
Db	1358	CTTGCAATTTGTTGACACAGATGTTGGTGTCTACTAGTAGGAGGCCCATGGATGATTG	1417
Qy	427	LeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVal	446
Db	1418	TTTGAGGAGGAAACTTGCTTGA-----TTTGTAGTTGGAGCAGTT	1459
Qy	447	GlyAlaGlyGlySerGly-----LeuLeuProProProAlaLeuCys	461
Db	1460	GCAGCTCGCGGAGCGCTGTTTATAGCACTCACAATTTGCCATCTCCACCTGCTGA-TGC	1518
Qy	462	GlyAlaSerAla	465
Db	1519	TAAGCCAGCAGT	1530

RESULT 31

US-08-786-555-3
; Sequence 3, Application US/08786555B
; Patent No. 5981181
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; INVENTOR: RIESMEIER, Jorg
; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE TRANSPORTER,
; TITLE OF INVENTION: PLASMIDS, BACTERIA AND PLANTS CONTAINING A TRANSPORTER
; TITLE OF INVENTION: AS WELL AS A PROCESS FOR PREPARATION AND TRANSFORMATION
; TITLE OF INVENTION: OF YEAST STRAINS FOR THE IDENTIFICATION
; FILE REFERENCE: Frommer
; CURRENT APPLICATION NUMBER: US/08/786,555B
; CURRENT FILING DATE: 1997-01-21
; EARLIER APPLICATION NUMBER: 08/356,340
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: PCT/EP93/01604
; EARLIER FILING DATE: 1993-06-22
; EARLIER APPLICATION NUMBER: DE P4220759.2
; EARLIER FILING DATE: 1992-06-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Spinacia oleracea
US-08-786-555-3

Alignment Scores:

Pred. No.: 4.6e-22 Length: 1773
Score: 330.00 Matches: 132
Percent Similarity: 42.94% Conservative: 93
Best Local Similarity: 25.19% Mismatches: 194
Query Match: 11.53% Indels: 106
Gaps: 20

US-09-593-793A-113 (1-553) x US-08-786-555-3 (1-1773)

Qy 4 ArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeu 23
Db 89 AAGCTATGG-----AAAATATAGTTGTAGCTCC 118
Qy 24 LeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValProLeuLeu 43
Db 119 ATAGCTGCTGGGTCAATTTGGTGGCTCTTACGCTCTCTTCTTACACCTTATGTT 178
Qy 44 LeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGlyProValLeu 63
Db 179 CAATTGCTCGGAATTCCTCATAAATTCCTCTTTTATTTGGCTTTGTGGACCGATTCT 238
Qy 64 GlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGly 83
Db 239 GGTATGATTGTTACAGCCAGTTGTTCGGCTACTACAGTGATAATTGCTCCCGCTTCGGT 298
Qy 84 ArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIle 103
Db 299 CGCCCGCCGCAATTCATTGCCCGCGGAGCTGCATTTGATGATTGGCTTTCTCTCATC 358
Qy 104 ProArgAlaGlyTrpLeuAlaGlyLeu-----LeuCysProAsp 116
Db 359 -----GGATTGCGCGCGACCTTGGTCACGCTCCGGTGACACTCTCGGAAAGGA 409
Qy 117 ProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGly 136
Db 410 TTTAGCCCGCAATTCGCGCTTTTCGTCGCGCTTTTGGATCCTTGGATCTTCTTAAC 469
Qy 137 GlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp--- 155
Db 470 AACATGTTACAGGCGCCATGAGACACTACTGGCTGATCTCTCCGCGGAAATCCCGC 529
Qy 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 1519 TAAGCCAGCAGT 1530

Db 530 AGGATGAGAACAGCAAAATGCTTTTCTCATTTCTTCATGGCGTCGGAACAATCTGGGG 589
Qy 176 TyrLeuLeuProAlaIleAspTrp-----AspThrSerAla 187
Db 590 TAGCGCGCGGTTCATATTCACCTCTTAAAGTATTTCCCTTCTCAAAAACCAAGCC 649
Qy 188 LeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe---GlyLeuLeuThrLeuIle 206
Db 650 TCGCATGTACTCGCAAAATCTGAAGAGTTGTTCTTTCATCGCTATATTCCTTTACTC 709
Qy 207 PheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu---AlaAlaLeuGlyPro 225
Db 710 AGCTTAAACAACCATAGCCTTAACCTTAGTCGGGAAAACGAGCTCCCGAGAAACAGAG 769
Qy 226 ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245
Db 770 CAAGAAATCGAGAGAAATAGCCGCGCGCGA-----AAA 805
Qy 246 AlaArgLeuAlaPheArgAsnLeuLeuAlaLeuProArgLeuHisGlnLeuCysCys 265
Db 806 TCGAAAGTACCGTTT-----TTCGGTGAATTTTGGGGCTTTGAAAGAAATTA----- 853
Qy 266 ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285
Db 854 -----CCTCGACCGATGTGGATTCTTATTAGTAACCTGTTCGAACGTGCGTGG 907
Qy 286 MetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValPro 305
Db 908 TTTCCCTTTTCTTATACGATACAGATTGGATGGCTAGGAGGTTTTCGGTGA----- 961
Qy 306 ArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySer 325
Db 962 -----CAAGTCGGTGAT-----CGAGGTGTACGATTTCGGGTACGCCCTGGTGA 1009
Qy 326 LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 1010 ATGGGATTACTGTGCAATCTGTGTTCTAGGTTTATGTACATTCTGGGGTTTGAATCTTA 1069
Qy 346 ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365
Db 1070 GGAAGAAGATGGT---GGTCTAAGAGTTATCGGGAATTTTGAACCTTTGTTTG--- 1123
Qy 366 AlaGlyAlaThrCysLeuSerHisSerValAlaValAlaVal----- 378
Db 1124 -----GCTATTGCTTGGCTATGACCATTTTGGTCACAAATGCGCGAGAAATCTCGC 1177
Qy 379 -----ThrAlaSerAlaAlaLeuThrGlyPheThr----- 388
Db 1178 CAGCAGCAGCCCGCGGACACTTATGGGCGCGACGCTGTGTAAATCGGTGCCTTG 1237
Qy 389 -----PheSerAlaLeuGlnIle-----LeuProTyrThrLeu 399
Db 1238 CTTCTCTTTGGCGCCCTTGGTATTCCTCTTGGCGCAACTTTTAGTATTCCATTTCTTG 1297
Qy 400 AlaSerLeuTyrHisArgGluLys----- 407
Db 1298 GCATCTATATTCTAGTAATCGTGTTCAGCACAAAGTTTGTCTACTAGGAGTGTCAAT 1357
Qy 408 ---GlnValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSer 426
Db 1358 CTTGCAATTTGTTACCACAGATGTTGTTGTCACCTAGTAGGAGGCCCATGATTTG 1417
Qy 427 LeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVal 446
Db 1418 TTTGGAGGAGAAATCTGCCGGA-----TTTGTAGTTGGAGCAGTT 1459
Qy 447 GlyAlaGlySerGly-----LeuLeuProProAlaLeuCys 461
Db 1460 GCAGCTGCGCGAGCGCTGTTTAGCACTCAAAATGTTGCCATCTCCACCTGCTGA-TGC 1518
Qy 462 GlyAlaSerAla 465
Db 1519 TAAGCCAGCAGT 1530


```
Db 1195 ATTGCAATATTATTCCTT-----GCTGTTTGTAGCTATGAGGGTG 1236
Qy 376 AlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeu 395
Db 1237 ---TTAGTTACTAAGTCCCGCAA----- 1257
Qy 396 ProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArg 415
Db 1258 ---CACCCTCCGTATGATGACCCACCATATTATG----- 1284
Qy 416 GlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPro 435
Db 1284 ----- 1284
Qy 436 LysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPro 455
Db 1285 -----GGCTCCGCGTCCCTCGG 1302
Qy 456 ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGly 475
Db 1303 CCGCGCGCTGCT-----GGCTTAAGGTGGCGCTTTGGCTATCTTTGCCGCTTCTTGT 1356
Qy 476 GluProThrGluAlaArgVal---ValPro----- 484
Db 1357 ATCCCTCTTGGCATCCTTTCAGTATCTCTTGGCCTTGGCGTCAATCTTTTCAGCATCT 1416
Qy 485 ---GlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGln 503
Db 1417 TCCGGTTCAGGACAGGTCTTCTCTAGGAGTCTCAACCTCGCCATCGTGTGACCCCG 1476
Qy 504 Val-----AlaPro 506
Db 1477 ATGTTTGTGTCGTACAAAGTGGCCATGGGATGCAATGTTTGGTGGAGAAATTTGCCA 1536
Qy 507 SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyr 523
Db 1537 GCATTCGTGGTGGGAGCTGTAGCAGCAACAGCCAGTCAGTCTTTCATTT 1587

RESULT 34
US-09-071-710-5
; Sequence 5, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
```

```
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083-US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-710-5
Alignment Scores:
Pred. No.: 1,84e-15 Length: 231
Score: 247.00 Matches: 57
Percent Similarity: 98.28% Conservatives: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 8.63% Indels: 1
DB: 3 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-071-710-5 (1-231)
Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515
Db 3 GATAGTGCCTCTCCTGCTGCCAGGTGCCCATCCCTGTTTATGGCTCCATTTGCCAG 62
Qy 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
Db 63 CTCACGCCAGTCTGTCACCTGCCTATATGTTGTTCTGCCGAGGCTG-GGTCTGGTCCGCA 121
Qy 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 122 TACTTTGCTACACAGGTAGTATTTCACAGAGCGACTTGGCCAAATATCTACGCG 175

RESULT 35
US-09-525-397-5
; Sequence 5, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525.397
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/071.710

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6083.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-525-397-5

Alignment Scores:

Pred. No.:	1.84e-15	Length:	231
Score:	247.00	Matches:	57
Percent Similarity:	98.28%	Conservative:	0
Best Local Similarity:	98.28%	Mismatches:	1
Query Match:	8.63%	Indels:	1
DB:	4	Gaps:	0

US-09-593-793A-113 (1-553) x US-09-525-397-5 (1-231)

Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515

Db 3 GATAGTGCCTTCTCCTGCTGCCAGGTGGCCCATCCCTGTTATGGCTCCATTGTCACG 62

Qy 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535

Db 63 CTCACCCAGTCTGTCACCTATATGTTGTCGCCGAGGCTG-GGTCTGGTCGCCATT 121

Qy 536 TyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553

Db 122 TACTTTGTACACAGGTAGTATTTCACAGAGCGACTTGGCCAAATACATCAGCG 175

RESULT 36

US-08-056-200-93/c

Sequence 93, Application US/08056200

Patent No. 5616500

GENERAL INFORMATION:

APPLICANT: Steinert, Peter M.

APPLICANT: Lee, Seung-Chul

APPLICANT: Kim, In-Gyu

APPLICANT: Chung, Soo-Il

APPLICANT: Park, Sang-Chul

TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and

TITLE OF INVENTION: Methods of Using Same

NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/056.200

FILING DATE: 30-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502

INFORMATION FOR SEQ ID NO: 93:

SEQUENCE CHARACTERISTICS:

LENGTH: 9551 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1507..1644

FEATURE:

NAME/KEY: intron

LOCATION: 1645..2511

FEATURE:

NAME/KEY: CDS

LOCATION: 2512..8070

US-08-056-200-93

Alignment Scores:

Pred. No.:	0.000289	Length:	9551
Score:	155.50	Matches:	157
Percent Similarity:	35.78%	Conservative:	62
Best Local Similarity:	25.65%	Mismatches:	198
Query Match:	5.44%	Indels:	198
DB:	1	Gaps:	31

US-09-593-793A-113 (1-553) x US-08-056-200-93 (1-9551)

Qy 7 ValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPhe 26

Db 6471 CTGACGCAGTTGCTCGCGCTCTCTCGAGCGCAGCTTCCTCTTCGCGGAATTT 6415

Qy 27 GlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuGluVal 46

Db 6414 TCTCTCCCGTTC-----CTCGCGCAGCGCTGTTCCTC----- 6382

Qy 47 GlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyVal 66

Db 6381 ---CTCGAGGAATT-TTCTCCCTTGTCTCTGATGAGCAGAGTTCCTCTTCGCGGAATTTTC 6326

Qy 67 CysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrArgArgArg 86

Db 6325 TGTCACGCTCTTGGCGGAGCAGCGCT----- 6293

Qy 87 ProPhe-----IleTyrAlaLeuSerLeuGlyIleLeu 97

Db 6292 CCCTTCTCTGGAGCAGCTGTTCCTCTCTCGCGGAATTTCTGTCTCTTCACGCGCTC 6233

Qy 98 LeuSerLeuPheLeuIlePro----- 105

Db 6232 TCTTCTCTT---CTCTTCTCTCTCAGCACTGCTTTTCTTCCTTTGGGACTTCTCTGTCTCGC 6176

Qy 106 AlaGlyTrpLeuAla---GlyLeuLeuCysProAspProArgProLeu----- 120

Db 6175 GCCTTTTGGCTTCTCTTTTGTCTCTTCGCTCCAGCTGTTCCTTCCTCGGAAATCCCTGT 6116

Qy 121 -----GluLeuAlaLeuLeuGlyVal 129

Db 6115 TGGCTGTGCGCAGCGCTCTCTCTTGTCTCAGATCTCTCTCTGCTGTTTACCCAGCA 6056

Qy 130 GlyLeuLeuAspPheCysGlyGlnValCysPheThrPro----- 142

Db 6055 GGTGTGCAGATCTTGTCTGGGATGTCTCGCGCACCTGGGAATCTTCCAACTCCGCGA 5996
Qy 143 ---LeuGluAlaLeu-----LeuSerAspLeuPhe 151
Db 5995 ACTGTTTCATCTCTCTGCGCTTTGCAGTAACCTTGTATATACGAAGTGCATTTCTTTT 5936
Qy 152 ArgAspPro-----AspHisCysArgGlnAlaTyrSerValTyrAlaPheMet 167
Db 5935 CTGTTTCCCACTGCCATTCAGATCACTGCGTGATCTCCATCCCGGTATCGCT----- 5882
Qy 168 IleSerLeuGlyGlyCysLeuGly-TyrLeuLeuProAlaIleAspTrpAspThrSerAl 187
Db 5881 GTTCTTTTCTGGCGCTGAAGCTCTCTCTCCCGATATTGCGTATTCAGCTCTCGGCT 5822
Qy 187 a-----LeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLe 205
Db 5821 GCCTTCTCTCTCCGCTTCTC-----TCTCAGCAGCTGCTCTTCCCTCTCTCGCTG 5768
Qy 205 uIlePheLeuThrCysValAlaAlaThrLeuLeu-----ValAl 218
Db 5767 CCTCTTCTCCCGACATTCCTCTCCCGCTCTCGCGCTTCTCTCTCCGCTTCTCTC 5708
Qy 218 aGluGluAlaLeuGlyPro-----ThrGluProAl 229
Db 5707 TCAGCA-GCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5649
Qy 229 aGluGly-----LeuSerAlaProSerLeuSerProHisCysC 242
Db 5648 TCTTGGCGCTTCTCGTCTCCCGTTCCTCTCCAGAGCTGCTCTCTCTCTCTCTCTCT 5589
Qy 242 sProcysArgAlaArgLeuAlaPheArgAsnLeuGly----- 254
Db 5588 TCCTCTCTCTCCCGATATTGCTCTCCCGCTCTCGAGTCTTCTTCTCCGTTCTCTCT 5529
Qy 255 -----AlaLeuLeuProArgLeuHisGlnLeuCysCysArg-MetProArgThrL 271
Db 5528 CTCAGCAGCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5469
Qy 271 eu-----ArgArgLeuPheValAlaGluLeu 280
Db 5468 TCTTGGCGCTTCT 5416
Qy 280 ysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGlyL 300
Db 5415 -----CTGCAACT 5364
Qy 300 eutyGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 320
Db 5363 TTTCTCGGTTCT 5305
Qy 320 lyValArgMetGlySerLeuGlyLeuPhe-----L 330
Db 5304 ATATTGCT 5245
Qy 330 euGlnCysAlaIleSerLeuLeuPheSerLeuValMetAspArgLeuValGlnArgPhe 350
Db 5244 TTTCT 5185
Qy 350 lyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThr 370
Db 5184 CTCTCTCGCGCT 5141
Qy 370 ysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPhe- 389
Db 5140 -----GCAGCTGCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5095
Qy 390 -----SerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeu 403
Db 5094 GTACAGCGTGTGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5041
Qy 403 yrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSer 423
Db 5040 TTGGT-----CGCGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5011

i LOCATION: 2512..8070
US-08-800-644-93

Alignment Scores:
Pred. No.: 0.000289 Length: 9551
Score: 155-50 Matches: 157
Percent Similarity: 35.78% Conservative: 62
Best Local Similarity: 25.65% Mismatches: 198
Query Match: 5.44% Indels: 198
DB: 2 Gaps: 31

US-09-593-793A-113 (1-553) x US-08-800-644-93 (1-9551)

QY	7	valSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPhe	26
		::::::::::::	
Db	6471	CTGACCAGATTGCTCGCGCTCTCGAGCGCAGCTGTTGTTCCCTC--CTTAAGGAATTT	6415
QY	27	GlyLeuGluValCysLeuAlaLaGlyIleThrTyrValProProLeuLeuLeuGluVal	46
Db	6414	TCCTCCCGTTC-----CTCGCGCAGCGCTGTTCCTC-----	6382
QY	47	GlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal	66
		:::	
Db	6381	---CTCGAGGAATT-TTCTCCCTTGTCTGATGAGCAGTTCTCTTCGCGGAATTTTC	6326
QY	67	CysValProLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArg	86
Db	6325	TGTCACGCTCTTTGGCGGACAGCGCT-----GTTCCCT	6293
QY	87	ProPhe-----IleTrpAlaLeuSerLeuGlyIleLeu	97
Db	6292	CCCTTTCTGGACAGCTGTTCTCTCGGGAATTTTCTGTGTCTCTTGACGGCGTC	6233
QY	98	LeuSerLeuPheLeuIlePro-----	105
Db	6232	TCTTCTCTT--CTCTTTTCTCTCTCAGCAACTGTTTCTCTTGGAAGTCTCTGTCGC	6176
QY	106	AlaGlyTrpLeuAla--GlyLeuLeuCysProAspProArgProLeu-----	120
Db	6175	GCCTTTTGCTCTCCTTTTGCTCTTCTCGCTCCAGCTGTTTCTCTCGGAAATGCTGT	6116
QY	121	-----GluLeuAlaLeuLeuIleLeuGlyVal	129
		:::	
Db	6115	TGGCCTTGCTGCAGCGCCTCTCTTGTCTCAGCATCTCTCTGTGTTACCCACGA	6056
QY	130	GlyLeuLeuAspPheCysGlyGlnValCysPheThrPro-----	142
Db	6055	GGTGCTGCAGATTGCTGGGATTGCTGTCGCGCACCTGGGAATCTTCAACTGCGCGA	5996
QY	143	---LeuGluAlaLeu-----LeuSerAspLeuPhe	151
		:::	
Db	5995	ACTGTTTCATCTCTCTGCGCTTTGCACTAAACCTGTTATCAGAACTGCATTTTCTTTT	5936
QY	152	ArgAspPro-----AspHisCysArgGlnAlaTyrSerValTyrAlaPheMet	167
Db	5935	CTGGTTCCCACTGCCATTTACAGATCACTGCGCTGATCTCATCCCGGTATGCT	5882
QY	168	IleSerLeuGlyGlyCysLeuGly--TyrLeuLeuProAlaIleAspTrpAspThrSerAl	187
Db	5881	GTTTCTCTTCTGGCGCTGAAGCTCTTCTCTCCGATATTTGCTCTCCAGCTCTCTGCG	5822
QY	187	a-----LeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLe	205
Db	5821	GCTTCTCTCTCCCGTTCCTC-----TCTCAGCAGCTGCTCTTCTCTCTGCTGCAGCT	5768
QY	205	ullePheLeuThrCysValAlaAlaThrLeu-----ValAl	218
		:::	
Db	5767	CCTTCTTCTCCGACATTGCTCTCCCGCTCTCTGCGGCTTCTCTTCTCCGGTTCCTCTC	5708
QY	218	aGluGluAlaLeuLeuGlyPro-----ThrGluProAl	229
		:::	
Db	5707	TCAGA-GCTGCTCTTCTCTGCTGTCAGCTCTCTCTCTTCCGATATTTGCTCTCTCCAGC	5649

[illegible]

; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 59
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-199-737-3

Alignment Scores:

Pred. No.: 0.00618 Length: 1417
Score: 128.50 Matches: 115
Percent Similarity: 29.53% Conservative: 43
Best Local Similarity: 21.50% Mismatches: 178
Query Match: 4.49% Indels: 199
DB: 4 Gaps: 21

US-09-593-793A-113 (1-553) x US-09-199-737-3 (1-1417)

QY 66 ValCysValProLeuLeu-----GlySerAlaSerAspHisTrp---ArgGly 80
DB 20 CTCCTGCTCTCCCTCTCCATCTCCACAGAGCTTCCAGCCCAACACACCTGGCCAGACCC 79
QY 81 ArgTyrGlyArg-----ArgArgProPheIleTrpAlaLeuSerLeuGly 95
DB 80 AGGTGGGGGAGTTAGATCCCGGGGTCAAGCAACAGAACTGGGGCTCTTCCCTGAGGA 139
QY 96 Ile-----LeuLeuSerLeuPheLeuIleProArgAla--- 106
DB 140 TTCCAGCTTCTCTCCAGGTGCGCTCTGATGGGAGATGCTGATGCCAGACATTT 199
QY 106 ----- 106
DB 200 CACTGGACAGCCAGGAGTGTGGGGCGGTGGCAGTGCCTGTGCTTTCCTTAATCT 259
QY 107 -----GlyTrp---LeuAlaGlyLeuLeuCysProAspProA 118
DB 260 TCCTGCTGGGCACAGTGGCAATGGCTGTGCTGGCAGTGTCTCTGAGCCTGGCCCGA 319
QY 118 rgProLeuGlu-----LeuAlaLeuLeuIleLeuGlyValGlyLeuLeuA 133
DB 320 GTGCTGGCAGGAGCTGGCAGCACACAGGACCTGTTCATCCTCAACCTGGCGGTGGCTG 379
QY 133 spPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgA 153
DB 380 ACCTCTGCTTTCATCTGTGCTGCTGCTGCTTCCAGGCCACCATC----- 423
QY 153 spProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyC 173
DB 423 ----- 423
QY 173 ysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuG 193
DB 424 -----TACACGTGGATGCC-----TGG----- 441
QY 193 lyThrGlnGluCysLeuPheGlyLeuLeuThr-----LeuIleP 207
DB 442 -----CTCTTTGGGGCCCTCGTCTGCAAGCCCGTGCACCTGCTCATCT 484
QY 207 heLeuThrCysValAlaAlaThrLeuValAlaGluAlaLeuGlyProThrG 227
DB 485 ACCTCACCATGTACGCCAGCAGCTTTACG----- 513
QY 227 luProAlaGluGlyLeuSerAlaProSerProHisCysCysProCysArgAlaA 247
DB 514 -----CTGGCTGCTGCTCCGTGGACAGGTAC----- 540
QY 247 rgLeuAlaPheArgAnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgM 267

DB 541 -----CTGGCGCTGCGG----- 571
QY 267 etProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetT 287
DB 572 CCTCGGCACGCGGTACGCGCGGCGAGTGGGGCTGTGTGGCTGTGGCTGGCGGCCG 631
QY 287 hrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgA 307
DB 632 TCTTCTGGCGGCCCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 691
QY 307 laGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuG 327
DB 692 GCGTCCCGCGCTGGGAGGACGCGCGCGCGCGCTGGACGTGGCCACCTTCCTGCTGCCG 751
QY 327 lyLeuPheLeuGlnCysAla---IleSerLeuValPheSerLeuValMetAspArgLeuV 346
DB 752 GCTACTGCTGCGGTGGCTGTGTGGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 811
QY 346 alGlnArgPheGly-----ThrArgAlaValTyrL 356
DB 812 GGGCGCGCTGGTCCCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 871
QY 356 euAlaSerValAlaAlaPheProValAlaAla----- 366
DB 872 GCGCGGCGCGCGCCATGCTGGCGGTGGCGCGCTCTACGCGCTCTGCTGGGTGCCACAC 931
QY 367 -----GlyAlaThrCysLeuSerHisSerValAlaValV 378
DB 932 AGCGCTCATCTCTGCTTCTGTGTAGCGCGCTTTCGCTTACGCGCGCGGCGGCGGCGG 991
QY 378 alThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrT 398
DB 992 GCGCGCTGGCGCTCACACTGCTGTGGCTAGCGCAACTCTCTGCTCAACCGCTCGTCTACG 1051
QY 398 hrLeuAlaSerLeuTyr----- 403
DB 1052 CGCTCGCTCGCGCCACTTCCGCGCGCGCTTCCGCGCGCTGTGGCGGTGGCGCGCGGAC 1111
QY 404 -----HisArgGlnLysGlnValPheLeuProLysTyrArg----- 415
DB 1112 GCGCGCACGCGTCCGCGCGCGCGC---TTGCGTGGCTGGCGCGCGGCTCTCGGGCCAC 1168
QY 416 --GlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyP 435
DB 1169 CGCGTCCCGGAGAGCGCGCGCTAGCGGAGGCTGTGCTGTGGTGGCGGCGGCGGCG 1228
QY 435 roLysPro---GlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuL 454
DB 1229 CGAGGCCAGGAGGAGGCCCTCCACGCGGAGAGGCTGCCCGGAGGACCGGAATAACCC 1288
QY 454 euProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValV 474
DB 1289 TGCCCGCTGGACTCCGCTGTGCTCGTGTCTACTCCGCTTCTCC----- 1335
QY 474 alGlyGluProThrGluAlaArgValValProGlyArgGly 487
DB 1336 -----GAAGGCGGACGCCACCGGCGGCGGCA 1362

RESULT 39
US-09-058-333A-3
; Sequence 3, Application US/09058333A
; Patent No. 6368812
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Reili E
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas

QY 474 aIGlyGluProThrGluAlaArgValValProGlyArgGly 487
Db 1336 -----GAAGCGGACGCCACCGCGGCGGGA 1362

RESULT 40

US-09-453-702B-197
; Sequence 197, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Plunkett, Guy
; Welch, Rod

TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-Dec-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 197:

SEQUENCE CHARACTERISTICS:

LENGTH: 4021

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 197:

US-09-453-702B-197

Alignment Scores:
Pred. No.: 0.0464 Length: 4021
Score: 126.50 Matches: 102
Percent Similarity: 33.00% Conservative: 61
Best Local Similarity: 20.65% Mismatches: 153
Query Match: 4.42% Indels: 178
DB: 4 Gaps: 26

US-09-593-793a-113 (1-553) x US-09-453-702B-197 (1-4021)

QY 19 LeuLeuValAsnLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyr 38

Db 1057 CTGATCATGAATTTCTACCTTT----- 1080

QY 39 ValProProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGly 58

Db 1081 -----TTCTACACCGACGTTTTTGA 1101

QY 59 IleGlyPro-----ValLeuGlyLeuValCys 67

Db 1102 TTAACCTCCGCGCTGTTGGCACGCTGTTATTGCACTGCGCGTGTGTTGATGCCATCTCC 1161

QY 68 ValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTrglyArgArgPro 87
Db 1162 GACCCGGTGATGGCGTCATTGCGACCGGACGAAAGCGGATGGGGCGCTTCCTCGCCG 1221
QY 88 Phe-----IleTrp---AlaLeuSerLeuGlyIleLeu---LeuSerLeuPheLeuLeuPro 104
Db 1222 TGGCAGCTATGATGATGCCATTCCTCCATCGCATTTATCGGATCTGACGTTCAACCGTGCCA 1281
QY 105 ArgAla-----GlyTrpLeuAlaGlyLeuLeuCysProAspProArg 118
Db 1282 GATGCCAGCATGGGAGTAAAAATCGCTGGCGTTCGGT----- 1320
QY 119 ProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeu-----LeuAspPhe 134
Db 1321 -----ACTTACCTGCTCTTTCAGTCGGTTATACCGCCATCAACGATACGCTAC 1368
QY 135 CysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspPro 154
Db 1369 TCGCGCGGATC-----AACACCATGACCCCGCCGCAATGAATG 1410
QY 155 AspHisCysArgGln-----AlaTyrSerValTyrAlaPheMetIleSerLeu 170
Db 1411 ATCTCTGCGCATCTCGGGATTCGTTCTCTGCGGGTAGCGGGATTTCTGGTTTCGGTA 1470
QY 171 GlyGlyCysLeuGlyTyrTrpLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaPro 190
Db 1471 GGC-----TTACCGTGGATGCTAGCTCTCTTCGGTCAGGCAACGCTGCACGCGCTAT 1524
QY 191 TyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuLeuPheLeuThrCys 210
Db 1525 CAACCTGGCGTCGGGTATTTGTC-----GCCATTGCGTGGTGTATGTTCTGTCTGT 1578
QY 211 ValAlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGlu 230
Db 1579 TTC-----TTCGTGGTTCGTGAACGGTG-----CCGCTCTCC 1611
QY 231 GlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPhe 250
Db 1612 ACAATGGGGAATTTACCTCGCGCAACATCTTGC-----GGCGTG 1653
QY 251 ArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThr 270
Db 1654 CGGAACAACGACCACTGCTG----- 1674
QY 271 LeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeu 290
Db 1675 -----CTGATGCTGTCATGTTCTTCTGCTG 1701
QY 291 PheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGly 310
Db 1702 ATTAACGCTTTTAACATTCGCGCGGTGGGTATATG----- 1737
QY 311 ThrGluAlaArgArgHisTrpAspGluGlyValArgMetGlySerLeuGly----- 327
Db 1738 -----TACTTCAATACCTACGTCCTTACAGAGCAGCAGCGGTACACGTCG 1782
QY 328 LeuPheLeuGlnCysAla-----IleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 1783 CTGTCTTTCACCATGGTCACCTTCGCTCCATTTATGCGTCTGGTGTATGACCCGTTA 1842
QY 346 ValGlnArgPheGlyThrArgAlaValTyr-----LeuAlaSerVal 359
Db 1843 ACGCGCGCTTTCGATACCGTCAAAATTTATTACTACCAACCTGCTCTCTCGCTCACGTCG 1902
QY 360 AlaAlaPhePro-----ValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 377
Db 1903 GCGGTGTTGATGTTGCTGCTCCCGCTCCCGCGGTATATCAACGCTGTGGTGGCGGTG 1962
QY 378 ValThrAlaSerAlaAlaLeuThrGlyPheThrPheSer-----AlaLeuGlnIle 394
Db 1963 ATCTCTCGGTAAATGGCGTGATCTTGGCTTCACATTCGCCACTGCACCTTCATTTGATGGCC 2022

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QY 395 -LeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTy 414
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Db 2023 TTTCCGATGACTACGCGCAGT----- 2044

QY 414 rArGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProL 434
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Db 2045 -----GGAACCCACGTACGTTCTTCGCG 2070

QY 434 y----ProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLe 453
      ||| ||| ::| |||
Db 2071 ATGAACCTCGCCCTCAATCTGTTTTCATCAAGCTGGCTGGG----- 2113

QY 453 uLeuProProProAlaLeuCysGlyAlaSerAlaCys 466
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Db 2114 ----CCTCCAGCGCCG-----GGATCATCAGCCTGC 2140

RESULT 41
US-08-494-907-13/C
; Sequence 13, Application US/08494907
; Patent No. 5955298
; GENERAL INFORMATION:
; APPLICANT: Thomasshow, Linda S
; APPLICANT: Bangera, Mahalaxmi
; APPLICANT: Weller, David M
; APPLICANT: Cook, R. James
; TITLE OF INVENTION: Sequences for Production of
; 2,4-Diacetylphloroglucinol and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0009.95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1269 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas fluorescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (1..1269)
; OTHER INFORMATION: /note= "phLE DNA sequence. SEQ ID
; OTHER INFORMATION: NO:14 is translation (protein) of SEQ ID NO:13."
US-08-494-907-13

Alignment Scores:
Pred. No.: 0.0176 Length: 1269
Score: 123.00 Matches: 84
Percent Similarity: 41.33% Conservative: 40

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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 5076 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens

FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (4285..5076)
OTHER INFORMATION: /note= "phIA, transcribed from
OTHER INFORMATION: right to left"

FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (2606..3313)
OTHER INFORMATION: /note= "phIB, transcribed from
OTHER INFORMATION: right to left"

FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (3085..4251)
OTHER INFORMATION: /note= "phIC, transcribed from
OTHER INFORMATION: right to left"

FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (1398..2444)
OTHER INFORMATION: /note= "phID, transcribed from
OTHER INFORMATION: right to left"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 3514..4767
OTHER INFORMATION: /note= "phIR, transcribed from left
OTHER INFORMATION: to right"

FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (2..1270)
OTHER INFORMATION: /note= "phIE, transcribed from
OTHER INFORMATION: right to left"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..5076
OTHER INFORMATION: /note= "SEQ ID NO:2 contains genes
OTHER INFORMATION: involved in synthesis, activity, and/or export of
OTHER INFORMATION: PhI."

US-08-494-907-2

Alignment Scores:

Pred. No.:	0.143	Length:	5076
Score:	123.00	Matches:	84
Percent Similarity:	41.33%	Conservative:	40
Best Local Similarity:	28.00%	Mismatches:	124
Query Match:	4.30%	Indels:	52
DB:	2	Gaps:	12

US-09-593-793A-113 (1-553) x US-08-494-907-2 (1-5076)

Qy 269 ArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe 288
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Db 1226 AAGAGCGATGGTCGTCTTTTCGCTGAGCTT-----CGGCGTGGTAGGACTTGA 1176
Qy 289 ThrLeuPheThrAspPheVal---GlyGluGlyLeuTyrGlnGlyValProArgAla 307
:::|||||
Db 1175 TCGATTCATATCAGCGCGTGTTCCTCCCGGTGATCATGACCTGCGCCCTGGAGCTATCA 1116
Qy 308 GluProGlyThrGluAlaArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327
|||||
Db 1115 GCACCTGGCGCTGTATCGGC-----GATCTGCGCATTTGCTCGGGAGGCTCGGC 1065
Qy 328 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGl 347
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Db 1064 CCTCTTCATGGCGCTTGCTATC-----AG 1041
Qy 347 nArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGl 367
:::|||||
Db 1040 GCGATTGGCCACCAAGCACTGCTGCTTTCGATTACCTTGGTATGCTCTCGCTCGCGG 981
Qy 367 yAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyph 387
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Db 980 CGCATCTCGTTGATCTCAAGCCTTATGGCGCTGCTCTCGCGCTTGTATGGGAT 921
Qy 387 eThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLy 407
:::|||||
Db 920 CTGCAAGCGCC-----TTCACCGCGTCAACATCATGTCCACCAT-- 878
Qy 407 sGlnValPheLeuProLysTyrArg-GlyAspThrGlyGlyAlaSerSerGluAspSerL 427
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Db 877 -GAAGTTTCGCGACCGTCCGCGCGGCTCAACC---TGGGCATCCACGACGACTGTT 822
Qy 427 euMetThrSerPhe-LeuProGlyProLysProGly----- 438
:::|||||
Db 821 TCCCATCATCGCGCTGCTGCTGGCGCGCTGCTGGCGCGTATTGTTTGAATGTTCCG 762
Qy 439 -----AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGly----- 452
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Db 761 ATCGTGGCGCGCGCTGTTGCGCATCATCTCGTTCGCGCGCTGCTGGCGCTGATCT 702
Qy 453 -----LeuLeuProProAlaLeuCysGlyAlaSerAlaCysAspValSerVal 470
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Db 701 GTATCGAACCTACCAACGAGCGCGCCCATCCAGCGCGCTCTAGAACCTCCCG 642
Qy 471 ArgValValValGlyGluProThrGluAlaArgValAlProGlyArgGlyLeuCysLeu 490
:::|||||
Db 641 CAGCCAATGGCGAACAGCCCTGTCCAGCGGCAACGTGGCGCTCAACAT-----TGCCTT 588
Qy 491 Asp-LeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPhe 510
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Db 587 GATGCTATGCATCTGACGTGCGCAATTCGCTGCGCGCTGCTGCCAGG---TACCT 531
Qy 510 tGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLe 530
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Db 530 GACAGAGCTCTTGACCTGACGAATTTCTCCATGCCCATGATCATCTCCGATCGGCT 471
Qy 530 uGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAsp 547
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Db 470 GGGT-----GGTTTTTCGGCGAGCTCGTTCATTCGCGTTGCTCTGAC 428

RESULT 44

PCT-US96-10986-2/c

; Sequence 2, Application PC/TUS9610986

; GENERAL INFORMATION:

; TITLE OF INVENTION: Sequences for Production of

; TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN

; STREET: 600 N. West Shore Boulevard, Suite 1000

; CITY: Tampa

; STATE: FL

; COUNTRY: USA

; ZIP: 33609

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; APPLICATION NUMBER: PCT/US96/10986

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Pendorf, Stephan A.

; REGISTRATION NUMBER: 32665

; REFERENCE/DOCKET NUMBER: A700.320

TELECOMMUNICATION INFORMATION:

TELEPHONE: (813) 289-2966

TELEFAX: (813) 289-2967

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5076 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Pseudomonas fluorescens

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (4285..5076)

OTHER INFORMATION: /note="phlA, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (2606..3313)

OTHER INFORMATION: /note="phlB, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (3085..4251)

OTHER INFORMATION: /note="phlC, transcribed from

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FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (1398..2444)

OTHER INFORMATION: /note="phlD, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 3514..4767

OTHER INFORMATION: /note="phlR, transcribed from left

OTHER INFORMATION: to right"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (2..1270)

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FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..5076

OTHER INFORMATION: /note="SEQ ID NO:2 contains genes

OTHER INFORMATION: Involved in synthesis, activity, and/or export of

OTHER INFORMATION: Phl."

PCT-US96-10986-2

Alignment Scores:

Pred. No.: 0.143 Length: 5076

Score: 123.00 Matches: 84

Percent Similarity: 41.33% Conservative: 40

Best Local Similarity: 28.00% Mismatches: 124

Query Match: 4.30% Indels: 52

DB: 5 Gaps: 12

US-09-593-793A-113 (1-553) x PCT-US96-10986-2 (1-5076)

QY 269 ArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe 288

Db 1226 AAGACCGATGGTCTTTCTTTGTCGTGAGCTT-----CGGGCTGTAGGACTTGA 1176

QY 289 ThrLeuPheTyrThrAspPheVal---GlyGluGlyLeuTyrGlnGlyValProArgAla 307

Db 1175 TCGATTATTATCATGCCCTGTGTCTCCGGTGATCATGACCTGGCCCTGGACTATCA 1116

QY 308 GluProGlyThrGluAlaArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327

Db 1115 GGACCTGGGCGCTGTTATCGGC-----GATCCTGGCATTTGCTGGGGAGGCTCGGC 1065

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,907
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 30043
REFERENCE/DOCKET NUMBER: 0009.95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (4285..5076)
OTHER INFORMATION: /note= "pHIA, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (2606..3313)
OTHER INFORMATION: /note= "pHIB, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (3085..4251)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (1398..2444)
OTHER INFORMATION: /note= "pHID, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3514..4767
OTHER INFORMATION: /note= "pHIE, transcribed from
OTHER INFORMATION: left to right"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (2..1270)
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FEATURE:
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LOCATION: 5781..6170
OTHER INFORMATION: /note= "pHIF, truncated,
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6170
OTHER INFORMATION: /note= "SEQ ID NO:4 contains genes
OTHER INFORMATION: involved in synthesis, and modulation of synthesis
OTHER INFORMATION: of PhI."
US-08-494-907-4
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Pred. No.: 0.192 Length: 6170
Score: 123.00 Matches: 84
Percent Similarity: 41.33% Conservative: 40
Best Local Similarity: 28.00% Mismatches: 124
Query Match: 4.30% Indels: 52
DB: 2 Gaps: 12

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US-09-593-793A-113 (1-553) x US-08-494-907-4 (1-6170)
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DB 1226 AAGACGCATGTCGTTCTTTTGTCTGCTGAGCTT-----CGGCTGGTAGGACTGA 1176
QY 289 ThrLeuPheThrArgPheVal---GlyGluGlyLeuTyrGlnGlyValProArgala 307
DB 1175 TCGATTCAATTATATCGCGGTTGTTCCCGGTGATCATGATGACCTGGCCCTGGCATATCA 1116
QY 308 GluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetClySerLeuGly 327
DB 1115 GGACCTGGGCGCTTATCGGC-----GATCTGGCATTTGCTGGGAGGCTCGGC 1065
QY 328 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValG1 347
DB 11064 CCTCTTCATGGCGTGTCTATC-----AG 1041
QY 347 nArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaPheProValAlaAlaG1 367
DB 1040 GCGATTGGGCACCAAGCAACTGCTGCTTTCGATTACCTTGGTATCGCTCTCGCCGG 981
QY 367 yAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPh 387
DB 980 CGCATCTGCTGTTGATCTCAAGCCTTATGGGCGCTGCTCTCGCGCGCTTGTATGGGAT 921
QY 387 eThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLy 407
DB 920 CTGCGAAGCGCC-----TTCACCCCGGTACGATCATCTGTCCCGAT--- 878
QY 407 sGlnValPheLeuProLysTyrArg-GlyAspThrGlyGlyAlaSerGluAspSerL 427
DB 877 -GAAGTTTCGCGAGCGGCGCGGCGGCTCAACC---TGGGCATCCAGCAGCAGCTGTT 822
QY 427 eumethThrSerPhe-LeuProGlyProLysProGly----- 438
DB 821 TCCCATCTCGGCGCTGCTGCGGCGCGCTGCTGCGGCGCGCTGTTTGAATGTTTCGG 762
QY 439 -----AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGly----- 452
DB 761 ATCGTGGCGCGCGCTGTTGCGCATCATCTGCTTGGCGGCGCTGCTGCTGGTATCT 702
QY 453 -----LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerVal 470
DB 701 GTATCGAACTTACCAACCGAGCGCGCCCATCCAGGCGCTCGTAGAACCTCCGG 642
QY 471 ArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeu 490
DB 641 CAGCAATGGCGAACAGCCCTGTCCAGCGGCAACGTGGCGCTCAACAT-----TGCCTT 588
QY 491 Asp-LeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMe 510
DB 587 GATGCTATGCTACTGACGTGCGCAATTCCTGCTGGCGCGCTGCTGCCAGC---TACTT 531
QY 510 tGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLe 530
DB 530 GACAGCGCTGTGCACCTGAGCAATTTCTCCATGCCCATGATCATCTCCGATCGGCT 471
QY 530 uGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAsp 547
DB 470 GGGT-----GGTTTTTTCGGCCAGCTGCTCATTCGCGGTTTGTCTGAC 428

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Search completed: February 19, 2003, 05:11:16
Job time : 147 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:53:29 ; Search time 232 seconds
(without alignments)
1214.034 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 2861

Sequence: 1 MVQRLWVSRLLRKRAQLL.....AIYFATQVVFDSKLAKYSA 553

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Database : Published Applications_NA.*

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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	2861	100.0	3410	9	US-09-232-880-110
3	2861	100.0	3410	9	US-10-012-896-110
4	2861	100.0	3410	9	US-09-895-793-110

5	2861	100.0	3410	9	US-09-895-814-110	Sequence 110, App
6	2861	100.0	3410	10	US-09-745-288-100	Sequence 100, App
7	2861	100.0	3410	10	US-09-759-143-110	Sequence 110, App
8	2861	100.0	3410	10	US-09-780-669-110	Sequence 110, App
9	2861	100.0	3410	10	US-09-030-606-110	Sequence 110, App
10	2861	100.0	3410	10	US-09-822-827-110	Sequence 110, App
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12	2716.5	94.9	4034	9	US-10-012-896-704	Sequence 704, App
13	2716.5	94.9	4034	9	US-09-895-814-704	Sequence 704, App
14	2716.5	94.9	4034	10	US-09-759-143-704	Sequence 704, App
15	2716.5	94.9	4034	10	US-09-780-669-704	Sequence 704, App
16	2716.5	94.9	4034	10	US-09-822-827-704	Sequence 704, App
17	2538.5	88.7	4894	9	US-10-012-896-702	Sequence 702, App
18	2538.5	88.7	4894	9	US-09-895-793-702	Sequence 702, App
19	2538.5	88.7	4894	9	US-09-895-814-702	Sequence 702, App
20	2538.5	88.7	4894	10	US-09-759-143-702	Sequence 702, App
21	2538.5	88.7	4894	10	US-09-780-669-702	Sequence 702, App
22	2538.5	88.7	4894	10	US-09-822-827-702	Sequence 702, App
23	2538.5	88.7	4894	10	US-10-012-896-705	Sequence 705, App
24	2144	74.9	6976	9	US-09-895-793-705	Sequence 705, App
25	2144	74.9	6976	9	US-09-895-814-705	Sequence 705, App
26	2144	74.9	6976	10	US-09-759-143-705	Sequence 705, App
27	2144	74.9	6976	10	US-09-780-669-705	Sequence 705, App
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36	1403.5	49.1	1203	9	US-09-895-793-851	Sequence 851, App
37	1403.5	49.1	1203	9	US-09-895-814-851	Sequence 851, App
38	1403.5	49.1	1203	10	US-09-759-143-851	Sequence 851, App
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40	1403.5	49.1	1203	10	US-09-822-827-851	Sequence 851, App
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42	919	32.1	789	9	US-09-232-880-10	Sequence 10, Appl
43	919	32.1	789	9	US-09-895-793-10	Sequence 10, Appl
44	919	32.1	789	9	US-10-012-896-10	Sequence 10, Appl
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49	919	32.1	789	10	US-09-030-606-10	Sequence 10, Appl
50	919	32.1	789	10	US-09-822-827-10	Sequence 10, Appl
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52	328.5	11.5	1785	9	US-09-938-842A-1709	Sequence 1709, App
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54	279.5	9.8	1542	9	US-09-938-842A-1624	Sequence 1624, App
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56	144.5	5.1	1715	10	US-09-919-781-3	Sequence 3, Appli
57	144.5	5.1	1917	10	US-09-919-781-1	Sequence 1, Appli
58	138	4.8	15231	10	US-09-917-800A-1505	Sequence 1505, App
59	132	4.6	6433	10	US-09-995-542-1	Sequence 1, Appli
60	128.5	4.5	1417	9	US-10-007-132-3	Sequence 3, Appli
61	127.5	4.5	1857	10	US-09-970-516-3	Sequence 3, Appli
62	127.5	4.5	2380	10	US-09-817-676A-13	Sequence 13, Appl
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68	120	4.2	7563	10	US-09-776-167A-5	Sequence 5, Appli
69	120	4.2	8750	10	US-09-776-167A-8	Sequence 8, Appli
70	119.5	4.2	53522	9	US-09-904-968A-1	Sequence 1, Appli
71	119	4.2	7469	10	US-09-776-167A-6	Sequence 6, Appli
72	119	4.2	7771	9	US-09-832-292-38	Sequence 38, Appl
73	119	4.2	14800	10	US-09-954-456-1601	Sequence 1601, App
74	118.5	4.1	4030	9	US-09-990-046-1	Sequence 1, Appli
75	118	4.1	1830	9	US-09-978-295A-419	Sequence 419, App
76	118	4.1	1830	9	US-09-978-697-419	Sequence 110, App
77	118	4.1	1830	9	US-09-978-192A-419	Sequence 419, App

78 118 4.1 1830 9 US-09-999-832A-419 Sequence 419, App
79 118 4.1 1830 9 US-09-978-189-419 Sequence 419, App
80 118 4.1 7755 10 US-09-764-847-1331 Sequence 1331, Ap
81 117 4.1 1587 9 US-10-024-623-6 Sequence 6, Appli
82 117 4.1 2218 9 US-10-098-841-56 Sequence 56, Appl
83 117 4.1 2230 9 US-10-024-623-4 Sequence 4, Appli
84 117 4.1 2264 10 US-09-833-381-883 Sequence 883, App
85 116.5 4.1 14537 10 US-09-962-832-232 Sequence 232, App
86 115.5 4.0 1542 10 US-09-815-242-7726 Sequence 7726, Ap
87 115 4.0 2263 9 US-10-212-980-1 Sequence 1, Appli
88 115 4.0 3960 10 US-09-909-849-1 Sequence 1, Appli
89 114.5 4.0 1835 10 US-09-216-393-80 Sequence 80, Appli
90 114 4.0 5959 10 US-09-954-456-1996 Sequence 1996, Ap
91 112.5 3.9 2062 10 US-09-834-975-821 Sequence 821, App
92 112 3.9 4747 9 US-09-854-133-729 Sequence 729, App
93 111.5 3.9 4391 9 US-09-909-280A-1 Sequence 1, Appli
94 111 3.9 60 9 US-10-012-896-972 Sequence 972, App
95 111 3.9 60 9 US-09-895-814-972 Sequence 972, App
96 111 3.9 2439 9 US-09-954-531-140 Sequence 140, App
97 111 3.9 2439 9 US-09-954-531-359 Sequence 359, App
98 111 3.9 5387 9 US-10-001-873-22 Sequence 22, Appl
99 111 3.9 6432 10 US-09-858-194-3 Sequence 3, Appli
100 111 3.9 6768 10 US-09-858-194-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-838-785-1
; Sequence 1, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
; APPLICANT: Lau, Ted
; APPLICANT: Lin, Rick
; APPLICANT: Parkes, Debbie
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; APPLICANT: Van Heult, Pam T
; APPLICANT: Wu, John
; TITLE OF INVENTION: DNA Encoding a No. US20020009455A1el PROST 03
; FILE REFERENCE: 51831AUSM1
; CURRENT APPLICATION NUMBER: US/09/838,785
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/200,065
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(1943)
US-09-838-785-1

Alignment Scores:
Pred. No.: 1.38e-259 Length: 3320
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-838-785-1 (1-3320)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 1422 TCAGCGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1481

Db 342 GTCAACCTCTAACCCTTGGCCTGGAGGTGTGTTGGCCGACAGGCATCACCTATGTGGCG 401
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 402 CCTCTGCTCTGGAAGTGGGGGTAGAGGAGAACTTCATCACCATGGTGTGGGCATTGGT 461
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 462 CCAGTGTCTGGCTGTCTGTCTCCGCTCTAGGCTACGCCAGTACCACCTGGCGTGA 521
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 522 CCCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTCTGTGAGCCCTC 581
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 582 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCGGATCCAGGCCCTTG 641
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 642 GAGCTGGCACTGCTCATCTGGCGGTGGGCGTCTGGACTTCTGTGCCAGGTGTGCTTC 701
QY 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 702 ACTCCACTGGAGGCCCTGCTCTGTGACCTCTCCGGGACCCGACACCTGTGCCAGGCC 761
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 762 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGCTGCCTGGGTACCTCTCTGCTGCC 821
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 822 ATTGACTGGGACACCACTGCTGCGCCCTACTTGGGCACCCAGGAGGAGTGCCTCTTT 881
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 882 GGCGTGTCTCACCTCTCTCCTCAGTACGAGCCACACCTGCTGTGTGGCTGAGGAG 941
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 942 GCAGCGCTGGGCGCCACCGAGCCAGCAGAGGGCTGTGCGCCCTCTCTTGTGCGCCAC 1001
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
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QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgPheValAlaGluLeuCys 280
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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1122 AGCTGGATGGCACTCATGACCTTCAGCGTGTTCACCGGATTCGTGGCGCGAGGGCTG 1181
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Db 1302 GTCATGGACCGGCTGGTGGCAGGATTCGCACCTCGAGCAGCTATATTGGCCAGTGTGGCA 1361
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Db 1362 GCTTTCCCTGTGGCTGCCGTCACATGCCATGCCGTGCCACAGTGTGCCGCTGGTGACAGCT 1421
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1422 TCAGCGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1481

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Db 1542 GCTAGCAGTGGAGACAGCTGTATGACCACTTCCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1601
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
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Db 1602 TTCCTAATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCCGGGCTC 1661
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QY 481 ArgValValProGlyArgGlyLeCysLeuAspLeuAlaLeuAlaLeuAspSerAlaPheLeu 500
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QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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Db 1842 ACTGCCATATGTTGTCGCCAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1901
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1902 GTAGATTGTGACAAGAGCAGCTTGCCCAATATCTCAGCG 1940

RESULT 2
US-09-232-880-110
; Sequence 110, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangqun
; APPLICANT: Dillon, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-110

Alignment Scores:
Pred. No.: 1.44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-232-880-110 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
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Db 344 GTCACACTGCTAACCTTTGGGCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 464 CCAGTGTCTGGGCTGTGTGTCTCCGCTCCCTAGGCTCAGCCAGTGACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Db 1364 GCTTTCCCTGTGGCTGGCGGTGCCACATGCTGTGCCACAGTGTGGCGCTGGTGCACACT 1423
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Db 1484 TCCTCTACACCGGAGAGCAGGTGTTCTCCGCCAAATACCGAGGGGACACTGGAGGT 1543
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Db 1544 GCTAGCAGTGAGGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
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Db 1604 TTCCCTAATGGACACGTGGGTGCTGGAGGACGTGGCTGCTCCACCTCCACCGCGCTC 1663
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RESULT 3

US-10-012-896-110
; Sequence 110, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-110

Alignment Scores:

Pred. No.: 1.44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x US-10-012-896-110 (1-3410)
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Db 284 ATGGTCCAGAGGCTGGGGTGAGCCGCTGCTGGGCACCCGGAAGCCAGCTCTTGTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTCTTAACCTTTGGCCTGGAGGTGTGTTTGGCCGAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGAGAAAGTTTCATGACCATGGTGTGGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTCTGGGCTGGTCTGTGTCGGCTCTTAGGCTCAGCCAGTACACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleThrPheAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTTCATCTGGGCACCTGCTCTGGGCATCTGCTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCGAGATCCACAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGGCGTGGGCTGTGGAGTCTTCTGGCCAGGTGTGCTTT 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGAGGCGCTGCTCTGACCTTTCGGGACCCCGGACCACCTGCTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGTGCTGGGTACCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCTGCTGGCCCTTACCTGGGCACCCAGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCTCATCTTCTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCCA 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGCGCGCGCTTGGCTTTCGGAACTTGGGCGCCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACAGCTGTGCTGCCGATGCCCGACCTGCGCGGCTCTTCTGGCTGAGCTGTGCTG 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
Db 1124 AGCTGGATGGCACCTCATGCTTACGCTGTTTATACAGGATTTCTGTGGCGGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTGGCCAGAGCTGAGCGGGCCACCGAGGCCGAGGAGACTATGATGAAGGC 1243

Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTTCGGATGGCAGCTGGGGGTGTTCTTCGTCAGTCGCACATCCCTGGCTTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyLeuAlaSerValAla	360
Db	1304	GTCAATGGACCGCGTGGTGACGGATTTCGGCACTTCAGCAGTCTATTGGCCAGTGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCTTTCCTGCTGGCTCCGGTGCACATGCCTGTCCACAGCTGTGGCGCTGGTCACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyThrLeuAla	400
Db	1424	TCAGCGCGCTCACCGGGTTCACTTCTCAGCGCTTCAGAGATCCCGCCTACACACTGGCC	1483
Qy	401	SerLeuTyHisArgGluLysGlnValPheLeuProLysTyArgGlyAspThrGlyGly	420
Db	1484	TCCTCTTACCACCGGAGAGCAGGTGTTCCTGTGCCAAATACCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerLeuAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGTAGACAGCTGTATGACCACTTCTTCGCAGGCCCTTAAGCTGTGGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGCCTTCCACCTCCACCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGGGGGGCCTCTGCCGTGATCTCCGTACGTGTGGTGGTGGTGAGCCACCGCAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTGTTCGGGCGGGGCATCTCCCTGGACCTCGCCATCTCTGGATAGTGCCTTCTGT	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATGTCTCCAGCTCAGCCAGCTGTCT	1843
Qy	521	ThrAlaTyMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyPheAlaThrGln	540
Db	1844	ACTGCCCTATATGTTCTCCCGCAGCCTGGGTCTGTGTCGCCATTTTACTTTCCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTySerAla	553
Db	1904	GTAGTATTTTGACAAGAGCAGCTTGGCCAAATACTCAGCG	1942

RESULT 4

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US-09-895-793-110						
: Sequence 110, Application US/09895793	:					
: Publication No. US20020192763A1	:					
: GENERAL INFORMATION:	:					
: APPLICANT: Xu, Jiangchun	:					
: APPLICANT: Dillon, Davin C.	:					
: APPLICANT: Mitcham, Jennifer L.	:					
: APPLICANT: Harlocker, Susan L.	:					
: APPLICANT: Jiang, Yuqiu	:					
: APPLICANT: Kalos, Michael D.	:					
: APPLICANT: Retter, Marc W.	:					
: APPLICANT: Stolk, John A.	:					
: APPLICANT: Day, Craig H.	:					
: APPLICANT: Vedvick, Thomas S.	:					
: APPLICANT: Carter, Darlick	:					
: APPLICANT: Li, Samuel X.	:					
: APPLICANT: Wang, AiJun	:					
: APPLICANT: Skeiky, Yasir A.W.	:					
: APPLICANT: Hepler, William T.	:					
: APPLICANT: Henderson, Robert A.	:					
: APPLICANT: Hural, John	:					
: APPLICANT: McNeill, Patricia D.	:					
: APPLICANT: Houghton, Raymond L.	:					
: APPLICANT: Vinals de Bassols, Carlot	:					

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QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGTGTCCATGCCGGCCCGCTTGGCTTTCCGAAACCTGGCGCCCTGCTTCCCGCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGlnLeuCys 280
Db 1064 CACCAGCTGTCTGCGCATGCCCCGACCCCTCGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGlnGlyLeu 300
Db 1124 AGCTGGATGSCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGlnProGlyThrGlnAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCTGCCAGAGCTGAGCGGGGCACCGAGGCGCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCCTGGGGCTGTTCTCTGACGTGGCCATCTCCCTGGTCTTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
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QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTCTGGCTGCGGTGTCACATGCTCTCCACAGTGTGGCGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCTCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACCCCGGAGAGCAGGTGTTCTCTGCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCCTGATGACAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
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QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGlnProThrGlnAla 480
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QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 5

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US-09-895-814-110
; Sequence 110, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
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; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-895-814-110
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Alignment Scores:

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Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-895-814-110 (1-3410)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTTGGCCGCGAGGCATCACCTATGTGCCG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGAAGCTGGGGGTAGAGAGAGTTCATGACCATGTGCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCGGGCGTGGGCTGCTGGACTTCTGTGCCAGGTGCTTCTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Qy 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
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Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTCGCCGATGCCCGCACCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGCGAGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTGGCCAGAGCTGAGCGGGCCAGCCGAGGCGCCGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCTGGGGCTGTCTCGAGTGGCGCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGACCGCGTGGTGACCGATTTCGGCACTCGGCAGTCTATTGGCCAGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCTTTCCTGTGGTGGCGGTGGCCACATGCTGTGCCACAGTGGCGGTGGTGCACAGCT 1423
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Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
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Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAAGCGGACTTGGCCAAATACTACGCG 1942
RESULT 6
US-09-745-288-100
; Sequence 100, Application US/09745288
; Patent No. US20010018058A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-745-288-100
Alignment Scores:
Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-745-288-100 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGGTGAGCGCTGCTGCGGACCCGGAAGCCAGCTCTTGTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCGAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGGTCTGGGCATTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCGCTGTGCTGCTCCCGCTCTAGGCTCAGCCAGTGACCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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Db 1304 GTCATGGACCGCTGGTCAGGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTGCTGGCTGCCGTGCCACATGCTGCTGCCAGTGTGGCGTGTGACAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACCCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGT 1543
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Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
... RESULT 7
US-09-759-143-110
; Sequence 110, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-110
Alignment Scores:
Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-593-793A-113 (1-553) x US-09-759-143-110 (1-3410)
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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGTGCGCACCGGAAAGCCAGCTCTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCC 403
Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGGAGAAAGTTCATGACCATGCTGTGGCATGTGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAAGTCTGGGCGCTGTGTGTCTCCGCTCTAGGCTCAGCCAGTCAGCCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTCTGCTGAGCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGTGTGTGCCCGGATCCCCAGGCCCTCG 643
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Qy	121	GlueuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCGGGCGGTGGGGCTGCCTGGACTTCTGTGGCCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGAGCACTGTGCGCAGGCC	763
Qy	161	TyTserValTyrrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrrLeuLeuProAla	180
Db	764	TACTCTGCTCATGCTTCATGATCAGTCTTGGGGCTGCCTGGGCTACTCTCGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrrLeuGlyThrGlnGluGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTAGTGCCTTGGCCCTTACCTGGGACCCAGAGGAGTGCCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTTGCTCACTCATCTTCTTCACTTCGCTAGCAGCACACTGCTGGTGGCTAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCGAGCGACAGAGAAGGCGTTCGGCCCTCTCTTGTGCGCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCGGGCGCGCTGGCTTTCGGAACCTGGGCGCCCTGTTCCCGCGGTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCACTGTGCTGCGCCGATGCCCGCGACCCCTGCGCCGCGCTCTGTGTGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGCACATCATGACCTTCACGCTGTTTTACACGGATTTTCGGGGCGAGGGCGTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGCGCTGCCAGAGCTAGCGGGGACCCGAGGCGCCGAGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTGCGATGGGACGCTGGGGCTGTTCCTTCAGCTGCGGCATCTCCCTGGTCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrrLeuAlaSerValAla	360
Db	1304	GTCA TGACCGCGCTGGTGACCGATTTCGGCACTCAGCAGAGTCTATTGGCCACGTGTGCCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCTTTCCTCTGGCTCGCGTGCCACATGCCTGTGCCACAGTGTGGCGTGGTGACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrrThrLeuAla	400
Db	1424	TCAGCGCCCTTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	1483
Qy	401	SerLeuTyrrHisArgGluLysGlnValPheLeuProLysTyrrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCCACCGGAGAGCAGGTGTTCCTGCCCAATACCCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGGAGACAGCTGATGACCAGCTTCCTGCCAGCCCTTAAGCCTGGAGCTCCC	1603
Qy	441	PheProasnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACCTGGGTGCTGGAGCAGTGGCTTCTCCCACTCCACCGCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGCGCTCTGCCCTGTGATGTCCTCGTACGTGTGTGGTGGGTGGAGCCACCGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500

Db	1724	AGGTGGTTCGGCGCGGGCATCTGCCCTGGACCTCGGCATCCCTGGATAGTGCCTTCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTGCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGTCACGCTCAGCAGTCGTGC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCTATATGGTGTCTGCCGCGAGCCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGATATTTGACAAGAGCGGACTTTGGCCAAATACTACAGG	1942
RESULT 8			
US-09-780-669-110			
; Sequence 110, Application US/09780669			
; Patent No. US20020051977A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqul			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Hepler, William			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C24			
; CURRENT APPLICATION NUMBER: US/09/780,669			
; CURRENT FILING DATE: 2001-02-09			
; NUMBER OF SEQ ID NOS: 943			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 110			
; LENGTH: 3410			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-780-669-110			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			
US-09-593-793A-113 (1-553) x US-09-780-669-110 (1-3410)			
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Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	
Db	344	GTCACCTGCTACCTTTGGCCTGGAGGTGTGTTTGGCCGCGCAGGCATCACCTATGTCCG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60	

Db 404 CCTCTGCTGCTGAAGTGGGGGTAGAGAGAAAGTTTCATGACCATGCTGCTGGGCATGTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTCTGGGCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTACCCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGATCCAGGCGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
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QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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QY 261 HisGlnLeuCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTGGCGCATGCCCGCACCCCTCGCGCGCTCTGCTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCAGCGTGTTCACCGATTTCTGTGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCCNAGACTGAGCGGGCACCGAGGCGCGGACACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCGCTGGGCTGTCTCTGCACTGCGCATCTCCTGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
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QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
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QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCGCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
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Alignment Scores:

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
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QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCGCTCTGCTGTGATGCTCCGACGCTGGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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Db 1784 CTGTCCCACTGGCCCATCTCCCTGTTTATGGCTCCATTTGCCAGCTCAGCCAGTCTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTTCTGCCGAGCCCTGGGTCTGGTCTGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGCGACCTTGGCCAAATACTCAGCG 1942

RESULT 9

US-09-030-606-110
; Sequence 110, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-110

Pred. No.:	1.44e-259	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-09-593-793A-113 (1-553) x US-09-030-606-110 (1-3410)			
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Db	284	ATGGTCCAGAGCGTGGGTGAGCGCGCTGCTGGCGCACCGAAGCCACGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCAACCTGCTAACCTTTGGCGCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTTCATGACATGTTGGTGGCATTTGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTGTGGCGCTGGTCTGTGTCGGCTCCTAGGCTCAGCCAGTGACCATGGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGTCTTGGGCATCTCTGCTGAGCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGGCGCGGTGCTAGCAGGGCTGTGTGCCGGATCCCGAGGCCCTGT	643
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACATGCTCCTGGGCGTGGGCTGTGGACTTCTTGGCGCAGGTGTCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCCCTCTCTGACCTCTCCGGGACCCGACCACTGTGCGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGTATGCTTTCATGATCAGTCTTGGGGCTGCCCTGGGCTACCTCTGCTGCTGC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACAGTGGCCCTGGCCCTACCTTGGGCACCCAGGAGGAGTGCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCCTGCTACCCCTCATCTTCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGTGGGCCCCACCGAGCAGCAGAGGGCTGTGCGGCCCTCTCTGTCGCCCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACTTGGCGCGCCCTGCTTCCCGCGGTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGCTCGCGCATGCCCGCACCTGCGCGCGGCTCTTCGTGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTTCCGTGGCGGAGGGGTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGlnAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGCGGTGCCAGAGCTGAGCCGGGCACCGAGGCGCGGAGACACTATGATGAAGGC	1243

Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCCGATGGCAGCCTGGGCTGTCTCTGCAGTGGCGCATCTCCCTGCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGGACCGCGCTGGTGACGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCTTTCCTCTGTCGCTGGCGTGCACATGCTGTCCCACAGTGGCGGTGGTGCAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCGCCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCTTCCCTACACACTGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCAACCGGAGAGCAGGTGTCTGCCCAATACCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTAGGACAGCCTGATCACCAGCTTCTTCCAGGCCCTAAGCCTTGGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCCCTAATGGACAGCTGGGTGCTGGAGCAGTGGCTGTCCACCTCCACCCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCTCTGCTGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTGTGTTCGGCGCGGGGCTGCTGCTGAGCCTCGCCATCTTGGATGTCCTTCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCAGGTGGCGCCATCCTGTTATGGCTCCATTTGCCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTCCCTATATGTGTCTGCGCGAGGCTTGGTGTGCTGCTGCTGCTGCTGCTGCTG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTTGACAAGAGCGACTTGGCCAAATACCTACGCG	1942

RESULT 10
US-09-822-827-110
; Sequence 110, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-822-827-110

Alignment Scores:
Pred. No.: 1.44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-822-827-110 (1-3410)
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Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCCTGAGAGGTGTGTTGGCCGAGGATCACCTATGTGGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluTysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGCAAGTGGGGCTAGAGGAGAAGTTTCATGACCATGCTGTGGGCATTG 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTCCCGCTCCCTAGGCTCAGCCAGTGCACACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACACTGCTCTGGGCATCTGCTGAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCACAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACCTCATCTCGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCACCTGGAGGCCCTGCTCTGACCTCTTCGGGACCCGGACCACTGTGCCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATGCCTTCATGATCAGTCTTGGGGCTGCCTGGGCTACCTCTCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCAAGTGCCTTGCCGCCCTTACCTTGGGCACCCAGGAGGTGCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGTCTCACCTCATCTTCTACCTGCTGAGGACCACTGCTGGTGGCTGAGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCCACCAGGACGACAGAGGGCTGTGGGCCCTCTCTTGTGCCCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGCTGCTTCGGAACCTTGGGCGCCCTGCTCCCGGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAAGCTGTGCTGGCATGCCCGACCTTGGCCCGGCTCTTCTGGCTGAGCTGTGC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGGCACCGAGGGCCGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGACGTGGGCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuLeuAlaSerValAla 360
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Db 1304 GTCATGGACGGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValaValValThrAla 380
Db 1364 GTTTTCCCTGTGGCTGCGGGTGCCACATGCTGTCCACAGTGTGCCGTGGGTGACAGT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCCTACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTAGGACAGCCTGATACCACTTCTTCCGAGGGCCCTAAGCCTGGAGCTCCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1604 TTCCCTAATGACACGTGGGTCTGGAGCAGTGGCTGTCTCCACCTCCACCCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyCluProThrGluAla 480
Db 1664 TGCGGGGCTCTGCTGTGATGCTCTCCGTACGTGTGTGGTGGTGGTGGTGGTGGTGG 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGGTTCGGGGCGGGGACATCTGCTGGACCTGGCCATCTGGATAGTCCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCCAGGTGGCCCCATCTCTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGCTGTCTGCCAGCGCTGGTGTCTGGTGGCCATTTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTGACAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 11
US-09-115-453-110
; Sequence 110, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115.453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-110
Alignment Scores:
Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-115-453-110 (1-3410)
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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGGTAGCGCCCTGCTGCGGCACCGAAAGCCAGCTCTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTCATGACCATGGTGTGGGCATTTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTCTGGGCTGTGTCTGCTCCGCTCTCTAGGCTCAGCCAGTGACCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CCCTATGGCCGCGCGGCCCTTCATCTGGGCACCTGTCTTGGGCATCTGCTGAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGTGGCTAGCAGGGCTGTGTCGCCGATCCCAAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyClnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGGCGTGGGCTGTCTGACTTCTGTGGCCAGGTGTGCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATGCTTTCATGATCACTTGGGGCTGCTGGGGTACTCTCTGCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGACACCACTGCTGCTGCGCCCTACCTGGGCACCCAGGAGGTGCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 884 GCGCTGCTACCGCTCATCTCTCACTGCGTAGCAGCACCACTGCTGCTGGCTGAGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCCCCACGAGCCAGCAGAGGCTGTGCGGCCCTCTCTGTGCGCCCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCGCATGCCCGCACCTGCGCGGCTTCTGCTGGCTGAGCTGTC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGGGCGAGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCGAGGGCCCGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCGCTGGGCTGTCTGTCAGTGGCGCATCTCCCTGGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCACCGATTGCGCACTGCGCAGCTATTTGGCCAGGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380

Db 1364 GCTTTCCCTGTGGCTGCGGTTGCCACATGCGCTGTCCCACAGTGTGGCGGTGGACGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTTCACCGGTTTCACCTTCTCAGCCCTGCGAGATCCTGCCCTACACACTGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCACCGGAGACGAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCCTGATGACCACTCTCTGCGCAGGCGCTAAGCCTGGAGCTCCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGACACAGTGGGTGCTGGAGCAGTGGCCCTGCCACCTCCACCCCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGGAGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTGTCCGGCGCGGCGCATCTGCTGGACCTGCGCATCTCGATAGTGCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCTAGGTGGGCCCCATCCTCTTTATGGGCTCCATGTGCCAGCTCAGCCAGTCTCTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTGCGCGCAGGCGCTGGGTCTGGTTCGCCATTTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGCGGACTTGGCCAAATACTACGCG 1942

RESULT 12
US-10-012-896-704

: Sequence 704, Application US/10012896
: Publication No. US20020183251A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqiu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William F.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Wantanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/012.896
: CURRENT FILING DATE: 2001-12-10

: NUMBER OF SEQ ID NOS: 1011									
: SOFTWARE: FastSeq for Windows Version 3.0									
: SEQ ID NO 704									
: LENGTH: 4034									
: TYPE: DNA									
: ORGANISM: Homo sapiens									
US-10-012-896-704									
Alignment Scores:									
Pred. No.:	7,21e-246	Length:	4034						
Score:	2716.50	Matches:	553						
Percent Similarity:	70.09%	Conservative:	0						
Best Local Similarity:	70.09%	Mismatches:	0						
Query Match:	94.95%	Indels:	236						
DB:	9	Gaps:	1						
US-09-593-793A-113 (1-553) x US-10-012-896-704 (1-4034)									
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20						
Db	281	ATGGTCCAGAGGCTGTGGGTGAGCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGCTG	340						
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40						
Db	341	GTCAACCTGCTAACTTTTGGCTGAGAGTGTTTGGCGCAGGCATCACCTATGTGGCG	400						
Qy	41	ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly	60						
Db	401	CCTCTGCTGGAAGTGGGGTAGAGAGAGATTATGACCATGAGTGGTCTGGGCATTGGT	460						
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80						
Db	461	CCAGTGCTGGCGCTGTGTGCTCCGCTCTAGGCTCAGCCAGTGACCACTGGCGTGA	520						
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100						
Db	521	CGCTATGGCCCGCCGCCCTTCTATCTGGGCATCTGCTTGGGCATCTGCTGGACCTC	580						
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120						
Db	581	TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGCTGTGTGCCGGATCCAGGCCCTG	640						
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140						
Db	641	GAGCTGGCACCTGCTCATCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC	700						
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160						
Db	701	ACTCCACTGGAGGCCCTGCTCTGTACCTTTCGGGACCTTCGGGGACCGGACCACTG	760						
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180						
Db	761	TACTCTGTCTATGCTTCATGATAGCTTGGGGCTGCCCTGGGCTACCTCTGCTGCC	820						
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200						
Db	821	ATTGACTGGGACACCACTGGCCCTGGCCCCCTACCTGGGCACCCAGGAGGTGCTCTTT	880						
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220						
Db	881	GGCTGTCTCAACCTCATCTTCTCACTTCGCTAGCAGCCACACTGCTGGTGGCTGAGG	940						
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240						
Db	941	GCAGGCTGGGGCCCCACCGCCAGCAGAGGGGTGTGGGGCCCCCTCCTTGTGGCCCCAC	1000						
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260						
Db	1001	TGCTGTCCATCCGGGGCCGCTTGGCTTTCGGAACTTGGGGCCCTGCTTCCCGGGCTG	1060						
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys	280						
Db	1061	CACCAGCTGTGCTGCCGATGCCCGCACCTCTGGCGGGCTTCTGCTGGCTGAGCTGGC	1120						

Qy 405 gLuLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAAGCAGGTGTTCTTCGCCAAATACCGAGGGACACTGGAGGTGTAGCAGTGAGGA 2260
Qy 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCAGCTTCCTGCCAGGCCCTTAAGCCTGGAGCTCCCTTCCTAATGGACA 2320
Qy 445 svalGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGCTGAGGAGCAGTGCCTGCTCCACCTCCACCGCGCTCTCGGGGCGCTCTGC 2380
Qy 465 aCysAspValSerValArgValValGlyGluProThrGluAlaArgValValProG1 485
Db 2381 CTGTGATGCTCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCCAGGGTGTTCGGG 2440
Qy 485 yArgGlyLecCysLeuAspLeuAlaLeuLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CCGGGGATCTGCCTGGACCTCGGCATCCTGGATAGTGCCCTTCCTGCTGCCAGGTGGC 2500
Qy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCCATCCCTGTTATGGCTCCATTGTCAGCTCAGCCAGTCTGTCTACTGCTATATGGT 2560
Qy 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCTGCCGAGCGCTGGGTCTGGTGGCCATTACTTTGCTACACAGGTAGTATTGCAA 2620
Qy 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACTTGGCCAAATACTACGCG 2645

RESULT 13

US-09-895-793-704
: Sequence 704, Application US/09895793
: Publication No. US20020192763A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqiu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121-534C2
: CURRENT APPLICATION NUMBER: US/09/895,793
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 704
: LENGTH: 4034
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-895-793-704
Alignment Scores:

Pred. No.: 7.21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 9 Gaps: 1
US-09-593-793A-113 (1-553) x US-09-895-793-704 (1-4034)
Qy 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGTGCGGCACCGGAAGCCACCACTCTTGTGCT 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGTGGAAGTGGGGTAGAGGAGAAGTTCATGACCATGGTGTCTGGGCATTGGT 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTCTGGGCCCTGGTGTGCTCCGCTCCTAGGCTCAGCCAGTGACCATGGCGTGG 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCCCGCGGCCCTTCATCTGGGCACCTGTCTTGGGCATCTCTCTGAGCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTyrPheAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGTGGCTAGCAGGGCTGTGTGCCGGATCCAGGCCCTCTG 640
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTCTGGGCTGTGGGCTGTGTGACTTCTGTGGCCAGGTGTGCTTC 700
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGGGAGCCGACCACTGTCTGCCAGGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 820
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTCACTGGGACACCACTGGCCCTGGCCCTTACCTGGGACCCAGGAGGAGTGCTCTTT 880
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCTGTCTACCTTCATCTCTCCTCCTGCTAGCAGCCACACACTGTGTGGTGGCTGAGGAG 940
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTCTGCGCCAC 1000
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATGCGGGGCCGCTTGGCTTTCGGAACTTGGGCGCCCTGCTTCCCGGCTG 1060
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACAGCTGTGCTGCCGATGCCCGCCACCTGCGCCGCGCTCTTCGTGGTGGCTGACTGTGC 1120
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGCACTCATGACCTTACACGCTGTTTACACGGATTTTCGTGGGCGAGGGCTG 1180
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGlnAlaArgArgHisTyrAspGlu--- 319
Db 1181 TACCAGGGCGTGGCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTATGATGAAGGT 1240

Qy 319 ----- 319
Db 1241 AAGGCTTTGGCAGCCAGCAGAGGCTGGTGTGGAGAGCCGCCACAGACGACACTCGGG 1300
Qy 319 ----- 319
Db 1301 GCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTGTCAGGAAAGTGGG 1360
Qy 319 ----- 319
Db 1361 ATGGAGCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCTGGGTTTC 1420
Qy 319 ----- 319
Db 1421 AGGAAGGCTCTGGCTGTCTAGGAGTCTGATCAGAGTCTGTGCCCCAGTTTGACAGAAG 1480
Qy 319 ----- 319
Db 1481 GAAAGCGGAGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTCAGAT 1540
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; Sequence 704, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-704
Alignment Scores:
Pred. No.: 7, 21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 9 Gaps: 1
US-09-593-793A-113 (1-553) x US-09-895-814-704 (1-4034)


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Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Db 2621 GAGCGACTTGGCCAAATACTCAGCG 2645
RESULT 15
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; Sequence 704, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-704
Alignment Scores:
Pred. No.: 7, 21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 1 Gaps: 1
US-09-593-793a-113 (1-553) x US-09-759-143-704 (1-4034)
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Db 2621 GAGCCAGCTGGCCAAATACTCAGCG 2645
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RESULT 16
US-09-780-669-704
: Sequence 704, Application US/09780669
: Patent No. US2002005197A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqui
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darriek
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C34
: CURRENT APPLICATION NUMBER: US/09/780,669
: CURRENT FILING DATE: 2001-02-09
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 704
: LENGTH: 4034
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-780-669-704

Alignment Scores:
Pred. No.: 7,21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-780-669-704 (1-4034)
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; Sequence 704, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28

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; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-704

Alignment Scores:
Pred. No.: 7,216-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 10 Gaps: 1

US-09-593-793a-113 (1-553) x US-09-822-827-704 (1-4034)

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QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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; Sequence 702, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 702
LENGTH: 4894
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-702

Alignment Scores:
Pred. No.: 5,33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 9 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-895-814-702 (1-4894)

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RESULT 21
US-09-759-143-702
; Sequence 702, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-702

Alignment Scores:
Pred. No.: 5.33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
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Query Match: 88.73% Indels: 526
Db: 10 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-759-143-702 (1-4894)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
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RESULT 22
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; Sequence 702, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-780-669-702

Alignment Scores:
Pred. No.: 5,33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 10 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-780-669-702 (1-4894)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyValPro 40
Db 334 GTCAACCTGTCAACCTTGGCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 393
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
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Db 513 CCTCTGCCCTGGGAGCTGCTTTGAGGGAGAGAGTGTGCTGCTGGGAAGCATTTGCTGGGCA 572
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Db 573 GGAGGTCACCCCTGGGCTGAGGGGGGCACACCAAGAGAAGAAGAAATACCAGACATA 632
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Db 1233 TTCTCAGGAGCTTGGTTTCCCTTCCCTTCCCTTTACTTTGCCAGCCATTGACTCAT 1292
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Db 1293 ACTACTTCCCTTTTCGACGCAATGTGTCCAGTGTGGGCTGTGTGTGTCGCCGCTCCA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
Db 1353 GGCTCAGCCAGTGACCACTGGCGTGAAGCTATGGCGCGCGGCGCTTCATCTGGGCA 1412
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTGGCATCTCTGTGAGCCTTTCTCATCCCAAGGCGCGCTGAGCAGGG 1472
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGCTGTGCCGATCCCAAGGCCCTTGGAGCTGGCACTGCTCATCTGGGCGTGGGCTG 1532
QY 132 LeuAspPheCysGlyGlnValCysPheTrpProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCCAGGTGTCTTCACTCCACTGGAGGCCCTGTCTCTGACCTCTTC 1592
QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1593 CGGAGCCCGGACCACTGTGCCAGGCTACTCTGTCTATGCTTATGCTTATGATCATGCTTGG 1652
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspTrpSerAlaLeuAlaProTyr 191
Db 1653 GGTGCTGGGTACCTTCTCTGCTGCGCATGTGCTGGACACCACTGCTGCTGGCCCTTAC 1712
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
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QY 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGCCACACTGTGTGGCTGAGGAGCGCTGGGCCCCACCCAGCAGCAGAGGG 1832
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTGGCCCCCTCTTGTGCCCCCACTGCTGTCCATGCGGGCGCGCTTGGCTTCCGG 1892
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGCGCCCTGTCTCCCGGCTGCACCACTGTGTGTGCGCATGCCCCCAGCCCTG 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
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QY 292 TyrThrAspPheValGlyGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACACGATTTCTGTGGCGAGGGCTGTACCAAGGCTGCCAGAGCTGAGCGGGCACC 2072
QY 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 2073 GAGGCCCGGAGACACTATGATGAAGGTAAAGCCCTTGGCAGCCAGCAGAGCTGTGTGG 2132
QY 319 ----- 319
Db 2133 AGCGGCCACAGAGACACTCGGGGCTGTCTCTGGGCTGTCTCTCCATCCTGGC 2192
QY 319 ----- 319
Db 2193 CCGGACTTCTCTCAGGAAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
QY 319 ----- 319
Db 2253 GTGTGAACATCTCTGCTTGGGTTTCAGGAAGSCCTCTGGCTGCTTAGAGTCTGATC 2312
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Db 2613 TTCTCTGAGGTCTAGTGAAGAACCTAGACTCCATTGCTAGAGGTAGAAAGGGAGAGG 2672
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QY 319 ----- 319
Db 2733 TTCTCATCTCCCTGAGACTGCTCCGACCCCTTCCCTCCAGGCTCTGTCTGATGGCCCCCTC 2792
QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCCTCTGCAGGCGTTCGGATGGCAGCCTGGGGCTGTCTCTCAGTGGCGCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356

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Db 2853 GGTCTTCTCTCTGGTCATGGACCGCTGGTGACGGATTTCGGCACTCGAGCAGTCTATT 2912
Qy 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GCCAGTGGGAGCTTTCCCTGTGGTGCCGGTGCCACATCCCTGTGCCACAGTGTGGC 2972
Qy 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGTGTACAGCTTCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCC 3032
Qy 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGl 416
Db 3033 CTACACACTGGCTCCCTCTACACCGGAGAGAGGTGTCTCTGCCCAATACCGAGG 3092
Qy 416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGTGCTAGCAGTGAGACAGCCTGATGACCACTTCTGCGCAGGCCCTAA 3152
Qy 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGGAGCTCCTCCCTAATGGACACGTGGGTGTGGAGCAGTGGCTCTCTCCACC 3212
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Db 3213 TCCACCCCGCTCTCGGGGCTCTGCCTGTGATCTCCGTACGTGTGGTGGTGA 3272
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Qy 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
Db 3333 TAGTGCCTCTCTGCTGCCAGGTGCCCATCCCTGTTATGGCTCCATTGTCCAGCT 3392
Qy 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536
Db 3393 CAGCCAGCTGTGCACTGCTATATGTGTCTGCCGAGCGCTGGGTCTGTGGTCGCATTTA 3452
Qy 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 3453 CTTTGTACACAGGTAGTATTGTGACAGAGCGACTTGGCCAAATACTCAGCG 3504
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RESULT 23

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US-09-822-827-702
; Sequence 702, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-702
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Alignment Scores:
Pred. No.: 5,33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 10 Gaps: 2
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US-09-593-793A-113 (1-553) x US-09-822-827-702 (1-4894)

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Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu 57
Db 394 CCTCTGCTGCTGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTCT -GGGTGAGTC 452
Qy 57 - 57
Db 453 ACTACATCCTCTCTCTCTCTCTCCATACATGCCACCTGGCATGTGGGACAGGAGTA 512
Qy 57 - 57
Db 513 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGGTGTCTCTGGGAAGGCATTGCTGGGCA 572
Qy 57 - 57
Db 573 GGAGGTGACCTTGGGCTGAGGGGGGCACACCAAGAGAAGAAGAAATACCAAGGACATA 632
Qy 57 - 57
Db 633 CCCCAGTCACCTCTGGATCCCTGCTGTCACAGAGCCTGGCTCATAGGAGACACTGGAG 692
Qy 57 - 57
Db 693 AAATGCTCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCTATTATGCG 752
Qy 57 - 57
Db 753 TTACAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAAGCAGAGCCTTTTAAGAGG 812
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Db 813 TTAGGTAAGTCTTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
Qy 57 - 57
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Qy 57 - 57
Db 1233 TTCTCAGGAGCTGGTTCCCTTCCCTTCCCTTCTTACTTGTCCAGCCATGTACTCAT 1292
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Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
```


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APPLICANT:	Dillon, Davin C.
APPLICANT:	Mitcham, Jennifer L.
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APPLICANT:	Day, Craig H.
APPLICANT:	Vedvick, Thomas S.
APPLICANT:	Carter, Darrick
APPLICANT:	Li, Samuel X.
APPLICANT:	Wang, Aijun
APPLICANT:	Skeiky, Yasir A.W.
APPLICANT:	Hepler, William T.
APPLICANT:	Henderson, Robert A.
APPLICANT:	Hural, John
APPLICANT:	McNeill, Patricia D.
APPLICANT:	Houghton, Raymond L.
APPLICANT:	Vinals de Bassols, Carlota
APPLICANT:	Foy, Teresa
APPLICANT:	Fanger, Gary R.
APPLICANT:	Wantanabe, Yoshihiro
APPLICANT:	Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	
FILE REFERENCE: 210121.427C27	
CURRENT APPLICATION NUMBER: US/10/012,896	
CURRENT FILING DATE: 2001-12-10	
NUMBER OF SEQ ID NOS: 1011	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 705	
LENGTH: 6976	
TYPE: DNA	
ORGANISM: Homo sapiens	
US-10-012-896-705	
Alignment Scores:	
Pred. No.:	1,166-191
Score:	2144.00
Percent Similarity:	30.48%
Best Local Similarity:	30.48%
Query Match:	74.94%
DB:	9
US-09-593-793A-113 (1-553) x US-10-012-896-705 (1-6976)	
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Db	165 ATGGTCCAGAGGCTGGGTGAGCGCCCTGCTGGCGCACCGAAGCCAGCTCTTGCTG 224
Qy	21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db	225 GTCAACCTGCTAACTTTGGCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCGG 284
Qy	41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db	285 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGCT-GGGTGAGTTC 343
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Db	344 ACTACATCCTCCTCCTTCCCTGTTCCAGTATACATGCCACCTGGCATGTGGGACAGAGTA 403
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Db	404 CCTCTGCCCTGGGAGCTGCTTGGAGGAGAGGTGGTCTGCTGGGAAGGACATTGCTGGGCA 463
Qy	57 ----- 57
Db	464 GGAGGGTGACCTGGGCTGAGGGGGCACACCAAGAGAAAGAGAGATACCAAGACATA 523
Qy	57 ----- 57

Db	524	CCCCAGTCACTCTTGGATCCCTGGTCTGCACAGAGCCTTGGCTCATAGAGACACTGGAG	583
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Db	584	AAATGCTCCTAAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC	643
Qy	57	-----	57
Db	644	TTACAACCACCATTTCAGGTGATCCATTTTACAGAGAGGAAGCAGAGCGCTTTTAAGAGG	703
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Db	704	TTAGTAACTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA	763
Qy	57	-----	57
Db	764	GGTCTCCCAGCGGAGCTTGTCTTACCCTTAGGACAGGGGTGGACTCCTGACTCTGCA	823
Qy	57	-----	57
Db	824	GATAAATTCTACAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACACCCCTCACCC	883
Qy	57	-----	57
Db	884	CCAGGAGAGGGGCCCTTGTGAGGATTGCGAGCTCTGGAGTCACACTGCTTGTGTGAAC	943
Qy	57	-----	57
Db	944	GCTGCTCTTACCCTCCCTAGGTCTCGGCTTTGAATAAGTATCATCTMTTGTGCTCC	1003
Qy	57	-----	57
Db	1004	ATGCCTCAGTTTGTCCATCTGAAATGGGGGCATCTGTAATGCCCTGTGTATGAGGAGTA	1063
Qy	57	-----	57
Db	1064	AATTACAGTCCCTGTGAAGAGTAGCACAGTGTGAGTACGGAATGTTATTTCATCC	1123
Qy	57	-----	57
Db	1124	TTCTCAGGAGCTTGGTTCCCTTCCCTTGGCCCTTTACTTGTCCAGGCATTTGACTCAT	1183
Qy	58	-----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71	
Db	1184	ACTACTTCCCTTCTTGCAGGCATTTGGTCCAGTGTGGGCTGTGTGTGTCGCTCTTA	1243
Qy	72	GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91	
Db	1244	GGCTCAGCCAGTGACACTGGCGTATGCCCGCCGCCCTTTCATCTTGGGCA 1303	
Qy	92	LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111	
Db	1304	CTGTCTTTGGGATCTCTGCTGAGCCTCTTCTCATCCCAAGGGCGGCTGGTAGCAGG 1363	
Qy	112	LeuLeuCysProAspArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131	
Db	1364	CTGCTGTGCCCCGGATCCCGAGGCCCTGGAGCTGGGACCTGCTCATCTGGGCTGGGCTG 1423	
Qy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151	
Db	1424	CTGGACTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTC 1483	
Qy	152	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171	
Db	1484	CGGGACCGGGACACTGTGCCAGGCCTACTCTGTCTATGCTTCAATCATCATGCTTGGG 1543	
Qy	172	GlyCysLeuGlyTyrLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191	
Db	1544	GGCTGCCCTGGGCTACTCTCTGCTTGCCTTGCCTGGGACACCAAGAGAGATACCAAGACATA 1603	
Qy	192	LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211	

Db	1604	CTGGCGCACCCAGGAGGAGTGCCCTCTTTTGGCCCTGCTCACCCCTCATCTTCTCCTCACCTTGGCGTA	1603
Qy	212	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly	231
Db	1664	GCAGCCACACTGCTGTGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGAGAGGG	1723
Qy	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg	251
Db	1724	CTGTGCGCCCCCTCTTGTGCGCCCCACTGCTGTCCATGCGGGCGCGCTTGGCTTCCGG	1783
Qy	252	AsnLeuGluAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu	271
Db	1784	AACCTGGCGGCCCTGCTTCCCCGGCTGCACCACTGTGCTGCCGATGCCCGACCCCTG	1843
Qy	272	ArgArgLeuPheValAlaGluLeuLeuLeuSerTrpMetAlaLeuMetThrPheThrLeuPhe	291
Db	1844	CGCCGGCTCTTCGTGGCTGAGCTGTCACGTGGATGGCACTCATGACCTTCACCGCTGTT	1903
Qy	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr	311
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Qy	312	GluAlaArgArgHisTyrAspGlu-----	319
Db	1964	GAGGCGCGGAGACACTATGATGAAGGTAAAGGCTTTGGCAGCCAGCAGAGCTGTGTGGG	2023
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Db	2084	CCCGACTTCTCTGCAGGAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2143
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Db	2144	GTGTGGAAACATCTCTGCTGCGGTTTCAGGAAGGCGCTGTGGCTGTCTPAGGAGTCTGATC	2203
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Db	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAGCGGGAGCTATTCAAAGTCTAGAGGGAG	2263
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Db	2264	TGAGGAGATTAAAGGCTGGATTTTCAGATCTGCCTGTTCCAGCGCAGTGTGCCCTCTGCT	2323
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Db	2324	CCCCCAACGACTTTTCCAAATAATCTACAGCGCGCTTCCAGCTCAGGCGTCTTGAAGCG	2383
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Db	2384	TCTTGAAGCCTATGGCCAGCTGCTCTTGTGTTCCTCTCACCCGCGCTGCTCTACAGCTG	2443
Qy	319	-----	319
Db	2444	AGACTCCAGGAACCTTCAGACTACCTTTCCTCTGCCCTTCAGAAAGGGCGTTGCCACAC	2503
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Db	2504	TTCTCTGAGGGTCAGTGGGAAGAACCTAGACTCCCATTTGCTAGAGGTAGAAAGGGGAGGG	2563
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Db	2564	TGCTGGGGACGAGGCTGGTCCACAGCAGGTCTCTGTGAGCAGGTACCTGTGGTTCGCC	2623
Qy	319	-----	319
Db	2624	TTCTCATCTCCCTGAGACTGCTCCGACCTTCCCTCCCGAGCTCTGTCTGATGCGCCCTC	2683
Qy	320	-----GlyValArgMetGlySerLeuLeuGlnCysAlaIleSerLe	336
Db	2684	TCCCTCTGCAGGGCTTCGATGGCAGCTCGGGGCTGTCTCTGAGCTGCGCATCTCCCT	2743

QY	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
DB	2744	GGTCTTCTCTGGTCTATGACCGGGTGTGCAGCGATTTCGCACATCGACAGCTATATT	2803
QY	356	uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl	376
DB	2804	GGCCAGTGTGCAGCTTTCCTGTGGCTGCCGTGCCACATGCCGTCCACAGTGTGGC	2863
QY	376	aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396
DB	2864	CGTGTGCACAGCTTCACGCCCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCCTGCC	2923
QY	396	oTyrThrIleuAlaSerLeuTyrHisArgGlyLysGlnVal	409
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DB	2983	AGTCAGGTGGGAGGGTGGTCTGGGTTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT	3042
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DB	3103	GGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGATTCTGGGAATGACTTCTCTGGG	3162
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DB	3163	TCAGGACTGTGTAGCACTTTGAATGGATGATTGCAGGAATGCAAAATACGATAGTGGAA	3222
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DB	3223	TCCGAAAGGTACAGGCACAGCAGGAGCCCTAGGCTTCTAGGCTGGTGTCTTATGGAGAGG	3282
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DB	3283	CAGGGCGTGAATCAGATGACCCCTGGGCCATTTCAGCCTCAGCAGACGGGAGTGGGAATG	3342
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DB	3403	TCTGGTCTCTGAGATGGGCGAGCTCTTCTTCCCTACCCCTTCTTCTTCTGGCTATTTTCT	3462
QY	409	-----	409
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QY	409	-----	409
DB	3523	TCCCTTCCCTTCCCTCTGGCGAGATCTCGAGCTTGACACCTGCACCCACTCCTCTGGG	3582
QY	409	-----	409
DB	3583	CACGTGTGAAGTTGGGGACCTCTTCTTCTTCTCGATCCTCCTTTGGCCTCTTCCCTCTCCAG	3642
QY	409	-----	409
DB	3643	GGGCCCTTTCTTGGGAAGCCACCTAACCCAGTAGTGTGGTCAATCTTGTCCCTTCCA	3702
QY	409	-----	409
DB	3703	CTGACCTCACTGAGCTACAAACCTCTGGTGTCTGGACTCTGCCTTGAGGGGCATGAAGTTGG	3762
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DB	3763	GGTGTCCCAAGGAGGAGGAGTGCAGGACTCTCTCATAGAGCTCTCAGACTCTAGGGGA	3822

APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 705
LENGTH: 6976
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-705

Alignment Scores:

Pred. No.: 1.16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 9 Gaps: 3

US-09-593-793a-113 (1-553) x US-09-895-793-705 (1-6976)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 165 ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGTGCGGCACCGGAAAGCCAGCTCTTGCTG 224
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
DB 225 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGAGGATCACCTATGTGCGG 284
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu 57
DB 285 CTTCTGCTGCTGGAAGTGGGGTAGAGGAGATTCATGACCATGCTGCT-GGGTGAGTC 343
QY 57 57
DB 344 ACTACATCTCTCTTCTTCTTCTTCCAGATACATGCCACCTGGCATGTGGGACAGAGTA 403
QY 57 57
DB 404 CCTCTGCCCTGGAGCTGCTTGGAGGAGAGGTGCTGCTGTGGAGGCAATTGCTGGGCA 463
QY 57 57
DB 464 GGAGGGTGACCTGGCTGAGGGGACACACAGAGAAAGAGAAATACCAAGACATA 523
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QY 57 57
DB 704 TTAGTAAGTCTTAGCCAAAGCAAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
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QY 57 57

DB 884 CCCAGGAAGAGGGGCCCTGTGAGGATTGACGGCTCTGGAGTCAACACTGCTTTGTTGAAC 943
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QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
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Db	2204	AGAGTCGTTGCCCGAGTTTGACAGAGGAAAGGGAGGACTTATTCAAAAGTCTAGAGGGAG	2263
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; Sequence 705, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-705
Alignment Scores:
Pred. No.: 1.16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 9 Gaps: 3
US-09-593-793a-113 (1-553) x US-09-895-814-705 (1-6976)

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RESULT 27

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US-09-759-143-705
; Sequence 705, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-705

Alignment Scores:
Pred. No.: 1.16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 10 Gaps: 3

US-09-593-793A-113 (1-553) x US-09-759-143-705 (1-6976)

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; Sequence 705, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
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; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-705

Alignment Scores:
Pred. No.: 1,16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservatives: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 10 Gaps: 3

US-09-593-793A-113 (1-553) x US-09-780-669-705 (1-6976)

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Db 2024 AGCCGCCCCACAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC 2083
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Db	3343	GTCCAGCCTTAGCA	CACACCTTTCTTCAGG	AGCAGCACTGACT	TAGCCTGTATCCTAC	3402		
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Db	3403	TCTGGTCTCTGAGAT	GGGGCAGGCTCCTTCCT	TACCCCTTTCTTCTGGCT	TATTTTTCT	3462		
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RESULT 29
US-09-822-827-705
; Sequence 705, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-705

Alignment Scores:
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Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 10 Gaps: 3

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US-10-012-896-703
; Sequence 703, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoilk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 703
LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-703

Alignment Scores:

Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
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US-09-593-793A-113 (1-553) x US-10-012-896-703 (1-2904)

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QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
DB 61 TGGGACACAGTGGCTGGCCCTTACCTGGGCACCCAGGAGGAGTGCCTCTTGGCCCTG 120
QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAla 222
DB 121 CTCACCTCATCTTCTTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAGGACGG 180
QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
DB 181 CTGGGCCCCACCCAGGACGACAGAGGGCTGTGGGCCCTCTTGTGCCCTGCTGT 240
QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
DB 241 CCATGCCGGGCCCTTGGCTTTCGGGAACCTTGGCGGCCCTGCTTCCCGGCTGCACGAG 300
QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
DB 301 CTGTGCTGCCGATGCCCGCACCTCGCCGGCTCTTCTGCTGGCTGAGCTGTGACGCTGG 360
QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGluGluGlyLeuTyrGln 302
DB 361 ATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGGGGGAGGGGCTGTACCAG 420
QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal --- 321
DB 421 GGCCTGGCCAGAGCTGTAGCCGGGACCCAGGCGCCGAGAGACTATGATGAAGGAAG -GCC 479
QY 321 ----- 321
DB 480 TCTGGCTGCTCTAGGAGTCTGATCAGAGTCTGTGGCCCGGTTGACAGAAGAGGCGG 539
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DB 660 TCCAGCTCAGGGCTCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGCTTTGTGTTCCT 719
QY 321 ----- 321

DB 720 CTCACCCGCTGTCTCTCAGCTGAGACTCCAGGAAACCTTTCAGACTACCTTCTCTCTGC 779
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DB 780 CTTTACGAAGGGGCGTTCGCCACATTCCTGAGGGCGTTCGGATGGGACGCTGGGGCTG 839
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DB 840 TTCCTGCAGTGGCCATCTCCCTGCTCTCTCTGTCATGACCGCGCTGTGTGACGCA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
DB 900 TTCGGCACTCGAGCAGTCTATTTCGCCAGTGTGTGGAGCTTTCCTCTGTGGCTGCGGTC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
DB 960 ACATCCCTGTCCACAGTGTGGCCGTGGTGGACAGCTTCAGCCGCTCTCACCGGGTTCACC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlyGln 408
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QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMet 428
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QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
DB 1140 ACCAGCTTCTTCCAGGCGCTAAGCTTGAGCTCCCTTCCCTTAATGGACACGTGGGTGCT 1199
QY 449 GlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
DB 1200 GGAGCAGTGGCTGCTCCACCTCCACCGGCTCTGGGGGCTCTGCGCTGTGATGTC 1259
QY 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
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QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
DB 1440 GGCCTGGGTGTGGTGGCATTACTTTGCTACACAGTAGTAGTATTTCACAAGAGCGACTG 1499
QY 549 AlaLysTyrSerAla 553
DB 1500 GCCAAATACCTCAGCG 1514
RESULT 31
US-09-895-793-703
; Sequence 703, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun

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; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-703

Alignment Scores:
Pred. No.: 3.6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
Db: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-895-793-703 (1-2904)

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Db 1 GTCTATGGCTTCATCATCAGCTTGGGGCTGCCCTGGGGCTACCTCTGCTGCCATTGAC 60

Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
Db 61 TGGGACACAGTGGCCCTGGCCCTACCTGGGCACCCAGGAGAGTGCCTCTTTGGCCTG 120

Qy 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
Db 121 CTCACCCCTCATCTTCCCTCACCTGCGTAGCAGCACACACTGCTGGTGGCTGAGGAGCAGG 180

Qy 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGGCCCCACCGACGACGAGAGGCTGTGCGCCCTCTCTTGTGCCCCACCTGCTGT 240

Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
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Qy 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGTGCTGCGCATGCCCGCCGACCCCTGGCGCGGCTCTTCTGGTGGCTGAGCTGTGACGCTGG 360

Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
Db 361 ATGGGCACATACACCTTACCGGTGTTTACACGGATTTCGTGGGGGAGGGGCTGTACCCAG 420

Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal --- 321
Db 421 GGCGTGCCACAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGAAG-GCC 479

Qy 321 ----- 321
Db 480 TCTGGCTGCTCTAGGAGTCTGATCAGAGTGTTCGCCAGTTTGTACAGAAGAAAGCGG 539

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Qy 322 ----- ArgMetGlySerLeuGlyLeu 328
Db 780 CTTCAAGAGGGCGGTGGCCACATTCTCTGAGGGCGTTCGGATGGCAGCCTGGGGCTG 839
Qy 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTTCTGTCAGTGGCCATCTCCCTGGTCTTCTCTGCTCATGGACCGGCTGGTGAGCGA 899
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Db 900 TTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCC 959
Qy 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaLeuThrGlyPheThr 388
Db 960 ACATGCTGTCTCCACAGTGTGGCGGTGACAGCTTCAGCGCCCTCACCGGGTTCCACC 1019
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Db 1020 TTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCTTACCACCGGAGAGACAG 1079
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Db 1080 GHTTCTCTCCCAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATG 1139
Qy 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTTCTGCCAGGCCCTAAGCGTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCT 1199
Qy 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
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Qy 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
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Qy 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
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Qy 549 AlaLysTyrSerAla 553
Db 1500 GCCAAATACTCAGCG 1514
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RESULT 32
US-09-895-814-703
; Sequence 703, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
```

APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 703
LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-703

Alignment Scores:
Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-895-814-703 (1-2904)

QY 163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
DB 1 GTCATGCTTCATGATCAGTCTGTGGGGCTGCCTGGGCTACCTCTGCTGCCATTGAC 60
QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
DB 61 TGGGACACCAAGTCCCTGGCCCTACCTGGGACCCAGGAGAGTGCCTCTTGGCCCTG 120
QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
DB 121 CTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGACGG 180
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DB 181 CTGGGGCCCCCAGGAGCCAGCAAGGGCTGTGGGGCCCCCTCTTGTGCCCCCACTGCTGT 240
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QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValClyGluGlyLeuTyrGln 302
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DB 480 TCTGGGTGCTCTTAGAGTCTGTATCAGAGTGTGTGCCCCAGTTTGTACAGAAGAAAGCGG 539
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DB 600 TCCAGCCGAGTGTGCCCTCTGTCTCCCCCAACGACTTTCAAAATAATCTCACCAGGCGCT 659
QY 321 ----- 321
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QY 322 ----- ArgMetGlySerLeuGlyLeu 328
DB 780 CTTTCAGCAAGGGCGTTCGCCACATTTCTGAGGGCGTTCGGATGGCAGCTGGGGCTG 839
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DB 840 TTCTCTGAGTGGCCCATCTCCCTGGTCTCTCTGTCATGACCGGGTGTGTGCAGCGA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
DB 900 TTGCGGCACTCGAGCAGTCTATTGCGCCAGTGTGGCAGCTTTCCCTGTGGCTGCGGGTGC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
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DB 1140 ACCAGCTTCTGCCAGGCCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACAGCTGTATG 1199
QY 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
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DB 1380 TTTATGGGTCTCATTTGCCAGCTCAGCCAGTCTGTCTACCTGCCTATATGTTGTGTGCGCA 1439
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DB 1440 GCGCTGGGTGCTGTGCCATTTACTTTGTCTACAGGTAGTATTTGACAAGACGCACTTG 1499
QY 549 AlaLysTyrSerAla 553
DB 1500 GCCAAATACACGC 1514
RESULT 33
US-09-759-143-703

; Sequence 703, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiongchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Ketter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-703

Alignment Scores:
Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 10 Gaps: 1
US-09-593-793a-113 (1-553) x US-09-759-143-703 (1-2904)

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QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
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Db 61 TGGGACACCAGTGCCCTGGGCCCTACCTGGGCACCCAGGAGGTGCTTTGGCCTG 120
QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuValAlaGluAlaAla 222
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Db 121 CTCACCTCATCTCTCTACCTCGGTAGCAGCCACACTGCTGGTGGCTGAGGAGGACGG 180
QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
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Db 181 CTGGGCCCCACCGACGACGAGAGGCTGTCGGCCCCCTCTCTGTCGCCCACTGCTGT 240
QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
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Db 241 CCATGCGGGCGGCTTGGCTTTCCGGAACCTGGGGCGCCCTGCTTCCCGGCTGCACACG 300
QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
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Db 301 CTGTGCTGGCGATGCCCCGACCCCTGCGCGGCTCTTGTGGCTGAGCTGTCAGCTGG 360
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Db 361 ATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGGCTGTACCAG 420
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Db 421 GGCGTCCCAGAGCTGAGCGGCGACCGGAGCCCGGAGACATATGATGAAGAAG-GCC 479
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Db 480 TCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTGTCCTCCAGTTTGACAGAAGAAAGCGG 539
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Db 600 TCCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCAAAATAATCTCACAGCGCCT 659
QY 321 ----- 321
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QY 322 -----ArgMetGlySerLeuGlyLeu 328
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Db 1260 TCCGTACGTGTGTGGTGGGTGAGCCACCGAGGCCAGGTGTTCCGGCGCGGCGCATC 1319
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QY 509 PheMetClySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
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QY 549 AlaLysTyrSerAla 553
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Db 1500 GCCAAATACTCAGCG 1514

RESULT 34

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US-09-780-669-703
; Sequence 703, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-703

Alignment Scores:
Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-780-669-703 (1-2904)

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Qy	283	MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeuTyrGln	303
Db	361	ATGCACATCATGACCTTCACGCTGTTTTACACAGGATTTCTGGGGAGGGGTGTACACG	420
Qy	303	GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal---	321
Db	421	GGCTGCCACAGCTGAGCGCGACCGAGGCGCGGAGACACTATGATGAAGAAG-GCC	479
Qy	321	-----	321
Db	480	TCTGGCTGCTCTAGGAGCTCTGATCAGAGTCGTGCCCCAGTTTGACAGAAAGAAAGCGGG	539
Qy	321	-----	321
Db	540	AGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGT	599
Qy	321	-----	321
Db	600	TCCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACACAGCGCT	659
Qy	321	-----	321
Db	660	TCCAGCTCAGCGCTCTAGAAAGCGTCTTGAAAGCCTATGCCACAGCTCTCTTGTGTTCCT	719
Qy	321	-----	321
Db	720	CTCACCCGCTGTCTCTCACAGCTGAGACTCCACAGAAACCTTCAGACTACCTTCCTCTGC	779
Qy	322	-----	322
Db	780	CTTCAGCAAGGGCGTTGGCCACATTCTCTGAGGGCTTCGGATGGCAGCGCTGGGGCTG	839
Qy	329	PheLeuGlnCysAlaIleSerLeuValPheSerLeuValIleAspArgLeuValGlnArg	348
Db	840	TTCTTCGAGTGGCCATCTCCCTGGTCTCTCTCTGGTCTATGCACCGGCTGGTGACGGA	899
Qy	349	PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla	368
Db	900	TTCGGCACCTCGACGAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGCTGCCGTGCC	959
Qy	369	ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr	388
Db	960	ACATGCTGTCCCACAGTGTGGCGTGGTGACAGCTTCAGCGCGCTCACCGGGTTCACC	1019
Qy	389	PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln	408
Db	1020	TTCTCAGCCCTGCAGATCTCTGCCCTACACAGCTGGCTCCCTCTACACCGGGAGAAGCAG	1079
Qy	409	ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet	428
Db	1080	GTGTTCTGCCCCAAATACCCAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATG	1139
Qy	429	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla	448
Db	1140	ACCAGCTTCTTGCAGGCCCCAAGACCTGGAGCTCCCTTCCCTTAATGGACACGTGGGTGCT	1199
Qy	449	GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal	468
Db	1200	GGAGGAGTGGCTGCTCCACCCTCCACCCTCCAGCGCTCTGGGGGCTCTGCTGTGATGTC	1259
Qy	469	SerValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle	488
Db	1260	TCCGTACGTGTGGTGGGTGAGCCCCAGGCGCAGGGTGTTCGGGGCGGGGCATC	1319
Qy	489	CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu	508
Db	1320	TGCCTGGACCTCGCCATCTCTGGATAGTGCTTCTCTCTCTCCAGGTGGCCCATCTCCCTG	1379
Qy	509	PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla	528
Db	1380	TTTATGGGCTCCATGTGCCAGCTACGCCAGTCTGTCTACCTGTGCTATATGGTGTCTGCCCA	1439
Qy	529	GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu	548

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|||||
Db 1440 GGCCTGGCTGCTGGCGCAATTTACTTTGCTACAGAGTAGTATTTGACAAGAGCGACTTG 1499
Qy 549 AlalystyrSerAla 553
Db 1500 GCCAAATACTCAGCG 1514

RESULT 35
US-09-822-827-703
; Sequence 703, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-703

Alignment Scores:
Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 10 Gaps: 1

US-09-593-793a-113 (1-553) x US-09-822-827-703 (1-2904)
Qy 163 ValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
Db 1 GTCTATGCTTCATGATCAGTCTTTGGGGCTGCCTGGGCTACCTCCTGCCCTGCATTGAC 60
Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeu 202
Db 61 TGGGACACCAAGTGGCCCTGGCCCTACCTGGGACCCAGGAGGAGTGCCTTTGGGCGTG 120
Qy 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
Db 121 CTCACCTCATCTTCCTCACCTGCTAGCAGCCACACACTGCTGGTGGCTGAGGAGCAGC 180
Qy 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGGCCCCACCGAGCCAGCAGAGGCTGTCGGGCCCTCCTTGTGCGCCCCACTGCTGT 240
Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
Db 241 CCATGCGCGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCCTTCCCGGCTGCACCG 300
Qy 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGTCGTCGCGCATGCGCCCGCACCTCGCGCGCTCTTCGTCGGCTGAGCTGTGACGTGG 360
Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
Db 361 ATGGCACTCATGACCTTCACGCTGTTTACAGGATTTCTGGGGGAGGGGCTGTACCAG 420
Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal--- 321
Db 421 GGCCTGCCAGAGTGAGCGCGGCGCACCGAGGCCGCGGACACTATGATGAAGGAAG-GCC 479
Qy 321 ----- 321
Db 480 TCTGGCTGCTTAGAGTCTGTATGATCAGAGTCTGTCGCCCGAGTTTGACAGAAGAGCGGG 539
Qy 321 ----- 321
```

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Db 540 AGCTTATTCAAAGTCTACAGGGAGTGGAGAGTTAAGCTGGATTTCAGATCTGCCTGGT 599
Qy 321 ----- 321
Db 600 TCCAGCCCGCAGTGTGCCCTCTGTCCCCCAACGAGATTTCCAAATAATCTCACCAGCGCT 659
Qy 321 ----- 321
Db 660 TCCAGCTCAGGCGTCTTAGAAGCGTCTTTGAAGCCTATGCGCAGCTGTCTTTGTGTCCCT 719
Qy 321 ----- 321
Db 720 CTCACCCCGCTGTCTCTACAGCTCAGACTCCAGGAAACCTTCAGACTACCTTCTCTGCG 779
Qy 322 ----- ArgMetGlySerLeuGlyLeu 328
Db 780 CTTTCAGCAAGGGCGTTCGCCACATCTCTCAGGGCGTTCGATGGGCGAGCGCTGGGGCTG 839
Qy 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTCCTGCAGTGGCCATCTCCTCGTCTCTCTGTGTCATGGACCGCTGGTGCGAGCGA 899
Qy 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCC 959
Qy 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
Db 960 ACATGCCCTGCCACAGTGTGGCGGTGGTACAGCTTCAGCCGCCCTCACCGGGTTCACC 1019
Qy 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
Db 1020 TTCTCAGCCCTGCAGATCTGCCCTACACACTGGCTCCTCTACCCACGGGAGAGCAG 1079
Qy 409 ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet 428
Db 1080 GTGTTCTCTGCCCAATACCGAGGGGACACTGGAGTGTAGCAGTGGAGCAGCGCTGATG 1139
Qy 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACAGTGGGTGCT 1199
Qy 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGCAGTGGCCCTGCTCCACCTCCACCGCGCTCTCGGGGCTCTCGCTGTGATGTC 1259
Qy 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
Db 1260 TCCGTACCTGTGGTGGTGGTGAGCCACCGAGGCGAGGTGGTTCCGGGCGCGGGCATC 1319
Qy 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
Db 1320 TGCCTGGACCTCGGCATCTCTGGATAGTCCCTTCCTGCTGCCAGTGGCCCAATCCCTG 1379
Qy 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
Db 1380 TTTATGGCTCCATGTGCCAGCTCAGCCAGTCTGTCACTGCTATATGCTGTGCCCA 1439
Qy 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
Db 1440 GGCCTGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTGACAAGAGCGACTTG 1499
Qy 549 AlalystyrSerAla 553
Db 1500 GCCAAATACTCAGCG 1514
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RESULT 36
US-10-012-896-851
; Sequence 851, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-851

Alignment Scores:
Pred. No.: 4,58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-10-012-896-851 (1-1203)

QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProLeuLeuLeu 44
Db 379 GTGACATTGGCCGAGGAGCCCGCCGGAATTATCACCTATGTGCCGCTCTGCTGTG 438
QY 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGTAGAGAGAGATTCTACCATGCTGGCATTTGGTCCAGTGGCTGGGC 498
QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGTCGCGCTCTAGGCTCAGCAGTGACCACTGGCGTGGAGCGCTATGSCCGC 558
QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTCACTCGGCACCTGCTTGGGCATCCTGCTGAGCCTCTTCTCATCCCA 618
QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGGTGTGTGCCGGATCCAGGCCCTGGAGCTGGCAGCTG 678
QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCTGGCGCTGGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAG 738
QY 145 AlaLeuLeuSerAspLeuPheArgProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GGCCTGCTCTGACCTCTTCCGGGACCGGACCACTGTGCGCAGGCGCTTACTTCTCTAT 798

QY 165 AlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATGATCAGTCTTGGGGCTGCTTGGGCTACTCTGCTGCATGACTGGGAC 858
QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGGCCTGGCCCTTACCTGGGACCCAGGAGAGTGCCTCTTTGGCCTGCTCACC 918
QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaLeuGly 224
Db 919 CTCATCTTCTCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCGCTGGC 978
QY 225 ProThrGluProAlaGluLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAAGGGCTGTGCGCCCTCTTGTGCGCCCACTGCTGTCCATGC 1038
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCCGCTTGGCTTTCGGAACTTGGCGGCTGCTTCCCGGCTGCACAGCTGTGC 1098
QY 265 CysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGGCGCATGCCCGCACCTGCGCGGCTTTCGCTGGCTGAGCTGTGACGTGGATGGCA 1158
QY 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTACGCTGTTTTTACACGGATTCGTGGGCGAG 1200

RESULT 37

US-09-895-793-851
Sequence 851, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-851

Alignment Scores:
Pred. No.: 4,58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0

Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-895-793-851 (1-1203)

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QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProProLeuLeuLeu 44
   ||| ||||| |||
Db 379 GTGACATTTGGCGAGGAGCCCGCGCGGAATTCATCACCTATGTGCGGCTCTGCTGTG 438

QY 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 GAAGTGGGGTAGAGAGAAGTTCATGACCATGGTGTGGGATGGTCCAGTGTGGGC 498

QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 499 CTGGTCTGTCTCCGCTCCTAGGCTCAGCCAGTACCCAGTGGCGCTATGGCCGC 558

QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 559 CGCGGCCCTTCTATCTGGGCATCTCTTGGGCATCTCTTCTCATCCCA 618

QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuLeuAlaLeu 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 619 AGGCGCGGCTGGCTAGCAGGCTGCTGTGCCGATCCAGGCCCTGGAGCTGGCATG 678

QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 679 CTCATCTCTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAG 738

QY 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 739 GCCCTGCTCTGACCTTCCGGACCCCGACCACTCTCCAGGCCCTACTCTGTCTAT 798

QY 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGCCCTGGCTACCTTCTGCCCTGCCATTGACCTGGAC 858

QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 38

US-09-895-814-851
; Sequence 851, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.

```
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fager, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C26  
; CURRENT APPLICATION NUMBER: US/09/895,814  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 990  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 851  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-895-814-851
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Alignment Scores:

Pred. No.: 4.58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-895-814-851 (1-1203)

```
QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProProLeuLeuLeu 44
   ||| ||||| |||
Db 379 GTGACATTTGGCGAGGAGCCCGCGCGGAATTCATCACCTATGTGCGGCTCTGCTGTG 438

QY 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 GAAGTGGGGTAGAGAGAAGTTCATGACCATGGTGTGGCATTTGGTCCAGTGTGGGC 498

QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 499 CTGGTCTGTCTCCGCTCCTAGGCTCAGCCAGTACCCAGTGGCGCTATGGCCGC 558

QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 559 CGCGGCCCTTCTATCTGGGCATCTCTTGGGATCCCTGCTGAGCCTCTTCTCATCCCA 618

QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuLeuAlaLeu 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 619 AGGCGCGGCTGGCTAGCAGGCTGCTGTGCCGATCCAGGCCCTGGAGCTGGCATG 678

QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 679 CTCATCTCTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAG 738

QY 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 739 GCCCTGCTCTGACCTTCCGGACCCCGACCACTCTCCAGGCCCTACTCTGTCTAT 798

QY 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGCCCTGGCTACCTTCTGCCCTGCCATTGACCTGGAC 858

QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-851

Alignment Scores:
Pred. No.: 4.58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-780-669-851 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----lleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCGGAGGAGCCCGCCGCAATTCATCAGCTATGTGCCGCTCTGCTG 438
Qy 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGGCGGATTGGTCCAGTGGTGG 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGly 84
Db 499 CTGGTCTGTGTCCGCTCTAGGCTCAGCCAGTACCATGGCGTGGAGCGTATGGCG 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuPro 104
Db 559 CGCGGCGCTTCTGACCTCTTCGGGACCCGACCACTGTGCCAGGCTACTCTGTCT 798
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGCTGTGTGCCGATCCAGGCCCTTGTGCTCATGCCA 678
Qy 125 LeuIleLeuGlyValGlyLeuAspPheCysGlyGlnValCysPheThrProLeu 144
Db 679 CTCATCTTGGCGGTGGGCTGTGTGGCTTCTGTGGCCAGGTGTGTCTTCTCAT 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerVal 164
Db 739 GCCCTGCTCTGTGACCTCTTCCGGGACCCGACCACTGTCCGAGGCTACTCTGT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrp 184
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGTGTGGCTACCTCTCTGCTGCTGCTG 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeu 204
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Qy 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGGCGGATTGGTCCAGTGGTGG 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGly 84
Db 499 CTGGTCTGTGTCCGCTCTAGGCTCAGCCAGTACCATGGCGTGGAGCGTATGGCG 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuPro 104
Db 559 CGCGGCGCTTCTGACCTCTTCGGGACCCGACCACTGTGCCAGGCTACTCTGTCT 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGCTGTGTGCCGATCCAGGCCCTTGTGCTCATGCCA 678
Qy 125 LeuIleLeuGlyValGlyLeuAspPheCysGlyGlnValCysPheThrProLeu 144
Db 679 CTCATCTTGGCGGTGGGCTGTGTGGCTTCTGTGGCCAGGTGTGTCTTCTCAT 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerVal 164
Db 739 GCCCTGCTCTGTGACCTCTTCCGGGACCCGACCACTGTCCGAGGCTACTCTGT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrp 184
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGTGTGGCTACCTCTCTGCTGCTGCTG 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeu 204
Db 859 ACCAGTGCCTTGGCGCCCTACCTGGGACCCAGGAGGAGTGCCTTTTGGCTG 918
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-880-10

Alignment Scores:
Pred. No.:          9,79e-78      Length:      789
Score:             919.00        Matches:    192
Percent Similarity: 96.50%      Conservative: 1
Best Local Similarity: 96.00%    Mismatches:  7
Query Match:       32.12%       Indels:     2
DB:                9            Gaps:         0

US-09-593-793A-113 (1-553) x US-09-232-880-10 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGTGCACGCTTCCCTGTGGCTGCCGGTCCACATGCTGTCCAC 62
QY 374 SerValAlaValAlaThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCCGTGGTGACAGCTTCACCGCCCTCAGCCGCTTCCCTTCTCAGCCCTGGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCCTGCCCTACACACTGGCCCTCCCTTACCACCGGGAGAACAGGTGTCTCGTCCCAA 182
QY 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
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QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GCCCTAAGCCCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGGAGGAGGTGGCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCACACCTCCACCGCCCTCTCGGGGGCCCTGCCTGTGATGCTCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCCGCCGANGCCAGGGTGTTCGGGCCCGGGGCATCTGCTTATGGGCTCCAT 422

US-10-012-896-10
; Sequence 10, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
```

QY 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
|||||
Db 423 ATCTGATAGTCC-ATCTGCTGCTCCANGTGGCCCATCCCTGTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
|||||
Db 482 GTCCAGCTACGACGCTGTCTGCTATATGCTGTCTGCCCAGCCCTGGGCTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValAlaPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 45

US-09-895-793-10
; Sequence 10, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G

US-09-895-793-10

Alignment Scores:
Pred. No.: 9,79e-78 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-10 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
|||||
Db 3 GTCTATNTGCCAGTGTGGCAGCTTTCCTGCTGGCTGCCGCGGCCACATGCTGTCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
|||||
Db 63 AGTGTGGCGGTGTGACAGCTTACAGCGCGCCCTACCGGGGTTACCTTCTCAGCCCTGCAG 122

QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlyLysGlnValPheLeuProLys 413
|||||
Db 123 ATCTCTGCCCTACACACTGGCTCCCTCTACACCGGAGACAGGTGTTCCTGCCCAAA 182
QY 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
|||||
Db 183 TACCGAGGGGACACTGGAGGTGCTAGCAGTAGGACAGCCTGATGACACAGCTTCCCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
|||||
Db 243 GGCCTTAACCTGGAGCTCCCTTCCCTAATGAGACAGCTGGGTGCTGGAGGAGTGGCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
|||||
Db 303 CTCCACACTCCACCCGCGCTCTGCGGGGCTCTGCTGTGTGTCTCTCCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
|||||
Db 363 GTGGGTGAGCCACCCGANGCAGGGTGTTCGCGGGCGGGCATCTGCTGGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
|||||
Db 423 ATCTCTGGATAGTGC-TTCTCTGCTGCCANGTGGCGCCCATCCCTGTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuVal 533
|||||
Db 482 GTCCAGCTCAGCCAGCTCTCTACTGCTATATGGTGTCTGCGCGCAGGCTGGGTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 542 CC-ATTACTTGTCTACACAGGTANTATTGTGACAAAGACGANTTGGCCAAATACTCAGCG 600

Search completed: February 19, 2003, 05:16:48
Job time : 402 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:45:09 ; Search time 1694 Seconds
(without alignments)
5286.956 Million cell updates/sec

Title: US-09-593-793a-113
Perfect score: 2861
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_esti:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_vrt:*
23: em_gss_fun:*
24: em_gss_man:*
25: em_gss_mus:*
26: em_gss_other:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1039	36.3	718	12	BE867241 601442309
5	1033	36.1	786	12	BG174399 602334219
6	906	31.7	885	14	BQ948390 AGENCOURT
7	904	31.6	592	10	AW412402 u078h02.y
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11	858	30.0	969	12	BG173136 602335411
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26	601	21.0	630	13	BI145201 602909395
27	578	20.1	520	12	BG364300 BB627844
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Db	780	CATGACCTTCAGCCTGTTTACCCGCGCATCTCGCTGGCGACGGGCTGTCCCCACGGCGT	839
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VERSION	BI107873.1	GI:14558766	
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 858)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-re@mail.nih.gov		
	Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	Clone Sequencing by: Incyte Genomics, Inc.		
	Clone Distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM11088 row: o column: 04		
	High quality sequence stop: 810.		
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	/strain="129,C57BL/6J,EVB/N"		
	/db_xref="taxon:10090"		
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	/clone_lib="NCI_CGAP_Mam3"		
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	/dev_stage="10 months"		
	/lab_host="DH10B"		
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	Site_2: NdeI; Cloned unidirectionally. Primer: Oligo dT.		
	Library constructed by Life Technologies. Investigators		
	providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH		
	Reference for transgenic model: Xu et al., Nature Genetics		
	22, 37-43 (1999)."		
BASE COUNT	133 a 265 c 245 g 215 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.28e-104	Length:	858
Score:	1196.50	Matches:	236
Percent Similarity:	89.49%	Conservative:	11
Best Local Similarity:	85.51%	Mismatches:	25
Query Match:	41.82%	Indels:	4
DB:	13	Gaps:	1
US-09-593-793a-113 (1-553) x BI107873 (1-858)			
Qy	122	LeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThr	141
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Qy	142	ProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyr	161
Db	73	CCATTGGAGGCTTACTCTCCGACCTCTTCCGGGACCCAGACCACTGCCCAAGCCTTC	132
Qy	162	SerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIle	181
Db	133	TCTGTCTAGCCCTTCATGATCAGCCTTGGGGCTGCGCTACCTCTTACCTGCATTC	192
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Qy	202	LeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAla	221
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Qy	262	GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer	281
Db	433	CAGCTGTGTCGCCGATGCTCGCACCTTACGCCGACTCTTGTGGCTGAGCTGTGCAGC	492
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Qy	342	-MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAl	361
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Qy	361	aPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal-ValThr-Ala	380
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Db	790	TCAATGGGCTTCACCGGGTTCACCTTCTCGGCTTGAAGATC	831
RESULT 3			
LOCUS	BG242597	602354010F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4482362 5',	
DEFINITION	mRNA sequence.		
ACCESSION	BG242597		
VERSION	BG242597.1	GI:12752412	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 1116)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-re@mail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM10319 row: c column: 03
High quality sequence stop: 666.
Location/Qualifiers

FEATURES
source

1. .1116
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4482362"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 209 a 349 c 314 g 244 t

ORIGIN

Alignment Scores:

Pred. No.: 3.9e-94 Length: 1116
Score: 1089.50 Matches: 232
Percent Similarity: 81.13% Conservative: 13
Best Local Similarity: 76.82% Mismatches: 42
Query Match: 38.08% Indels: 18
DB: 12 Gaps: 2

US-09-593-793A-113 (1-553) x BG242597 (1-1116)

QY 248 LeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMet 267
Db 11 CTGCTTTCGGGAATCTGGGTACCTCTTTCCCGCGCTGCAGCAGCTGTCTGCCCATG 70
QY 268 ProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThr 287
Db 71 CCTCGCACCTACGCCGACTCTTTGGCTGAGCTGTGCAGCTGGATGGACATTATGACT 130
QY 288 PheThrLeuPheThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAla 307
Db 131 TTCACACTGTCTACACGGACTTCGTGGGAGAGGGGCTGTACCAGGCTGTACCAGAGCC 190
QY 308 GluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327
Db 191 GAGCCAGGCCACCGAGGCCGAGACACTATGATGAAGGCATTGAAATGGGCACCTGGGG 250
QY 328 LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGln 347
Db 251 CTCTTCTGCAGTGTGCCATCTCCCTGGCTCTTCCCTGGTCTATGACAGGCTGGTACAG 310
QY 348 ArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGly 367
Db 311 AAGTTCGGCACACGGTCAGTCTATCTGCCAGGTGATGACCTTTCTCTGGCTGCCGCT 370
QY 368 AlaThrCysLeuSerHisSerValAlaValValThAlaSerAlaAlaLeuThrGlyPhe 387
Db 371 GCCACCTGCTGTCCACAGCGTGGTGTAGTAGACAGCCTCAGCTGCCCTCACCGGGTTC 430
QY 388 ThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLys 407
Db 431 ACCTTCTGGCCCTTGAGATCTCGCTTACACGCTCGCTTCCCTCTACACCGTGAGAG 490
QY 408 GlnValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeu 427
Db 491 CAGGTGTCTCTGCCAAATACCCAGGGAGCGCTGGAGGTAGCAGCGGTGAGGACGCCAG 550
QY 428 MetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGly 447
Db 551 ACAACCAAGCTTCTTGGCAGGCCCTTAAGCCAGGAGCTCTCTTTCCCAATGGACACGTGGC 610

QY 448 AlaGlyCysSerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAsp 467
Db 611 TCTGGCAACACGCGATCCTGGC-CCTCCACT-GCACTCTGTGGGCTCTTGTGCGAT 668
QY 468 ValSerValArgVal-ValValGlyGluProThrGluAlaArgValValProGlyArgG1 487
Db 669 GTTTCATCGATCGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 728
QY 487 YlleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPro-- 506
Db 729 CATTTCCTGGC-CTGGCCATTCTGGCGGTGCTTCTGTCTGCCAGTGGTGGCGCTG 787
QY 507 -----SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAl 522
Db 788 TCCTGGCCCATGCACGCTGACACTC-----TGCACCTGG 820
QY 522 aTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValVa 542
Db 821 CCATATGGGATCAGTCAGGATGCGCTTGTGGCGGATACTTTTGACACACCGGACTGG 880
QY 542 LPhe 543
Db 881 GTTC 884

RESULT 4
LOCUS BE867241 718 bp mRNA linear EST 20-OCT-2000
DEFINITION 601442309F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846411 5',
mRNA sequence.

ACCESSION BE867241
VERSION BE867241.1 GI:10316017
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9559 row: a column: 04
High quality sequence stop: 693.

FEATURES
source

1. .718
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3846411"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 112 a 227 c 210 g 168 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 1.4e-89 Length: 718
Score: 1039.00 Matches: 212
Percent Similarity: 98.15% Conservative: 0
Best Local Similarity: 98.15% Mismatches: 2
Query Match: 36.32% Indels: 2

DB:	12	Gaps:	0
US-09-593-793A-113 (1-553) x BE867241 (1-718)			
Qy	340	LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal	359
Db	2	CTGTGCATGGACCGCGTGCTGCAGCGATTCCGCACTCGAGCAGTCTATTTGCCAGTGTG	61
Qy	360	AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThr	379
Db	62	GCAGCTTTCCTGTGGCTGCCGCTGCCACATGCTGTCCCACAGTGTGGCGTGGTGACA	121
Qy	380	AlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeu	399
Db	122	GCTTCACGCGCCCTCACCGGGTTCCACTTCTCAGCCCTGCAGATCTGCTCCCTACACATG	181
Qy	400	AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly	419
Db	182	GCCTCCCTCTACCACCGGGAGAACAGGTCTCTGCCAAATACCGAGGGACACTGGA	241
Qy	420	GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAla	439
Db	242	GGTGCTAGCAGTAGGACAGCGCTCATGCCAGCTTCCTGCCAGGCCCTTAAGCCTGGAGCT	301
Qy	440	ProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProLa	459
Db	302	CCTTCCTTAATGACACAGTGGTGCTGGAGGCAGTGGCTTCCTCCACCTCCACCCGCG	361
Qy	460	LeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGlu	479
Db	362	CTCTGCGGGGCTCTGCTGTGATGTTCTCCGTAGTGTGGTGGTGGAGCCACCGAG	421
Qy	480	AlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPhe	499
Db	422	GCCAGGTGTGTTCGGCGCGGGCATCGCTGCAGCTCCCATCTGGTAGTGCCTTC	481
Qy	500	LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer	519
Db	482	CTGTGTGCCAGGTGGCCCCATCCCTGTTATGGGCTCCAPTGTCCAGCTCAGCAGTCT	541
Qy	520	-ValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle-TyrPheAlat	539
Db	542	TGTACTNGCTATATGTGTCTTCGCGAGGCTGGGTCTGGTCGCCAFITTACTTTGCTA	601
Qy	539	hrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	602	CACAGGTAGTATTGTACAGAGCGACTTGGCCAATACTACTCAGCG	645
RESULT 5	BGI74399	786 bp	mRNA linear EST 06-FEB-2001
LOCUS	BGI74399	602334219F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4457452 5'	
DEFINITION	mRNA sequence.		
ACCESSION	BGI74399		
VERSION	BGI74399.1	GI:12681102	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
TITLE	1 (bases 1 to 786)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapps-femail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		

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QY 323 tGlySerLeu---GlyLeuPheLeuGln---CysAlaIleSerLeuValPhe----- 338
Db 661 TGGGGCAGCCTGGGGCCCTCTTCCTGGAGGTGTCGCAATTCCTCCCTGCTCCCTGG 720
QY 339 -SerLeuValMetAspArgLeuValGlnArgPhe---GlyThrArgAlaValTyrLeuAl 357
Db 721 CTATTG-----GACAGGCTGGCTCCCGAAATTCGGGGCCACGCGCAATTAATCTTCG 774
QY 357 a 357
Db 775 G 775

RESULT 6
LOCUS BQ948390
DEFINITION AGENCOURT_8803099 Lupski_sciatic_nerve Homo sapiens cDNA clone
          IMAGC:6198823 5', mRNA sequence.
ACCESSION BQ948390
VERSION BQ948390.1 GI:22363868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 885)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapps-remail.nih.gov
          Tissue Procurement: Dr. James R. Lupski
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM13611 row: b column: 08
          High quality sequence stop: 615.
FEATURES
          Location/Qualifiers
            1..885
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:6198823"
              /clone_lib="Lupski_sciatic_nerve"
              /sex="male"
              /tissue_type="sciatic nerve"
              /dev_stage="adult, 70 yr"
              /lab_host="DH10B"
              /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
              NotI; Site_2: SalI; cDNA made by oligo-dT priming.
              Directionally cloned using the following adaptors:
              5'-TGACCCAGCGTCCG-3' and
              5'-GACTAGTTCTAGTCGCGAGCGCGCCCT(15)-3'. Size selected >
              1 kb for average insert length 1.87 kb. This is a primary
              library, non-amplified. Library constructed by Life
              Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
              College of Medicine) and is available through Life
              Technologies."
BASE COUNT 129 a 286 c 294 g 176 t
ORIGIN

Alignment Scores:
Pred. No.: 1-24e-76 Length: 885
Score: 906.00 Matches: 180
Percent Similarity: 92.86% Conservative: 2
Best Local Similarity: 91.84% Mismatches: 11
Query Match: 31.67% Indels: 3
DB: 14 Gaps: 0

US-09-593-793A-113 (1-553) x BQ948390 (1-885)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

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Db 259 ATGCTCAGAGGCTGTGGGTGAGCCGCTCTCGCGCACCGAAAGCCAGCTCTTCTG 318
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 319 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGACGATCACCATTGTCGCG 378
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 379 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGTGTGCTGGCATTTGGT 438
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 439 CCAGTGTGGCCCTGTGCTGTCCGCTCTAGGCTCAGCCAGTGACCATCGCGTGA 498
QY 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 499 CGCTATGGCCGCGCGGCCCTTTCATCTGGGCACTGTCTTGGGCACTCTGCTGAGGCCTC 558
QY 101 PheLeuIleProArgAlaGlyTyrLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 559 TTTCTCATCCCAAGGCCGCGCTGCTAGCAGGCTGCTGTGCCGGATCCAGGCCCTG 618
QY 121 GluLeuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 619 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGCTGGACTTCTGTGGCCCGGTGTGCTTC 678
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAsp-ProAspHisCysArgGlnAl 160
Db 679 ACTCCACTGGAGGCCCTGCTCTGAACCTCTCCGGGACCCCGACCATGTGCGCCAGGC 738
QY 160 atySerValTyrAlaPheMetIle--SerLeuGlyGlyCysLeuGlyTyrLeuLeuPro 179
Db 739 CTACTCTGTCTATGCCTTTCATGATCCGCTCTTGGGGGCTGCGCGGGCTACCTCTCTGCC 798
QY 180 AlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGly 193
Db 799 TGCCTTGGCTGGGAACACGAGGCGCTGGGCCCTAACTGGGC 840

RESULT 7
LOCUS AW412402
DEFINITION AW412402.y1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2648691 5',
          similar to TR:Q39231 Q39231 SUCROSE-PROTON SYMPORTER. [1] ;, mRNA
          sequence.
ACCESSION AW412402
VERSION AW412402.1 GI:6938274
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 592)
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Other ESTs: uc78b02.xl
          Contact: Robert Strausberg, Ph.D.
          Email: cgapps-remail.nih.gov
          Tissue Procurement: Gilbert Smith, Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          MGI:1029143
          Seq primer: -40RP from Gibco
          High quality sequence stop: 421.
FEATURES
          Location/Qualifiers
            1..592
              source

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:2648691"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 91 a 193 c 168 g 140 t
ORIGIN

Alignment Scores:
Pred. No.: 1,01e-76 Length: 592
Score: 904.00 Matches: 172
Percent Similarity: 89.85% Conservatives: 5
Best Local Similarity: 87.31% Mismatches: 20
Query Match: 31.60% Indels: 1
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW412402 (1-592)

QY 149 AspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIle 168
Db 2 GACCTCTCCGGGACCCAGACCACCTGCCGCCAGCCCTCTCTGTCTACGCCCTCATGATC 61
QY 169 SerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeu 188
Db 62 AGCCTTGGGGGCTGCCCTGGGCTACCTCTTACCTGCCATTGACTGGGACACCAGCGTCTG 121
QY 189 AlaProTyrLeuGlyThrGlnGluGlyCysLeuPheGlyLeuThrLeuIlePheLeu 208
Db 122 GCCCCCTACTGGGTACTCAGGAAGAATGCCCTTTGGGCTCCTCACCCCTCATTTTCCTC 181
QY 209 ThrCysValAlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluPro 228
Db 182 ATCTGCATGCGACCCACTCTGTTGTGACGAGGAGGAGTACTGGGCCACCCAGACCG 241
QY 229 AlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeu 248
Db 242 GCAGAAAGGTTGTGTGCTCTGCGGTGTCGCGCCGATGCTGCCATGCCACGTTGCCCTG 301
QY 249 AlaPheArgAsnLeuGlyAlaLeuProArgLeuHisGlnLeuCysCysArgMetPro 268
Db 302 GCTTCCCGGAATCTGGGTACCCCTGTTTCCCGGCTGCAGCAGCTGTGCTGCCGATGCCT 361
QY 269 ArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe 288
Db 362 CGCACCTACGCCGACTCTTTGGGCTGAGCTGTGCAGCTGGATGGCACTTATGACTTTC 421
QY 289 ThrLeuPheTyrThrAspPheValGlyGlyLeuTyrGlnGlyValProArgAlaGlu 308
Db 422 ACACCTGTTCTACACGGACTTCGTGGGAGAGGGGCTGTACACGGGTGTACCCAGACCGAG 481
QY 309 ProGlyThrCluAlaArgHisTyrAspGluGlyValArgMetGlySerLeuGlyLeu 328
Db 482 CCAGGCACCGGCGCGGAGACACTATGATGAAGGCAATTCGAATGGGCGAGCCTGGGCTC 541
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 542 TTCCCTGCATGTGCCATCTCCCTGGTCTCTCCCT-GTCATGGACAGGCTG 591

RESULT 8
BF785813 929 bp mRNA linear EST 12-JAN-2001
LOCUS 602112437F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240617
DEFINITION 5', mRNA sequence.
ACCESSION BF785813
VERSION BF785813.1 GI:12090849
KEYWORDS EST.
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house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9855 row: j column: 10
High quality sequence stop: 610.
Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240617"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"

BASE COUNT 190 a 275 c 262 g 202 t
ORIGIN

Alignment Scores:
Pred. No.: 8.85e-76 Length: 929
Score: 897.50 Matches: 195
Percent Similarity: 83.54% Conservatives: 8
Best Local Similarity: 80.25% Mismatches: 40
Query Match: 31.37% Indels: 5
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF785813 (1-929)

QY 177 LeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 196
Db 13 CTCCTTACCTGGCCAT-GACYGGGACACCGAGGTCTGGCCCCCTACCTGGGTACTCAGGAA 71
QY 197 GluCysLeuPheGlyLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeu 216
Db 72 GAATGCTCTTAGGCCCTCTCACCCCTCATTTTCCCTCATCTGCATGGCAGCCACTCTGTT 131
QY 217 ValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSer 236
Db 132 GTACGAGGAGGAGCAGTACTGGGCCCCACCCGAGCCGAGAGGGTGTGTGTTCTCTGCC 191
QY 237 LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 256
Db 192 GTGTCCGCCGATGCTGCCATGCCACGTTGGCTGGCTTCGGAATCTGGGTACCCCTG 251
QY 257 LeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheVal 276
Db 252 TTTCCCGGCTGCAGCAGCTGTGCTGCCGATGCCCTGCACCCCTAGCCGACTCTTTG 311
QY 277 AlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheVal 296
Db 312 GCTGAGCTGTGAGCTGGTGGCACTTATGACTTTTACACTGTCTTACACGAGCTTCG 371
QY 297 GlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrCluAlaArgHis 316
Db 372 GGAGAGGGGCTGTACAGGGTGTACCCAGAGCCAGGACCCAGGAGCCGAGACAC 431
QY 317 TyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeu 336

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|||||
Db 432 TATGATGAAGCATTCGAATGGGCAGCTGGGCTCTTCTCGAGTGTGCATCTCCCTG 491
QY 337 ValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeu 356
Db 492 GTCTTCCTCCCTGGTCATGGACAGCTGGTACAGAAGTTCGGCACACGGTCACTATCTG 551
QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaValThrCysLeuSerHisSerValAla 376
Db 552 GCCAGTGTGATGACCTTCCTGTGGCTGGCC--TGTCACCTGTCTGTCCACACGGTGGT 609
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
Db 610 GTAGTGACAGCCC--AGTGGCCCTCAGGGGTGCACCTTCTCGGG-CTGAGAGATACCGGCT 666
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 667 TACAGCAGCAGCTTC-CCTACCAACCGTGGCAAGCAGTGTCTGCCCAATACCGAGGGGC 725
QY 417 AspThrGly 419
Db 726 ACCTGAGGT 734

RESULT 9
BQ934815
LOCUS
DEFINITION BQ934815 934 bp mRNA linear EST 21-AUG-2002
TITLE IMAGE:6396364 5', mRNA sequence.
ACCESSION BQ934815
VERSION BQ934815.1 GI:22350198
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-(MGC 1 to 934)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Distribution: Agencourt Bioscience Corporation
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13892 row: 1 column: 05
High quality sequence stop: 634.
Location/Qualifiers
1..934
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6396364"
/clone_lib="NCI CGAP Co24"
/lab_host="PH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 164 a 278 c 273 g 219 t
ORIGIN
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Alignment Scores:

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Pred. No.: 1.14e-74
Score: 886.00
Percent Similarity: 81.17%
Best Local Similarity: 79.08%
Query Match: 30.97%
DB: 14
Length: 934
Matches: 189
Conservative: 5
Mismatches: 23
Indels: 22
Gaps: 4
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FEATURES source

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RESULT 10
BQ934815
LOCUS
DEFINITION BQ934815 549 bp mRNA linear EST 26-JAN-2001
TITLE H3066G04-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
ACCESSION H3066G04 5', mRNA sequence.
VERSION BQ934815
KEYWORDS BQ934815.1 GI:12564144
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-(bases 1 to 549)
JOURNAL National Institutes of Health
COMMENT Contact: George J. Kargul
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
```

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US-09-593-793A-113 (1-553) x BQ934815 (1-934)
QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 246 ATATCCAGAGGCTGTGGCCAGCCGCTCTACGGCACCCGGAAGCTCAGCTCCTGCTG 305
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 306 GTCAACCTGCTACCTTTGGCCCTGGAGGTGCTGCTGGCTGCCGCGCATTAACCTATGTGCCA 365
QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 366 CCCCTTCTGCTGAAGTCGGGGTGGAGGAAATTCATGACCATGGT----- 413
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
Db 414 -----TTGGGCTCAGCCAGTGCACCTGCGGTGGG 443
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 444 CGCTATGGCCGCGGAGACCTTTATCTGGGCTTTGTCCCTGGGTGCTCTGCTAAGCCTC 503
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 504 TTTTCTCATCCGAGGCTGGCTGGCTGGCAGGACTGCTGTACCCAGACACAGGCCCCCTG 563
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 564 GAGTTGGCCCTGCTGATCTTGGGAGTGGGCTGCTGGACTTTTGGGCCAGGTGTGCTTT 623
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 624 ACTCCATTGGAGCCCTTACTCTCCGACCTTCTCCGGGACCCACACCTGCGCCAGGCC 683
QY 161 TyrSerValTyrAlaPheMetIleSerLeu-GlyGlyCysLeuGlyTyrLeuLeuProAl 180
Db 684 TTCTCTGTCTACGCTTTCATGATCAGCCCTTTGGGGCTTGGGGCTGCTGGGTACTGCTTTACTGC 743
QY 180 alleAspTrpAspThrSerAlaLeu-AlaProTyrLeuGlyThrGln-GluGluCysLeu 199
Db 744 CATTGACTGGGACACCGAGCTTCTGGGCCCTTACCTGGGTACTCAGGGAAAAATGCTTT 803
QY 200 -PheGlyLeu---LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu-----Le 216
Db 804 CTTTGGCCCTCCCTCACCCTCATTTTCTCTCATCTGCAATGCGCAACCCACTCGCTTTT 863
QY 216 uValAlaGluGluAlaAlaLeuGlyProThr---GluProAlaGluGly 231
Db 864 GACCGGAAGAAGCAATACTTGGGGCCCAACCCCAACCCGCGCAAGGG 912
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503 TCAGCTGCCCCACACCGGGTTCACCTTCGCGCTTGCAGATCCGCTTACACGCTCGCC 302

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Db 1 AGCGTTCTGCGCCCTACCTGGGTACTACGAGAAGATGCTCTTTGGCCCTCTCACCCCTC 60
QY 206 ILePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaLeuGlyPro 225
Db 61 ATTTTCTCTCATCTGCATGGCAGCATCTGTTTGTACGAGGAGGAGCAGTACTGGGCCCA 120
QY 226 ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245
Db 121 CCCGAGCGCGCAGAGGGTGTGGTCTCTGCGCGTGTGCGCGCGATGCTGCCCATGCCAC 180
QY 246 AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys 265
Db 181 GTTGGCTGGCTTTCCGGAATCTGGTACCCCTGTTCCCGGCTGCAGCAGCTGTCTGTC 240
QY 266 ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285
Db 241 CGATGCTCGCACCTACCGCCACTCTTGTGGCTGAGCTGTGCAGCTGGATGGCAGCT 300
QY 286 MetThrPheThrLeuPheThrAspPheValGlyGluGlyLeuThrGlnGlyValPro 305
Db 301 ATGACTTTTACACTGTTTACACGGACTTCTGCGGAGAGGGGCTGTACCA-GGTGTACCC 359
QY 306 ArgAlaGluProGlyThrGluAlaAlaArgHisTyrAspGluGlyValArgMetGlySer 325
Db 360 AGAGCCGAGCCAGCCAGCCAGGC-CGGAGACACTATGATGAAGGCATTCGAATGGGCAGC 418
QY 326 LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 419 CTGGGCTCTTCTGCAGTGTGCATCTCCCTGGTCTTCTCCCTGGTATGGACAGGCTG 478
QY 346 ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365
Db 479 GTACAGAAGTTTGGCACACCGCTCAGTCTATCTGGCCAGTGTGTATGACCTTTCTCTG 538
QY 366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr 385
Db 539 CGCGCTGCCACCTGCTG-TCCCCACAGCTGGTGTAGTGACAGC-TCAGGTGCCCTCACC 596
QY 386 GlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArg 405
Db 597 GGGTTACCTTCTCCGGCTTGCAGATCCTGAC-TTAAAGATCGCTTCTTACACCGCTG 655
QY 406 -GluGlyGlnValPheLeuProGlyTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 656 AGAAGACCACTTCTCCGGCAAAT---AAGGAGGAGGCCCTCAAGCATGCCCGTGAAGA 712
QY 425 pSerLeuMetThrSerPheLeuProGlyProGlyProGlyAlaProPhePro 442
Db 713 ACGGCACAAACCGGTTTT---GGCGGGCTTAAAGCAGGAGCATCTTCCCA 761

RESULT 12
AF109299
LOCUS AF109299 Homo sapiens prostate adult Homo sapiens cdna ipca-2
DEFINITION
ACCESSION AF109299
VERSION AF109299.1 GI:6782692
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 482)
JOURNAL Walker M.G., Volkmut, W., Sprinzak, E., Hodgson, D. and Klingler, T.
MEDLINE Prediction of gene function by genome-scale expression analysis:
COMMENT prostate cancer-associated genes
20082966 Genome Res. 9 (12), 1198-1203 (1999)
Contact: Walker MG
Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304, USA
co-expressed with known prostate-cancer genes.
Location/Qualifiers

BASE COUNT 57 a 179 c 141 g 105 t
ORIGIN
Alignment Scores:
Pred. No.: 1,21e-69 Length: 482
Score: 829.00 Matches: 157
Percent Similarity: 98.12% Conservative: 0
Best Local Similarity: 98.12% Mismatches: 2
Query Match: 28.98% Indels: 1
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x AF109299 (1-482)
QY 129 ValGlyLeuLeuAspPheCys-GlyGlnValCysPheThrProLeuGluAlaLeuLeuSe 148
Db 4 GTGGGCTGTGGACATCTGTGGGCCAGGTGTCTTCACTCCACTGGAGGCCCTGCTCTC 63
QY 148 AspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIl 168
Db 64 TGACCTCTTCCGGGACCCGAGCAGCAGTGTGCCAGGCTACTGTGCTGTATGCTTCAATG 123
QY 168 eSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLe 188
Db 124 TAGCTTTGGGGCTGCTGGCTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
QY 188 uAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLe 208
Db 184 GGGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTTTGGCCTGCTCACCCTCATCTCTC 243
QY 208 uThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluPr 238
Db 244 CACCTCGGTAGACCCACACACTGCTGTGTGGCTGAGGAGGAGGAGGCTGGGCCACCGAG 303
QY 228 oAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLe 248
Db 304 AGCAGAAGGCTGTGCGCCCTCTGCTGTGCGCCACTGCTGTCCATGCGGGCCGCTT 363
QY 248 uAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetPr 268
Db 364 GGGTTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTGCACAGCTGTGCTGCGCATGCC 423
QY 268 oArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThr 287
Db 424 CCGCACCTTGGCGGCTCTTGTGTGGCTGAGCTGTGCAGCTGGATGGCATCATGACC 481

RESULT 13
BF581244
LOCUS BF581244
DEFINITION BF581244.1 GI:11654956
ACCESSION BF581244
VERSION BF581244.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 700)
JOURNAL NIH-MGC http://mgc.ncl.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
```


cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1AW9803 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 680.
Location/Qualifiers

FEATURES

source
1..700
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4220415"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 110 a 227 c 197 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 3.84e-69 Length: 700
Score: 826.50 Matches: 194
Percent Similarity: 85.90% Conservative: 7
Best Local Similarity: 82.91% Mismatches: 31
Query Match: 28.89% Indels: 9
DB: 12 Gaps: 1

US-09-593-793A-113 (1-553) x BF581244 (1-700)

Qy 177 LeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 196
|||||
Db 3 CTCCTACCTGCCAT-GACTGGACACACAGCGTTCTGGCCCTACTCGGTACTCAGGAA 61
Qy 197 GluCysLeuPheGlyLeuLeuThrLeuPheLeuThrCysValAlaAlaThrLeuLeu 216
|||||
Db 62 GAATGCCCTT-GGCTCTCTACCTCATTTTCTCATCTGCGTGGCAGCCACTCTGTT- 119
Qy 217 ValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSer 236
|||
Db 120 GTGACGGAGGAGGAGTACTGGGCCCCACCGAGCGCGAGAGGGTGTG-GTCTCTGCC 178
Qy 237 LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 256
|||||
Db 179 GTGTCGCCCGGATGTGCCCATGCCACGTTGGCCTTTCGGAACTGGGTACCCCTG 238
Qy 257 LeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheVal 276
|||||
Db 239 TTTCCCGCGTGCACACGCTGTGTCGCCGATGCTCGACCTACGCCGACTCTTTGTG 298
Qy 277 AlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheVal 296
|||||
Db 299 GCTGAGCTGTGCAGCTGGTGCACCTTATGACTTTTCACACTGTTCTACAGGACTTCGTG 358
Qy 297 GlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHis 316
|||||
Db 359 GGAGAGGGCGTGTACACCGTGTATCCAGCCGAGCCAGCCAGCCAGCGCGGAGACAC 418
Qy 317 TyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeu 336
|||||
Db 419 TATGATGAGGCAATTCGAATGGGACGCTGGGGCTTCTTCCGCTGTCGCTATCTCCCTG 478
Qy 337 ValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeu 356
|||||
Db 479 GTCTTCTCCCTGTCATGGACAGGTGTGTACAGAAGTTCCGGACACAGCTCATCTG 538
Qy 357 AlaSer-ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
|||||
Db 539 GCCACGTGTGATGACCTTTCTGTGGCTTTCCTGTTGCCACCTGCTG-TCCCACAGCGTGT 597

Qy 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
|||||
Db 598 GGTAGTGACAGCTCAGCTGC-CTCACCAGGTTACCTTCTCGC-TTGACATCTCG-- 653
Qy 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal 409
|||
Db 654 -CTTACAGTCTGCTCCCTCTACACCGTGAAGCGGTG 692

RESULT 14
BG864609
LOCUS 602798469F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4919513 5',
DEFINITION mRNA sequence.
ACCESSION BG864609
VERSION BG864609.1 GI:14215147
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 872)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10834 row: i column: 18
High quality sequence stop: 738.
Location/Qualifiers
1..872
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:4919513"
/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

BASE COUNT 157 a 242 c 276 g 197 t
ORIGIN
Alignment Scores:
Pred. No.: 4.49e-68 Length: 872
Score: 817.00 Matches: 173
Percent Similarity: 90.91% Conservative: 7
Best Local Similarity: 87.37% Mismatches: 15
Query Match: 28.56% Indels: 5
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG864609 (1-872)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||
Db 280 ATGATCCAGAGCTGTGGCCAGCGCTGTCTACGGCACCAGGAAAGCTCAGCTCTGCTG 339
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 340 GTCAACCTGCTCACCTTTTGGCTGGAGGTGTGCTGGCTGGCGGCAATTACCTATGTGCCA 399

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 400 GCCCTTCTGCTGGAAGTGGGGTGGAGGAAATTCATGACCATGTGTGGCGATTGGC 459
QY 61 ProValLeuLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 460 CCAGTGTAGCGCTGGTGTCTGCTCCACTCTAGGCTCAGCCAGTACCATGTGGCGTGGG 519
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 520 CGTATGGCCCGCGGAGACCTTTATCTGGCTTTGTCCCTGGGTGTCTGCTTAAGCCCTC 579
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 580 TTTCTCATCCGAGGCTGGCTGGCTGGCAGGACTGCTGTA-CCAGACACAGCGCCCTG 638
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys-GlyGln-ValCysP 140
|||||
Db 639 GAGTTGGCCCTGTGATCTTGGAGTGGGCTGTCTGGACTTTTGGTGGCAAGGTGTGCT 698
QY 140 heThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnA 160
|||||
Db 699 TTACTCATTTGGAGGCTTACTCTCGAGCTCTTCGGGACGCGAGAACATGTCGCGAAAG 758
QY 160 laTyrSer-ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuPro 179
|||||
Db 759 CCTTCTCTGCTACGCTTCATGATCAGCCTTGGGGCTGCTGGGTACTTTTACCT 818
QY 180 AlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
|||||
Db 819 GGCATTGACTGGAACAAG-GTGCTGGGCGCCCTACTCTGGGTAATCAG 865
RESULT 15
BG469520 894 bp mRNA linear EST 21-MAR-2001
LOCUS 602532833F1 NTH_MGC_15 Homo sapiens cDNA clone IMAGE:4660496 5',
DEFINITION mRNA sequence.
ACCESSION BG469520
VERSION BG469520.1 GI:13401795
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1458 row: a column: 09
High quality sequence stop: 671.
Location/Qualifiers
1. .894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4660496"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Orgn: colon; Vector: pORF7; Site:1; Xhol; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)*

BASE COUNT 173 a 272 c 264 g 185 t
ORIGIN

Alignment Scores:
Pred. No.: 4.92e-66 Length: 894
Score: 796.00 Matches: 163
Percent Similarity: 98.19% Conservative: 0
Best Local Similarity: 98.19% Mismatches: 1
Query Match: 27.82% Indels: 2
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG469520 (1-894)

QY 390 SerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal 409
|||||
Db 3 TCAGCCCTCGAGATCCTGCCCTACACACTGGGCTCCCTCTACCACCGGAGAGAGAGGTG 62
QY 410 PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThr 429
|||||
Db 63 TTCCTGCCCAATATCCAGGGGACACTGGAGGTGCTAGCAGTCAGGACAGCCTGATGACC 122
QY 430 SerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGly 449
|||||
Db 123 AGCTTCTCCAGGGCCTAAGCCTGGAGCTCCCTTAATGGACACGCTGGGTGCTGGA 182
QY 450 GlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSer 469
|||||
Db 183 GGCAGTGGGCTGCTCCCACTCCACCGGCTCTGGGGGCTCTGCCCTGTGATGCTCC 242
QY 470 ValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCys 489
|||||
Db 243 GTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 302
QY 490 -LeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPh 509
|||||
Db 303 CCTGGACCTCGCATCCTCGATAGTGCCTTCCTGTGTCCTCCAGGTGGCCCATCCCTGTT 362
QY 509 ehkGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla-G 529
|||||
Db 363 TATGGCTCCATGTGTCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGACGG 422
QY 529 lYleuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuA 549
|||||
Db 423 GCTGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 482
QY 549 laLysTyrSerAla 553
|||||
Db 483 CCAATACTCAGCG 496

RESULT 16
B1650119 901 bp mRNA linear EST 12-SEP-2001
LOCUS 603296208F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5337073 5',
DEFINITION mRNA sequence.
ACCESSION B1650119
VERSION B1650119.1 GI:15564355
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 901)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11855 row: p column: 02
High quality sequence stop: 778.
Location/Qualifiers
1. 901
/organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5337073"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
22, 37-43 (1999)."
BASE COUNT 151 a 260 c 288 g 202 t
ORIGIN
Alignment Scores:
Pred. No.: 1,38e-64 Length: 901
Score: 781.00 Matches: 174
Percent Similarity: 90.45% Conservativeness: 6
Best Local Similarity: 87.44% Mismatches: 11
Query Match: 27.30% Indels: 9
DB: 13 Gaps: 0
US-09-593-793a-113 (1-553) x BI650119 (1-901)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 318 ATGATCCAGAGCTGTGGCCAGCGCTGCTACGCGACCGAAGCTCAGCTCCTGCTG 377
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db 378 GTCAACCTGCTCACCTTGGCCCTGGAGGTGTGCTGTGGCGCATTTACCTATGTGCA 437
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 438 CCCCTTCTGCTGGAAGTCGGGTGGAGGAGAAATTCATGACCATGCTGTGGCATTTGC 497
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 498 CCAGTGCTAGGCTGTCTTCTGCTCCACTCTAGGCTAGGCTAGGCTAGGCTGGG 557
QY 81 ArgTrpGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 558 CGCTATGGCCCGCGAGACCCCTTTATCTGGGCTTTTCTCCCTGGGTGTCTGCTAAGCC 617
QY 101 PheLeuIleProAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 618 TTTTCATCCCGAGGCTGGCTGGCTGGGAGGACTGCTGTACCCAGACATCAGGCCCTG 677
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 678 GAGTTGGCCCTGCTGATCTTGGAGTGGGGCTGTGGACGT-TGTGGCCAGGTGTGCTTG 736
QY 141 -ThrPro-LeuGluAlaLeuLeuSerAsp-LeuPheArg-AspProAspHis-CysArgG 159
Db 737 TACTCCATTTGGAGCCCTTACTCTCCGAACCTCTTCCGGGGAGCCAGACCACTTGC 796
QY 159 InAlaTrpSerVal-TyrAlaPheMetIleSerLeuGlyCysLeu-GlyTyrLeuLe 178
Db 797 AGGCCTTCTCTTACGCCCTTCTGTATCAGCCCTTGGGGGCTGCTGGGGTTACTTCT 856
QY 178 uProAlaIleAspTrpAspThr-SerAlaLeuAlaProTyr 191

Db 857 TACTGCGCTGCTTGGGACACCCAGCGTCTTGGCCCCCTAC 897
RESULT 17
LOCUS BF972601
DEFINITION 602243025F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4331407 5',
mRNA sequence.
850 bp mRNA linear EST 22-JAN-2001
ACCESSION BF972601
VERSION BF972601.1 GI:12339816
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1196 row: a column: 08
High quality sequence stop: 675.
Location/Qualifiers
1. 850
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4331407"
/clone_lib="NIH_MGC_46"
/lab_host="DH10B (phage-resistant)"
/tissue_type="leiomyosarcoma cell line"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 128 a 266 c 261 g 195 t
ORIGIN
Alignment Scores:
Pred. No.: 1.57e-64 Length: 850
Score: 780.00 Matches: 157
Percent Similarity: 99.37% Conservativeness: 0
Best Local Similarity: 99.37% Mismatches: 1
Query Match: 27.26% Indels: 1
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BF972601 (1-850)
QY 396 ProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArg 415
Db 3 CCTACACTGGCTCCCTCTACCCACCGGAGAGCAGGTCTCTGCCCAATACCGA 62
QY 416 GlyAspThrGlyCylAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPro 435
Db 63 GGGGACACTGGAGGTGCTAGCAGTAGGACAGCCTGATCACCAGGTCTCTGCCAGGCC 122
QY 436 LysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyCylSerGlyLeuLeuPro 455
Db 123 AAGCTGGAGCTCCCTCTCCCTAATGACACGCTGGGTGGAGGACGTGGCTGCTCCCA 182
QY 456 ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGly 475


```

TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Dr. Mark Watson
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM2002 row: m column: 14
          High quality sequence stop: 485.
FEATURES   Location/Qualifiers
            1..1060
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="IMAGE:5480245"
             /clone_lib="NIH_MGC_113"
             /lab_host="DH10B (phage-resistant)"
             /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GCACGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."
BASE COUNT      282 a 294 c 314 g 169 t 1 others
ORIGIN

Alignment Scores:
Pred. No.:      6.1e-55      Length:      1060
Score:          682.00      Matches:     135
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    23.84%      Indels:      0
DB:             14          Gaps:         0

US-09-593-793A-113 (1-553) x BM914562 (1-1060)
QY  419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProGly 438
DB  3  GGAGGTGCTAGCAGTGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCGGA 62
QY  439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
DB  63  GCTCCCTCCCTTANGGACACGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 122
QY  459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
DB  123  GCGCTCTGCGGGGCCCTCTGCCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACC 182
QY  479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
DB  183  GAGGCCAGGGTGGTTCGGGGCGGGGCATCTGCCTGGACCTGCCATCTGGATAGTGCC 242
QY  499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
DB  243  TTCCCTGCTGCCAGGTGGCCCATCCCTGTTATGGGGTCCCATGTCCAGCTCAGCCAG 302
QY  519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
DB  303  TCTGTCACTGCCTATATGTGTCTGCCGAGGCCTGGGTCTGGTCGCCATTTACTTTTGCT 362
QY  539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB  363  ACACAGGTAGTATTTTGACAAGAGCGACTTTGGCCAAATACTACGC 407

RESULT 21
BF789072 759 bp mRNA linear EST 12-JAN-2001
LOCUS    BF789072
DEFINITION 602104930F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222998

5', mRNA sequence.
BF789072 GI:12094108
EST
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE  1 (bases 1 to 759)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM9810 row: 1 column: 07
          High quality sequence start: 3
          High quality sequence stop: 756.
FEATURES   Location/Qualifiers
            1..759
             /organism="Mus musculus"
             /strain="FVB/N"
             /db_xref="taxon:10090"
             /clone="IMAGE:4222998"
             /clone_lib="NCI_CGAP_Kid14"
             /lab_host="DH10B (T1 phage-resistant)"
             /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
             Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 1.75 kb. Constructed by Life
             Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT      131 a 218 c 243 g 167 t
ORIGIN

Alignment Scores:
Pred. No.:      4.68e-53      Length:      759
Score:          660.00      Matches:     143
Percent Similarity: 90.24%      Conservative: 5
Best Local Similarity: 87.20%      Mismatches: 12
Query Match:    23.07%      Indels:      6
DB:             12          Gaps:         1

US-09-593-793A-113 (1-553) x BF789072 (1-759)
QY  1  MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB  282  ATGATCCACAGGCTGTGGGCCAGCGCTGTCTAGGSCACCGGAAAGCTCAGCTCCTGCTG 341
QY  21  ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB  342  GTCAACCTCTCACTTTCCTGGCTGGAGGTGGCTGGCTGCCGCCATTAACCTATGTGGCCA 401
QY  41  ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB  402  CCCCTTCTGCTGGAAGTGGGGTGGAGGAGAAATTCATGACCATGCTGTGGGCATTGGC 461
QY  61  ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB  462  CCAGTGTCTAGGCTGTCTTCTTCTTCCACTCCTTAGGCTCAGCCAGTGACCCAGTGGCGTGG 521
QY  81  ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB  522  CGCATATGGCCG-CGGAGACCCCTTTATCTGGGGCTTTGTCCCTGGGTGCTCTGCTAAGCCCTC 580
QY  101  PheLeuIleProAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB  581  TTTTCATATCCCGAGGCTGGCTGGCTGGCAGGACTGCTGTACCCAGACACACGACCCCTG 640
```

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Oy 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 641 GAGTTGGCCCTGCTCATCTGGAGTGGGGCTGCTGGACTTTGTGG--CAGGTGTGCTTT 698

Oy 141 ThrProLeuGluAlaLeuSerAsp-LeuPheArgaspProAspHisCysArgGlnAl 160
|||||
Db 699 ACTCCATTGGAGGGCTTACTCTCCGACTCTT-----CCGGACCAGACATGCGCGAG 749

Oy 160 atYrSerVal 163
|||||
Db 750 CTTCTCTGTT 759

RESULT 22
AZ418156/c
LOCUS
DEFINITION
  1M0194E12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0194E12 F, DNA sequence.
ACCESSION
  AZ418156
VERSION
  AZ418156.1 GI:10542169
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 578)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0194 row: E column: 12
  Seq primer: CGTTGTAAACGACGGCCAGT
  Class: plasmid ends
  High quality sequence stop: 578.
FEATURES
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    1..578
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0194E12"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi14732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
```

```
BASE COUNT 148 a 156 c 174 g 100 t
ORIGIN
Alignment Scores:
Pred. No.: 3.77e-53 Length: 578
Score: 659.00 Matches: 129
Percent Similarity: 91.33% Conservative: 8
Best Local Similarity: 86.00% Mismatches: 13
Query Match: 23.03% Indels: 0
DB: 17 Gaps: 0

US-09-593-793A-113 (1-553) x AZ418156 (1-578)
Oy 403 TyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyAlaSer 422
|||||
Db 457 TTTTATCCCCCCTCAGGTGTCTGCCCCAATACCGAGGGGACGCTGGAGGTAGCAGC 398

Oy 423 SerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhePro 442
|||||
Db 397 GGTGAGGACAGCCAGACAACCAAGCTTCTTGGCAGGCCCTTAAGCCAGGAGCTCTCTTCCC 338

Oy 443 AsnGlyHisValGlyAlaGlyCysGlySerGlyLeuLeuProProAlaLeuCysGly 462
|||||
Db 337 AATGACACGTGGGCTCTGGCAGCAGCGCATCTCTGGGCCCTCCACCTGCACCTGTGGG 278

Oy 463 AlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArgVal 482
|||||
Db 277 GCCTCTGCTGGCATGCTCTCCATGCGAGTGGTGGTGAGCCACCTGAGGCCAGGGTT 218

Oy 483 ValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSer 502
|||||
Db 217 GTTACGGGACGGGGCATTTGCTGACCTGGCCATCTTGGACAGTGCCTTTCTGTGTCC 158

Oy 503 GlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAla 522
|||||
Db 157 CAGGTGGCTCCGTCCTCTTTCATGGGCTCCATTTGCCAGCTGAGCCACTCTGTCACTGCC 98

Oy 523 TyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValVal 542
|||||
Db 97 TATATGGTATCAGTCGACGGCTTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTG 38

Oy 543 PheAspLysSerAspLeuAlaLysTyrSer 552
|||||
Db 37 TTTGACAAGACGACTTGGCCAAATACGCG 8

RESULT 23
BG469487
LOCUS
DEFINITION
  BG469487 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660703 5',
  mRNA sequence.
ACCESSION
  BG469487
VERSION
  BG469487.1 GI:13401762
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 800)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cdapbs-re@mail.nih.gov
  Tissue Procurement: ATCC
  CDNA Library Preparation: Ling Hong/Rubin Laboratory
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: NIH Intramural Sequencing Center
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLCMI458 row: i column: 24
  High quality sequence stop: 741.
FEATURES
  Location/Qualifiers
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source
1..800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4660703"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 135 a 245 c 239 g 181 t
ORIGIN

Alignment Scores:
Pred. No.: 3,61e-49 Length: 800
Score: 620.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 21.67% Indels: 1
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG4649487 (1-800)
QY 426 SerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHis 445
|||||
Db 3 AGCCTGATGACCAAGCTTCCTGCCAGGCCCTAAAGCCCTGGAGCTCCCTTCCCTAATGACAC 62
|||||
QY 446 ValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAla 465
|||||
Db 63 GTGGGTGCTGGAGCACTGGCTGCTCCACCTCCACCGCGCTCTCGCGGCGCTCTGCC 122
|||||
QY 466 CysAspValSerValArgValValGlyGluProThrGluAlaArgValProGly 485
|||||
Db 123 TGTGATGTCCTGCTAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 181
|||||
QY 486 ArgGlyLeuCysLeuAspLeuAlaLeuAspSerAlaPheLeuLeuSerGlnValAla 505
|||||
Db 182 CGGGGATCTGCTGGACCTCGCATCTGCGATCTGCGATCTGCTGCTGCTGCTGCTGCTGCTG 241
|||||
QY 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
|||||
Db 242 CCATCCCTGTTATGGCTCCATGTCACAGCTCAGCCAGCTCTGCTACTGCTATATGGTG 301
|||||
QY 526 SerAlaAlaGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
|||||
Db 302 TCTGCCGACAGCGCTGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 361
|||||
QY 546 SerAspLeuAlaLysTyrSerAla 553
|||||
Db 362 ACGGACTTGGCCAAATACTCAGCG 385

RESULT 24
BG246497
LOCUS BG246497 844 bp mRNA linear EST 13-FEB-2001
DEFINITION 602360526F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:448895 5',
mRNA sequence.
ACCESSION BG246497
VERSION BG246497.1 GI:12756312
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10336 row: c column: 08
High quality sequence stop: 655.

FEATURES
source
1..844
/organism="Mus musculus"
/db_xref="FVB/N"
/db_xref="taxon:10090"
/clone_image="IMAGE:448895"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 152 a 251 c 262 g 179 t
ORIGIN

Alignment Scores:
Pred. No.: 9,55e-49 Length: 844
Score: 616.00 Matches: 135
Percent Similarity: 86.14% Conservative: 8
Best Local Similarity: 81.33% Mismatches: 20
Query Match: 21.53% Indels: 5
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG246497 (1-844)
QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 315 ATGATCCAGAGGCTGTGGGCCAGCGCTGCTACGCCACGGAAAGCTCAGCTCCTCGTGTG 374
|||||
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 375 GTCAACCTCTCACCCTTGGCTGGAGGTGCTGCTGGCTGCCGGCATTAACCTATGTGCCA 434
|||||
QY 41 ProLeuLeuLeuGlu-ValGlyValGluGlyLysPheMetThrMetValLeuGlyIleG1 60
|||||
Db 435 CCCCTTCTGCTGGACAGCTCGGGTGGAGGAGAAATTCATGACCATGCTGTGGGCATTGG 494
|||||
QY 60 yProValLeuGlyLeuVal-CysValProLeuLeuGlySerAlaSerAspHisTrpArgG 80
|||||
Db 495 CCCAGTGTAGGCTGTTTCTGTTCACCTCTAGGCTCAGCCAGTACCCAGTGGCGTG 554
|||||
QY 80 lyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerL 100
|||||
Db 555 GCGCGTATGCCGCCGAGACCCCTTTATCTGGGCTTCGCTGGGTGCTGCTGCTAAGCC 614
|||||
QY 100 euPheLeuIleProArgAlaGlyTyrLeuAlaGlyLeuLeuCysProAspProArgProL 120
|||||
Db 615 TCTTTCTCATCCGAGGGCTGCTGCTGGCTGGCAGGACTGCTGTACCCAGAGACCGCCCT 674
|||||
QY 120 euGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysP 140
|||||
Db 675 G-GAGTTGGCCCTGGTGATCTTGGAAAGTGGGCTGGAGCTTCTGCTGGCCAGTGGTGT 733
|||||
QY 140 he-ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGln 159
|||||
Db 734 TTAACCTCCATTGGAGCCCTTAATCTTCAGACCTTTTCGGGAGCCCAACACTGCCG-CAA 792
|||||
QY 160 AlaTyrSerVal 163
|||||
Db 793 GCGTTTCAGGTA 804
```


DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1137 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 630.
Location/Qualifiers

FEATURES

source

1. .630
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5050583"
/lab_host="NCI CGAP L19"
/lab_host="DH10B (Tr1 phage-resistant)"
/note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 114 a 180 c 199 g 137 t
ORIGIN

Alignment Scores:

Pred. No.: 1.66e-47 Length: 630
Score: 601.00 Matches: 118
Percent Similarity: 95.24% Conservative: 2
Best Local Similarity: 93.65% Mismatches: 6
Query Match: 21.01% Indels: 0
DB: 13 Gaps: 0

US-09-593-793A-113 (1-553) x BI145201 (1-630)

QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeu 20
||||:||||| 118
Db 251 ATGATCAGAGGCTGGGCCACCGCTGTCTACGACCGGAAAGCTACGCTCGCTG 310
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
Db 311 GTCAACTGCTACCTTTGGCCCTGGAGGTGCTGGCTGGCTGGCGCATACCTATGTGCCA 370
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 371 CCCCTTCTGCTGGAAGTCGGGGTGGAGAGAAATCATGACCATGTTGTGGGCATGGC 430
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 431 CCACTGCTAGGCTGTCTTCTGCTTCCACTCTAGGCTCAGCAGTACCGCTGGG 490
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 491 CGCTATGGCGCGGAGACCCCTTATCTGGGCTTGTCCCTGGGTGCTGCTGAAGCCTC 550
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 551 TTTCTATCCCGAGGCTGGCTGGCTGGAGGACTGCTTACCACGACACGAGCCGCTG 610
QY 121 GluLeuAlaLeuLeuIle 126
Db 611 GAGTAGCCCTGCTGATC 628
RESULT 27
BG364300 520 bp mRNA linear EST 08-MAR-2001
LOCUS dab86b09.y1 NICHDXGC Emb2 Xenopus laevis cDNA clone IMAGE:4404424
DEFINITION S' similar to TR:Q9VSV1 Q9VSV1 CG4484 PROTEIN. ;, mRNA sequence.
ACCESSION BG364300
VERSION BG364300.1 GI:13253397
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.

REFERENCE

1 (bases 1 to 520)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wyllie,T., Underwood,K., Theising,B., Bowers,Y., Person,
B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Other_ESTs: dab86b09.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Library constructed by Life Technologies. DNA Sequencing by:
Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers

FEATURES

source

1. .520
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4404424"
/clone_lib="NICHDXGC Emb2"
/tissue_type="embryo, stage 17/19"
/lab_host="DH10B (phage-resistant)"
/note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Life Technologies."
BASE COUNT 121 a 119 c 113 g 167 t
ORIGIN

Alignment Scores:

Pred. No.: 3.88e-45 Length: 520
Score: 575.00 Matches: 106
Percent Similarity: 77.38% Conservative: 24
Best Local Similarity: 63.10% Mismatches: 38
Query Match: 20.10% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG364300 (1-520)

QY 248 LeuAlaPheArgAsnLeuGlyAlaLeuLeuProAlaHisGlnLeuCysCysArgMet 267
||| |||:||||| 118
Db 10 CTGACATTGAGAAAGCGCTTGTCTTTTCCACGCTCATGACATCTCTTCCAAAGTG 69
QY 268 ProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThr 287
||| |||:||||| 118
Db 70 CCGGTTACTCTTGGCGCCTCTTGTATCACAGTTTGTCTCGATGGTCTTATGACA 129
QY 288 PheThrLeuPheThrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAla 307
||| |||:||||| 118
Db 130 TTTATGCTCTTTTACACTGACTTTGTGGGTGGGGTGTGTACAAAGGTGTTCACAAATGA 189
QY 308 GluProGlyThrGluAlaArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327
||| |||:||||| 118
Db 190 AAGCCAGGACAGAGACAGACACTTCCTTATGATGAGGAGATGAAGATGGAGCTTGGGG 249
QY 328 LeuPheGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGln 347
||| |||:||||| 118
Db 250 CTCTTCCTTCAGTCTCTGGTTCTATGATGCTCTCTCTCATGATCATCTAATCAAA 309
QY 348 ArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaGly 367
||| |||:||||| 118
Db 310 ATGTTGGCACCGAGCCATTATGTTGGCAGCATAGTTTGCCTCCCATTTGCTACAATA 369
QY 368 AlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThrGlyPhe 387
||| |||:||||| 118
Db 370 GTAATGCTGCTTCTCAAGTACGATTACCGTGTGTGCAATAATACGCTGCCATGACAGCCTTC 429

TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 348.
FEATURES
source
1. .348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1629790"
/sex="male"
/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium; Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT 78 a 99 c 118 g 53 t
ORIGIN
Alignment Scores:
Pred. No.: 3,81e-42 Length: 348
Score: 541.00 Matches: 113
Percent Similarity: 97.41% Conservative: 0
Best Local Similarity: 97.41% Mismatches: 3
Query Match: 18.91% Indels: 1
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x AA984323 (1-348)
QY 326 LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db CTGGGGCTGTTCCTCGAGTGGCCATCTCCCTGGTCTTCTCTGTCATGGACCGGCTG 289
QY 346 ValGlnArgPheGlyThrArgAlaValTyrrLeuAlaSerValAlaAlaPheProValAla 365
Db GTCCAGCGATTCCGACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCT 229
QY 366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaLeuThr 385
Db GCCGGTGCCACATGCTGTCCACAGTGTGGCGTGGTGACAGCTTCAGCGGACCTCACC 169
QY 386 GlyPheThrPheSerAlaLeuGlnIleLeuProTyrrThrLeuAlaSerLeuTyrrHisArg 405
Db GGTTTCACTTCACCTTCAGCCCTCGAGATCTCGCCCTCACACTGGCCCTCCCTCTACCAACCG 109
QY 406 GluLysGlnValPheLeuProLysTyrrArgGlyAspThrGlyGlyAlaSerSerGluAsp 425
Db GAGAACAGGTGTCTCTGCCCAANTACCGAGGGGACACTGGAGGTCTGTCAGTGGAGGAC 49
QY 426 SerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db AGCCTGATGACCAAGTCTCTGTGCA-GGCCCTAAGCCTGGAGCTCCCTTC 2
RESULT 30
BQ950805 959 bp mRNA linear EST 21-AUG-2002
LOCUS BQ950805

DEFINITION AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204253 5', mRNA sequence.
ACCESSION BQ950805
VERSION BQ950805.1 GI:22366283
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt/Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13625 row: d column: 14
High quality sequence start: 2
High quality sequence stop: 490.
FEATURES
source
1. .959
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6204253"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 139 a 312 c 308 g 200 t
ORIGIN
Alignment Scores:
Pred. No.: 1.15e-40 Length: 959
Score: 533.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.63% Indels: 0
DB: 14 Gaps: 0
US-09-593-793A-113 (1-553) x BQ950805 (1-959)
QY 446 ValGlyAlaGlyCysGlyLeuLeuProProAlaLeuCysGlyAlaSerAla 465
Db GTGGGTGCTGGAGGAGTGGCTTCCACCTCCACCGCGCTCTGCGGGCTCTGTC 67
QY 466 CysAspValSerValArgValValGlyGluProThrGluAlaArgValProGly 485
Db TGTGATGTCCTCGTAGCTGTGGTGGGTGAGCCACCGAGGCGAGGTTCGGGGC 127
QY 486 ArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAla 505
Db CGGGGCATCTGCCTGGACCTCGCATCTGGATAGTCTCTCTGCTGCCAGGTGCC 187
QY 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
Db CCATCCCTCTTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGCTACTATATGGTG 247

```

Qy 526 SerAlaAlaGlyLeuGlyValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
|||||
Db 248 TCTGCGCAGGCGCTGGTCTGGTCGCACTTACTTGTCTACACAGTAGTATTGCACAG 307

Qy 546 SerAspLeuAlaLysTyrSerAla 553
|||||
Db 308 AGCGACTTGGCCAAATACTACGCG 331

RESULT 31
BG828841 602752813F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4905674 5', linear EST 22-MAY-2001
LOCUS mRNA sequence.
DEFINITION BG828841
ACCESSION BG828841
VERSION BG828841.1 GI:14176428
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1807 row: i column: 03
High quality sequence start: 3
High quality sequence stop: 602.
Location/Qualifiers
1..1035
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4905674"
/cclone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: muscle; Vector: pOT87; Site_1: EcoRI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 227 a 273 c 341 g 194 t

Alignment Scores:

Pred. No.: 1,33e-39 Length: 1035
Score: 522.50 Matches: 127
Percent Similarity: 77.71% Conservatve: 9
Best Local Similarity: 72.57% Mismatches: 20
Query Match: 18.26% Indels: 20
DB: 12 Gaps: 7

US-09-593-793A-113 (1-553) x BG828841 (1-1035)

```

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 279 ATGGTCCAGAGCGCTGGGTGAGCGCGCTGCTGGCGCACCGAAGCCAGCTCTGTGCTG 338

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 339 GTCAACCTGCTAACCTTTGGCGCTGGAGGTGTGTTTGGCGCGCAGGCATCACCTATGTGCGG 398
```

```

Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 399 CTTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGGTGGCATGGT 458

Qy 61 ProValLeuGlyLeuValCysValPro-LeuLeuGlySer-AlaSerAspHisTrpArgG 80
|||||
Db 459 CCAGTGTGGGCGCTGGTCTGTCTGCCGATCTAGGCTCACGCCAGTACCATCGCGGTG 518

Qy 80 LysArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuLeuLeu 98
|||||
Db 519 GACGCTATGGCGCGCGCGCGCTTCATCTGGAGCACTGTCTTGAGGCATCCTGACTT 578

Qy 99 --SerLeuPheLeuLeuProArgAla-GlyTrpLeu--AlaGlyLeuLeuCysPro-As 116
|||||
Db 579 GAGCATCTTCTTCATCCCAAGCGCGGCTGGCTAGACAAGGAGTGTCTGTGCCAGGA 638

Qy 116 pProArgProLeuGluLeuAlaLeuLeuLeuGlyVal---GlyLeuLeuAspPheCys 135
|||||
Db 639 TACCAGGACCTGGAGCTGGA-CTGCTCATCATGGGAGTGGGAGCTGCTGGAACCTCTG 697

Qy 135 sgly-----GlnValCysPheThrProLeuGluAlaLeuSerAspLeu----- 150
|||||
Db 698 TGGGGCCAAAGGAGTGTGTCATTACATCCAAACATGCGG-----AGGACCTGGGATCCTC 751

Qy 151 -----PheArgAspProAspHis----CysArg 158
|||||
Db 752 TGAACATACACTTCCGGACCGGACGACACATGTAGG 788

RESULT 32
BF854825/c 322 bp mRNA linear EST 16-JAN-2001
DEFINITION RC6-FN0202-271000-011-A03 FN0202 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF854825
VERSION BF854825.1 GI:12242569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 322)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
271000-011-A03&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 321.
Location/Qualifiers
1..322
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone_lib="FN0202"
/dev_stage="Adult"
/notes="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
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```

QY 542 ValPheAspLysSerAspLeuAlaLysTyrSer 552
|||||.....:|||||.....:|||||.....:
Db 300 GTCTTTGACAAAGACGACTTGGCCAAATACTCA 332

RESULT 36
BG068547/c
LOCUS
DEFINITION
H3066G04-3 NIA Mouse 15K cDNA Clone Set Mus musculus linear EST 26-JAN-2001
H3066G04 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 466)
Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
,T.S., Carter,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set
Unpublished (2001)
Other_ESTs: H3066G04-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3066 row: G column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 466
POLYA=yes.

FEATURES
Source
Location/Qualifiers
1..466
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:H3066G04-3"
/db_xref="taxon:10090"
/clone="H3066G04"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/db_stage="Clones arrayed from a variety of cDNA
libraries"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearrayed set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos
, and E12.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned unidirectionally with Oligo(dT
)-Not primers. References include: (1) Genome-wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray, 2000,
Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."
BASE COUNT 121 a 138 c 126 g 81 t
ORIGIN

Alignment Scores:
Pred. No.: 6 5e-35 Length: 466
Score: 468.00 Matches: 95
Percent Similarity: 96.08% Conservatives: 3
Best Local Similarity: 93.14% Mismatches: 4

```

```

Query Match: 16.36% Indels: 0
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BG068547 (1-466)

QY 451 SerGlyLeuLeuProProAlaLeuCysGlyAlaSerAlaCyspValSerVal 470
|||||:|||||.....:|||||.....:|||||.....:
Db 465 AGCGGCGATCTGCGCCCTCCACCTGCCTGCTGGGGCCTCTCGCTGCGATGTCCTCATG 406
|||||:|||||.....:|||||.....:|||||.....:
QY 471 ArgValValValGluProThrGluAlaAatgValValProGlyArgGlyIleCysLeu 490
|||||:|||||.....:|||||.....:|||||.....:
Db 405 CGAGTGGTGGTGAGCCACCTGAGGCCGGTGTACGGGACGGGCATTTGCCTG 346
|||||:|||||.....:|||||.....:|||||.....:
QY 491 AspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMet 510
|||||:|||||.....:|||||.....:|||||.....:
Db 345 GACCTGGCCATCTGCACAGTGCCTTTCTGCTGCCAGGTGGCTCCGTCCTGTTTCATG 286
|||||:|||||.....:|||||.....:|||||.....:
QY 511 GlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeu 530
|||||:|||||.....:|||||.....:|||||.....:
Db 285 GGCTCCATTGTCAGCTGAGCCACTCTGTCACTGCTATATGTTATCAGCTGAGGCTTG 226
|||||:|||||.....:|||||.....:|||||.....:
QY 531 GlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLys 550
|||||:|||||.....:|||||.....:|||||.....:
Db 225 GGTCCTGGTGGCCTTACTTTGCTACACAGGTAGTGTGTGACAGACGACTTGGCCAAA 166
|||||:|||||.....:|||||.....:|||||.....:
QY 551 TyrSer 552
|||||
Db 165 TACTCA 160

RESULT 37
BB707065
LOCUS
DEFINITION
musculus cDNA clone 7420496101 3', mRNA sequence.
ACCESSION
BB707065
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 317)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akashira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Muramatsu,M. and Hayashizaki,Y.
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .

```


10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

Location/Qualifiers
source
1..317
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7420496101"
/clone_lib="RIKEN full-length enriched, in vitro
fertilized eggs"
/sex="female"
/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGTCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGATTCGAGTAAATTAATTAATTCGCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pluciscript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI"
BASE COUNT 53 a 108 c 91 g 65 t
ORIGIN

Alignment Scores:
Pred. No.: 6.24e-34 Length: 317
Score: 455.00 Matches: 90
Percent Similarity: 90.38% Conservative: 4
Best Local Similarity: 86.54% Mismatches: 9
Query Match: 15.90% Indels: 1
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x BB707065 (1-317)

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuProTyrThrLeuAla 400
Db 3 TCAGCTGCCCTCACCAGGTTACCTCTCGGGCTTGCAGATCCTCGCTTACAGCTCGCC 62
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 63 TCCCTCTACCACCGTGAAGAGGAGGTTTCTTGCCTCCCAATACCGAGGGACCTGGAGTT 122
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 123 AGCAGCGGTGAGGACGACGACACACACAGCTTCTTCCAGGCGCCCTAAGCCAGGAGCTCTC 182
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 183 TTCCCCAATGGACAGTGGGCTCTCGACAGCGCATCTCGGCCCTCCACCTGCATCTC 242
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGlu-Al 480
Db 243 TGTGGGGCTCTGCTCGCATGCTCTCCATGCGAGTGGTGGTGGTGAACCACTGAGGGC 302
QY 480 aArgValVal 483
Db 303 CAGGGTTGTT 312

RESULT 38
AW787124

LOCUS 120845 MARC IPIG Sus scrofa cDNA 537 bp mRNA linear EST 09-JUL-2000
DEFINITION AW787124
ACCESSION AW787124
VERSION AW787124.1 GI:7843900
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 537)
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGCG
Plate: 45 row: C column: 12
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers

FEATURES
source

1..537
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC IPIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: Sall;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 96 a 161 c 186 g 94 t
ORIGIN

Alignment Scores:
Pred. No.: 7.88e-32 Length: 537
Score: 437.00 Matches: 85
Percent Similarity: 98.85% Conservative: 1
Best Local Similarity: 97.70% Mismatches: 1
Query Match: 15.27% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW787124 (1-537)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 276 ATGGTCCAGAGACTTGGATGAGCCGCTGCTGCGGCATCGGAAAGCCAGCTCTCTG 335
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 336 GTTAACTGCTGACGTTCCGCTGGAGGTGCTGCTGGCGCAGGATACCTACGTGCA 395
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 396 CCCCTGCTGTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGCATCGGT 455
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 456 CCAGTGTGGGCTGTCTCCCTCCACTCTTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 515
QY 81 ArgTyrGlyArgArgPro 87

```
|||||
Db 516 CGCTATGGTCCGCGGAGGCC 536
RESULT 39
BG745565
LOCUS BG745565 717 bp mRNA linear EST 15-MAY-2001
DEFINITION 602723976F1 NTH_MGC_113 Homo sapiens cDNA clone IMAGE:4850347 5',
mRNA sequence.
ACCESSION BG745565
VERSION BG745565.1 GI:14056218
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
NTH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium {LLNL}
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1691 row: 9 column: 20
High quality sequence start: 8
High quality sequence stop: 580.
Location/Qualifiers
FEATURES
source
1. .717
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4850347"
/clone_lib="NTH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; site 1: XhoI; site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NTH_MGC Library."
BASE COUNT 113 a 211 c 209 g 184 t
ORIGIN
Alignment Scores:
Pred. No.: 9,46e-30 Length: 717
Score: 417.50 Matches: 122
Percent Similarity: 83.78% Conservatives: 2
Best Local Similarity: 82.43% Mismatches: 9
Query Match: 14.59% Indels: 15
DB: 12 Gaps: 1
US-09-593-793A-113 (1-553) x BG745565 (1-717)
QY 418 ThrGlyGlyAlaSerSerGluAspSerLeu-MetThr-SerPheLeuPro-GlyProLys 436
|||
Db 2 ACTGCAGGTCTATCAGTGAGGACAGCTGGATGACCAAGCTTCCTGCCATGCCCTAAG 61
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
|||||
Db 62 CTTGGAGCTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGGCTGCTGCCACCT 121
QY 457 ProProAlaLeuCysGlyAlaSerAlaCys-AspValSerValArgValValGlyG1 476
|||||
Db 122 CCACCCCGCTCGCGGGCCCTGCTGCTGATGCTCCGTACGTCGTGGTGGTGA 181
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCys-LeuAsp-LeuAlaIleLeu 495
|||||
```

```
Db 182 GCCACCGAGGTCCAGGTGCTCCGGCGCGGCATCTGCTCTGGATCTTCGCCATCCTG 241
QY 496 -AspSerAlaPheLeuLeuSer-GlnValAlaPro-SerLeuPheMetGlySerIleVal 514
|||||
Db 242 TGATAGTGCCTTCTGCTGTCCTCCAGGTGCCCGCATCCTGTTATGGCTCCATGTA 301
QY 515 -GlnLeuSerGln-SerValThrAlaTyMetValSerAlaAla-GlyLeuGlyLeuVal 533
|||||
Db 302 CCAGCTCAGCAGTACTGCTCACTGCTATATGCTGCTGCCGCGATCCCTGGCTGGTC 361
QY 534 Ala---IleTyPheAlaThrGlnValVal-PheAspLys-SerAspLeuAlaLys 550
|||||
Db 362 GGCATATTAACTTGTCTACACAGGTAGTATTTCGACAAATGAGGCACTTGGCCAAA 417
RESULT 40
BF371417/c
LOCUS BF371417 265 bp mRNA linear EST 24-NOV-2000
DEFINITION RCO-FN0140-040800-023-h03 FN0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF371417
VERSION BF371417.1 GI:11333442
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?li-RC0st2-RC0-FN0140-
040800-023-h03st3-2000-08-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 265.
Location/Qualifiers
FEATURES
source
1. .265
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0140"
/dev_stage="Adult"
/note="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 68 a 72 c 94 g 31 t
ORIGIN
Alignment Scores:
Pred. No.: 2,38e-30 Length: 265
Score: 416.50 Matches: 83
Percent Similarity: 96.55% Conservatives: 1
Best Local Similarity: 95.40% Mismatches: 3
Query Match: 14.56% Indels: 2
```

```
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BF371417 (1-265)

QY 122 LeuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThr 141
Db 261 GTGGTCTCTCATCTCTGGCGTGGGGTCTGTGGAGCTTCTGTGGCAGGTGTCTTCACT 202
QY 142 ProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyr 161
Db 201 CCACCTAGAGGCGCTCTCTGACCTCTTCCGGGACCCGACCACTGTGCGCAGGCCCTAC 142
QY 162 SerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIle 181
Db 141 TCTGTCTATGCTTCATGATCAGTCTTGGGGCTGCCTGGGCTACCTCTGCTGCCATT 82
QY 182 AspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGly 201
Db 81 GACTGGAC-ACCAGTGC-CTGGCCCCCTACCTGGGCACCCAGGAGGTGCTCTTTGGC 24
QY 202 LeuLeuThrLeuIlePheLeu 208
Db 23 CTGCTCACCTCATCTTCTTA 3

RESULT 41
AWB22644 523 bp mRNA linear EST 17-MAY-2000
LOCUS uq13q05.y1 Ren Stubbs mouse thymus Mus musculus cDNA clone
DEFINITION IMAGE:2802392 5', mRNA sequence.
ACCESSION AWB22644
VERSION AWB22644.1 GI:7915661
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 523)
Marra.M., Hillier.L., Kucaba.T., Martin.J., Beck.C., Wylie.T.,
Underwood.K., Steptoe.M., Theising.B., Allen.M., Bowers.Y., Person
,B., Swaller.T., Gibbons.M., Pape,D., Harvey.N., Schurk.R., Ritter
,E., Kohn.S., Shin.F., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Other ESTs: uq13q05.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:1041916
Seq primer: Primer name ambiguous
High quality sequence stop: 474.
FEATURES
source
1. 523
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:2802392"
/clone_lib="Ren Stubbs mouse thymus"
/sex="mixed"
/lab_host="3 weeks"
/lab_host="DH10B"
/note="Pac1; 1st strand cDNA was primed with an oligo(dT)
Site 2: Pac1; 1st strand cDNA was ligated using 5' linker
primer; double-stranded cDNA was ligated using 5' linker
ggccgcat and 3' linker aactggaagcttaatt. Library is
size-selected >2.5 kb and average insert size is 3.5 kb.
Clones were arrayed from primary plating; non-amplified.
Library constructed by X. Ren and L. Stubbs (Lawrence
```

```
Livermore National Laboratory and DOE Joint Genome
Institute, 7000 East Ave., L-453, Livermore, CA 94550)."
BASE COUNT 102 a 146 c 170 g 105 t
ORIGIN
Alignment Scores: 9.1e-29 Length: 523
Pred. No.: 405.00 Matches: 79
Score: 405.00
Percent Similarity: 96.39% Conservative: 1
Best Local Similarity: 95.18% Mismatches: 3
Query Match: 14.16% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x AWB22644 (1-523)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 273 ATGATCCAGAGGCTGTGGGCCAGCGCTGTCTACGGCACCCGAAAGCTCAGCTCTGCTG 332
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
Db 333 GTCAACCTGCTCACCTTTGGCTGGAGGTGTGCTGGTGGCGGCATTACCTATGTGCCA 392
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 393 CCCCTTCTGCTGGAAGTCGGGGTGGAGGAGAAATTCATGACCATTGCTTGGCATTTGGC 452
QY 61 ProValLeuLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 453 CCAGTGTAGGCGTGGTTTCTTCTCCACTCTAGCTCAGCCAGTGACCAAGTGGCGTGGG 512
QY 81 ArgTyrGly 83
Db 513 CGCTATGGC 521
RESULT 42
CNS050VL 1020 bp DNA linear GSS 26-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 006H14 of library C from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL347178
VERSION AL347178.1 GI:8240948
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1020)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
REFERENCE 2 (bases 1 to 1020)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
REFERENCE 3 (bases 1 to 1020)
Genoscope.
Direct Submission
TITLE Submitted (12-APR-2000)
JOURNAL This sequence is a single read and was generated as part of a large
COMMENT scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
Location/Qualifiers
```



```

Db 670 TGTGCTGATCCAGGGCCCTGGAGGCTAGACTTGCTCA-----ATCCTGGGTTGGG 723
Qy 130 yLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeu 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 CTTGTCATCTTGTGGGCCAGGTTTC-GTCCCTTCCCTTGGAGGCTGCTCTGGC---CT 779
Qy 150 uPheArgAspPro 154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 780 TTTCCGGGGACCG 792
RESULT 44
AA112574
LOCUS      228 bp      mRNA      linear      EST 23-DEC-1997
DEFINITION  zM28c12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:526966 3', mRNA sequence.
ACCESSION  AA112574
VERSION    AA112574.1 GI:1665121
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 228)
AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favell,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,K. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
TITLE      Contact: Wilson RK
JOURNAL    Washington University School of Medicine
MEDLINE    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
COMMENT    Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
WARNING:   There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd from Amersham.
FEATURES   Location/Qualifiers
            source
            1..228
            /organism="Homo sapiens"
            /db_xref="GDB:3918395"
            /db_xref="taxon:9606"
            /clone="IMAGE:526966"
            /clone_lib="Stratagene pancreas (#937208)"
            /lab_host="SOLR cells (kanamycin resistant)"
            /note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
            EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
            Oligo dT. Pancreatic adenocarcinoma cell line. Average
            insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
            sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5'
            CTCAGATTTTCTTTTCTTTT 3'"
BASE COUNT 40 a 81 c 62 g 45 t
ORIGIN
Alignment Scores: 2.51e-27 Length: 228
Pred. No.: 384.00 Matches: 76
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 13.42% Gaps: 0
DB: 9

US-09-593-793A-113 (1-553) x AA112574 (1-228)

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```

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1 GCTTTCCCTGTGGTGGCGGTGCCACATGCTGTCACAGTGTGCCCGTGTGACAGCT 60
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ACCESSION  BF854834
VERSION    BF854834.1 GI:12242578
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 428)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL    Contact: Simpson A.J.G.
MEDLINE    Laboratory of Cancer Genetics
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           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           Project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6&t2=RC6-FN0202-
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            ; Site:2: SmaI; A mini-library was made by cloning
            products derived from ORESTES PCR (U.S. Letters Patent
            application No. 196,716 - Ludwig Institute for Cancer
            Research) profiles into the pUC 18 vector. Reverse
            transcribed of tissue mRNA and cDNA amplification were
            performed under low stringency conditions."
BASE COUNT 111 a 111 c 137 g 68 t
ORIGIN
Alignment Scores: 1.21e-26 Length: 428
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Score: 77.57% Conservative: 7
Percent Similarity:

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